

STIC-Biotech/ChemLib

166285

From: Dunston, Jennifer
Sent: Tuesday, September 20, 2005 11:49 AM
To: STIC-Biotech/ChemLib
Subject: Sequence Search 10/705757

Please do a sequence search for SEQ ID NOS: 1, 3 and 5 against the commercial protein databases.
SEQ ID NOS: 1, 3 and 5 are 2623, 1302 and 942 nt in length, respectively.

Thank you.

Jennifer Dunston, Ph.D.
USPTO Art Unit 1636
REM 2B76
Mailbox: REM 2C70
(571) 272-2916

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: 9/23
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus.n2p model

Run on: September 22, 2005, 16:20:36 ; Search time 68.9838 Seconds

(without alignments)
5676.828 Million cell updates/sec

Title: US-10-705-757-1

Perfect score: 4789

Sequence: 1 gaagagagccgagagagagtc.....atacaaaccttcgtcctt 2623

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBLOP=6 -DELEXT=7

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5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.dep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.dep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1670	34.9	313	3	US-09-237-543-9
2	1670	34.9	313	3	US-09-644-450-9
3	1657	34.6	313	2	US-08-463-0818-26
4	1657	34.6	313	2	US-08-463-379A-26
5	1657	34.6	313	2	US-08-463-390B-26
6	1657	34.6	313	3	US-08-463-074B-26
7	1657	34.6	313	3	US-08-465-585C-26
8	1657	34.6	313	3	US-08-652-446-26
9	1636	34.2	313	3	US-09-237-543-8
10	1636	34.2	313	3	US-09-644-450-8
11	1582	33.0	313	3	US-09-237-543-7
12	1582	33.0	313	3	US-09-644-450-7

13	1296.5	27.1	257	2	US-07-857-224B-41	Sequence 41, Appli
14	1149.5	24.0	455	3	US-09-237-543-5	Sequence 5, Appli
15	1149.5	24.0	455	3	US-09-644-450-5	Sequence 5, Appli
16	1133	23.7	326	3	US-09-237-543-2	Sequence 2, Appli
17	1133	23.7	326	3	US-09-644-450-2	Sequence 2, Appli
18	1105	23.1	323	3	US-09-237-543-6	Sequence 6, Appli
19	1105	23.1	323	3	US-09-644-450-6	Sequence 6, Appli
20	1079.5	22.5	254	3	US-09-237-543-4	Sequence 4, Appli
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22	903.5	18.9	372	4	US-09-949-016-7140	Sequence 7140, Ap
23	390	8.1	1323	3	US-09-770-170-2	Sequence 38, Appl
24	384.5	8.0	630	4	US-10-355-975A-11	Sequence 11, Appl
25	384.5	8.0	631	4	US-09-579-664B-18	Sequence 11, Appl
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27	383	7.9	776	4	US-09-523-849-34	Sequence 34, Appl
28	376	7.9	1101	3	US-09-770-170-8	Sequence 8, Appli
29	371.5	7.8	778	4	US-10-116-326-2	Sequence 2, Appli
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31	367	7.7	1356	3	US-09-770-170-6	Sequence 6, Appli
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36	356	7.4	602	4	US-09-949-016-7417	Sequence 7417, Ap
37	356	7.4	602	4	US-09-949-016-7418	Sequence 7418, Ap
38	354.5	7.4	722	4	US-08-817-832B-32	Sequence 32, Appl
39	354	7.4	504	4	US-09-554-726A-10	Sequence 10, Appl
40	353.5	7.4	722	4	US-09-984-890-4	Sequence 4, Appli
41	353.5	7.4	724	4	US-10-274-194-4	Sequence 2, Appli
42	352.5	7.4	724	4	US-09-984-890-2	Sequence 2, Appli
43	352.5	7.4	724	4	US-10-274-194-2	Sequence 2, Appli
44	352.5	7.4	1005	3	US-09-770-170-4	Sequence 4, Appli
45	348	7.3	418	4	US-09-248-796A-18441	Sequence 18441, A

ALIGNMENTS

RESULT 1
US-09-237-543-9
; Sequence 9, Application US/09237543A
; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-237-543-9

Alignment Scores:

Pred. No.: 3.94E-117
Score: 1670.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 34.87%
DB: 3
Gaps: 0

US-10-705-757-1 (1-2623) x US-09-237-543-9 (1-113)
QY 351 ATGCTCTGTCGCAATTCACCTGCTGCCACCTGCGCGCGCTGCAAGACCTG 410
DB 1 MetLeuLeuSerYsIleSenSerLeuAlaHisLeuArgAlaIaProCySaenApleu 20
QY 411 CAGCCACCAAGCTGCGCGCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 470
DB 21 HisAlaThrIysLeuAlaProGlyIyIeGluIyIeGluProLeuGluSerGlnIyIeVal 40

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QY 471 GGCCGCTACTGGGACGGGGGCTTCGGCTCGGCTCACTCAGGACATCCGCGTCTCGAC 530
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Db 41 G1YProleuLeuLysSerGlyGlyPheGlySerValTyrSerGlyIleArgValSerAsp 60
QY 531 AACTGCGCGGTGGCCATCAAAACAGTGGAGAGACCGGATTTCCGACTGGAGAGACTG 590
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QY 591 CCTAATGGCACTGAGTGGCCCATGGAAGTGTCTCTGCTGAAGAAGGTAGCTGGGTTTC 650
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Db 81 ProAsnGlyThrArgValProMetGluValIleuLeuLysValSerSerGlyPhe 100
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RESULT 2
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; Sequence 9, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HK1D-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/644,450
; NUMBER OF SEQ. ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 313
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-644-450-9

Alignment Scores:
Pred. No.: 3,94e-117
Score: 1670.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 34.87%
DB: 3
Gaps: 0

US-10-705-757-1 (1-2623) x US-09-644-450-9 (1-313)

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QY 531 AACTGCGCGGTGGCCATCAAAACAGTGGAGAGACCGGATTTCCGACTGGAGAGACTG 590
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 SOFTWARE: Patentin Release #1.0,
 SOFTWARE: Version #1.25
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 APPLICATION NUMBER: US/08/461,379A
 FILING DATE: 5-JUNE-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USSN 08/330,108; 08/104,736
 APPLICATION NUMBER: 4,077,96,066
 FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
 ATTORNEY/AGENT INFORMATION:
 NAME: Viviana Amzel, Ph. D.
 REGISTRATION NUMBER: 30,930
 REFERENCE/DOCKET NUMBER: DART-070
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610)470-0700
 TELEFAX: (610)470-0701
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 313 amino acids
 TYPE: peptide
 STRANDEDNESS: n.a.
 TOPOLOGY: n.a.
 MOLECULE TYPE: peptide
 US-08-461-379A-26

Alignment Scores:
 Pred. No.: 3,72e-116 Length: 313
 Score: 1657.00 Matches: 311
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 Best Local Similarity: 99.36% Mismatches: 2
 Query Match: 34.60% Indels: 0
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US-10-705-757-1 (1-2623) x US-08-461-379A-26 (1-313)

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 QY 471 GGGCGGCTACTGGGCGAGGCGGCTTGGCTGCTGCTCACTGAGGATCCGCGCTCGGAC 530
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 QY 531 AACTTGGCGGTGGCCATCAAAACAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 590
 DB 61 AsnLeuProValAlaIleuYbHleValGluLybAAspArgIleSerAapTrpGlyIuLeu 80
 QY 591 CTTAAATGGCACTGAGTGGCCCATGAAAGTGGCTCTGCTGAAGAGAGAGAGAGAGAG 650
 DB 81 ProAbnGlyIyHArArgValIProMetGluValIValIleuLeuYbValSerSerGlyPhe 100
 QY 651 TCCGGGCTACTTGGGCTTGGCTGAGTGGTGGAGAGGCGGACGATTTCGCTGAGACTG 710
 DB 101 SerGlyValIleArgIeuleuAAspTrpPheGluArgProAspSerPheValIleuIleu 120
 QY 711 GAGAGGCGGAGCGGCTGCAAGATCTTTCGACTTCATCAAGAGAGAGAGAGAGAGAG 770
 DB 121 GluArgProGluProValGlnAAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
 QY 771 GAGAGGCTGGCGCGAGCTTCTTCTGGCAGGTGCTGGAGGCGCTGGCGGCACTGCCA 830
 DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValIleuGlnAlaValAlaArgHisCybHleAAsn 160
 QY 831 TGGGGGGTGTCTACACGCGGACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 890
 DB 161 CybGlyValIleuHleAAspArgIleYbAspGluAsnIleuIleAspLeuAAspArgGly 180
 QY 891 GAGCTCAAGCTCATGACTTCGCGGTGGGGCGCTGCTCAAGAGACCGTCTACAGCGAC 950

DB 181 GluLeuYbLeuIleAAspPheGlySerGlyAlaLeuLeuYbAAspThrValIyThrAap 200
 QY 951 TTGCAATGGACCCGAGGTATATGCCCCCTCAGAGTGGATCCGCTACCATGCTCAACATGGC 1010
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 QY 1071 CCTTCAGACATGACGAAGAATCATCAGGGGCGAGGTTTCTTCAGGCGAGAGGTTCT 1130
 DB 241 PropheGluHleAAspGluGluIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
 QY 1131 TCAGAAATGCAGATCTCATTTGATGAGTGGCTTGGCGCTGAGACCATCATGATGGCCACC 1190
 DB 261 SerGluCybGlnHleIleuIleArgTrpCybLeuAlaLeuArgProSerAAspArgProThr 280
 QY 1191 TCGAAGAATCGACAGACCATCATGATGCAAGATGTTCTGCGCCCGAGAAACTGCT 1250
 DB 281 PheGluGluIleGlnAAspHleProTrpMetGlnAAspValIleuLeuProGlnIuHleAla 300
 QY 1251 GAGATCCACTTCACAGCCTGTGCGCGGCGCGGAGAGAGAGAGAGAGAGAGAGAG 1289
 DB 301 GluIleHleLeuHleSerIeuSerProGlyProSerIySg 313

RESULT 5
 US-08-462-390B-26
 Sequence 26, Application US/08462390B
 Patent No. 5882894
 GENERAL INFORMATION:
 APPLICANT: Smith, K. A., & Beadling, C.
 TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESSES:
 ADDRESSES: Ratner & Prestia
 CITY: Valley Forge
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19482
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/462,390B
 FILING DATE: 5-JUNE-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USSN 08/330,108
 FILING DATE: 27-OCT-1994
 APPLICATION NUMBER: USSN 08/104,736
 FILING DATE: 10-AUG-1993
 APPLICATION NUMBER: USSN 07/796,066
 FILING DATE: 20-NOV-91
 ATTORNEY/AGENT INFORMATION:
 NAME: Viviana Amzel, Ph. D.
 REGISTRATION NUMBER: 30,930
 REFERENCE/DOCKET NUMBER: DART-040
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610)407-0700
 TELEFAX: (610)407-0701
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 313 amino acids
 TYPE: peptide
 STRANDEDNESS: n.a.
 TOPOLOGY: n.a.
 MOLECULE TYPE: peptide
 US-08-462-390B-26

Alignment Scores:

Pred. No.: 3,72e-116 Length: 313
 Score: 1657.00 Matches: 311
 Percent Similarity: 99.36% Conservative: 2
 Best Local Similarity: 99.36% Mismatches: 0
 Query Match: 34.60% Indels: 0
 DB: 2 Gaps: 0

US-10-705-757-1 (1-2623) x US-08-463-390B-26 (1-313)

QY 351 ATGCTCTGTGTCGAAATCACTGCTGCTGCGCGCGCGCGCTGCAAGCACTG 410
 DB 1 MetleuLeuSerlySileAenSerleuAlahleuArgAlaCyshenAepLeu 20
 QY 411 CAGCCCAACCAAGCTGGCGCGCGCGCAAGAGAGAGAGCCCTGAGTGGCACTG 470
 DB 21 HleAlathrlYleuAlaProGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 40
 QY 471 GCGCGCTACTGGGAGCGCGCGCTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTG 530
 DB 41 GlyProleuLeuGlySerGlyGlyPheGlySerValTySerGlyLeArgValSerAap 60
 QY 531 AACTTGGCGGTGCGCATCAACACGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 590
 DB 61 AsnleuProValAlaIleuYshIeValGlyLysAapArgIleSerAapTrpGlyGlnleu 80
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 DB 81 ProhenGlythraArgValPrometGlyValValleuLeuYshYshValSerSerGlyPhe 100
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 DB 101 SerGlyValIleArgLeuLeuAapTrpPheGlyLysGlyLysGlyLysGlyLysGly 120
 QY 711 GAGAGCG 770
 DB 121 GlnArgProGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGly 140
 QY 771 GAGAGCTGGCGCGCGCGCTTCTTCTGCGAGTGGCTGCGAGCGCGCGCGCGCGCG 830
 DB 141 GlnGlyLeuAlaIleuYshIeValGlyLysAapArgIleSerAapTrpGlyGlnleu 160
 QY 831 TCGCGCGCTCATAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 890
 DB 161 CyshIeValIleuYshIeValGlyLysAapArgIleSerAapTrpGlyGlnleu 180
 QY 891 GAGCTCAAGCTCATGAGCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 950
 DB 181 GlnleuYshIeValIleuYshIeValGlyLysAapArgIleSerAapTrpGlyGlnleu 200
 QY 951 TTCAGTGGAGCCGAGTGTATAGCCCTTCAGAGTGTATAGCCCTTCAGTGTATAG 1010
 DB 201 PheArgGlythraArgValTySerProGlyLysGlyLysGlyLysGlyLysGly 220
 QY 1011 AGGTTCGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1070
 DB 221 ArgSerIleAlaValIleuYshIeValGlyLysAapArgIleSerAapTrpGlyGlnleu 240
 QY 1071 CTTTTCAGAGTGTATAGCCCTTCAGAGTGTATAGCCCTTCAGAGTGTATAGCCCT 1130
 DB 241 ProhenGlythraArgValPrometGlyValValleuLeuYshYshValSerSerGlyPhe 260
 QY 1131 TCAGAGTGTATAGCCCTTCAGAGTGTATAGCCCTTCAGAGTGTATAGCCCTTCAG 1190
 DB 261 SerGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGly 280
 QY 1191 TTCAGAGAGTGTATAGCCCTTCAGAGTGTATAGCCCTTCAGAGTGTATAGCCCTTCAG 1250
 DB 281 PheGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGly 300
 QY 1251 GAGATCCAGCTTCAGAGTGTATAGCCCTTCAGAGTGTATAGCCCTTCAGAGTGTATAG 1289

DB 301 GlnleuLeuSerlySileAenSerleuAlahleuArgAlaCyshenAepLeu 313

RESULT 6
 US-08-463-074B-26
 Sequence 26, Application US/08463074B
 Patent No. 6020155
 GENERAL INFORMATION:
 APPLICANT: Smith, Kendall A. & Beadling, Carol
 TITLE OF INVENTION: Nucleic Acids Encoding CRI Fusion Protein, Vector an
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
 ADDRESS: (B) STREET:
 CITY: Los Angeles
 STATE: California
 COUNTRY: USA
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0,
 SOFTWARE: Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/463,074B
 FILING DATE: 5-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/104,736
 FILING DATE: 10-AUG-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/796,066
 FILING DATE: 20-NOV-91
 ATTORNEY/AGENT INFORMATION:
 NAME: Viviana Amzel, Ph. D.
 REGISTRATION NUMBER: 30,930
 REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 622-7700
 TELEFAX: (213) 489-4210
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 313 amino acids
 TYPE: peptide
 STRANDEDNESS: n.a.
 TOPOLOGY: n.a.
 MOLECULE TYPE: peptide
 US-08-463-074B-26
 Alignment Scores:
 Pred. No.: 3,72e-116 Length: 313
 Score: 1657.00 Matches: 311
 Percent Similarity: 99.36% Conservative: 0
 Best Local Similarity: 99.36% Mismatches: 2
 Query Match: 34.60% Indels: 0
 DB: 3 Gaps: 0

US-10-705-757-1 (1-2623) x US-08-463-074B-26 (1-313)

QY 351 ATGCTCTGTGTCGAAATCACTGCTGCTGCGCGCGCGCGCTGCAAGCACTG 410
 DB 1 MetleuLeuSerlySileAenSerleuAlahleuArgAlaCyshenAepLeu 20
 QY 411 CAGCCCAACCAAGCTGGCGCGCGCGCAAGAGAGAGAGAGCCCTGAGTGGCACTG 470
 DB 21 HleAlathrlYleuAlaProGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 40
 QY 471 GCGCGCTACTGGGAGCGCGCGCTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTG 530
 DB 41 GlyProleuLeuGlySerGlyGlyPheGlySerValTySerGlyLeArgValSerAap 60
 QY 531 AACTTGGCGGTGCGCATCAACACGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 590
 DB 61 AsnleuProValAlaIleuYshIeValGlyLysAapArgIleSerAapTrpGlyGlnleu 80

QY 951 TTGATGGAGCCGAGTGTATAGCCCTCAAGATGATCGGTACCACTGCTACCAATGC 1010
 DB 201 PheAepGlyThrArgValIYrSerProGluTrpIleArgIYrHisArgIYrHisGly 220
 QY 1011 AGGTGGCGGAGCTGTGGTCCCTGGGAGATCCCTGTATGATATGATGTGTGAGATATT 1070
 DB 221 ArgSerIleAlaValITPserIleGlyIleLeuLeuYrHisPheValCYsGlyAspIle 240
 QY 1071 CCTTCGAGCATGACGAGAGATATCAAGGGGCGAGGTTTCTTCAGCAGAGGGTCTCT 1130
 DB 241 ProPheGluIleHisArgGluGluIleIleArgGlyGluValIlePhePheArgGluArgValIser 260
 QY 1131 TCGAATGTCAGCATCTCATTAAGATGATGCTGCTGGCCCTGAGACATGAGATAGGCCAAC 1190
 DB 261 SerGluGlySerGlnHisLeuIleArgIYrCYsLeuAlaLeuArgProSerAspArgProThr 280
 QY 1191 TTCGAGAATTCGACGACATCCATCCATGATGATGATGATGATGATGATGATGATGATGAT 1250
 DB 281 PheGluGluIleGlnHisLeuIleArgIYrMetGlnHisPheValLeuLeuProGluGluThrAla 300
 QY 1251 GAGATCCAGCTCCACAGCTGTGCGCGGGGCCGACGAAA 1289
 DB 301 GluIleHisLeuHisSerLeuSerProGlyProSerIYs 313
 RESULT 8
 US-08-652-446-26
 Sequence 26, Application US/08652446
 Patent No. 6057427
 GENERAL INFORMATION:
 APPLICANT: Smith, Kendall A. & Beadling, Carol
 TITLE OF INVENTION: Nucleic Acids Encoding CMS
 TITLE OF INVENTION: Polypeptide, Vector and Transformed Cell Thereof, and
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
 CITY: Los Angeles
 STATE: California
 COUNTRY: USA
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0,
 SOFTWARE: Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/652,446
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP App. # 96921319.8
 FILING DATE: 5-JAN-1998
 APPLICATION NUMBER: PCT/US/96/09194
 FILING DATE: 5-JUN-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/330,108
 FILING DATE: 27-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/463,074
 FILING DATE: 5-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/462,337
 FILING DATE: 5-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/462,390
 FILING DATE: 5-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/465,585
 FILING DATE: 5-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/463,081
 FILING DATE: 5-JUN-1995

444 South Flower St. - Suite 1900

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/461,379
 FILING DATE: 5-JUN-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/739,523
 FILING DATE: 29-OCT-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Viviana Amzel, Ph. D.
 REGISTRATION NUMBER: 30,930
 REFERENCE/DOCKET NUMBER: FP66 40035
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 622-7700
 TELEFAX: (213) 489-4210
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 313 amino acids
 TYPE: peptide
 STRANDEDNESS: n.a.
 TOPOLOGY: n.a.
 MOLECULE TYPE: peptide
 US-08-652-446-26
 Alignment Scores:
 Pred. No.: 3,72e-116 Length: 313
 Score: 1657.00 Matches: 311
 Percent Similarity: 99.36% Conservative: 0
 Best Local Similarity: 99.36% Mismatches: 2
 Query Match: 34,60% Indels: 0
 DB: 3 Gaps: 0
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 DB 1 MetLeuLeuSerIYrIleAsnSerLeuAlaHisLeuArgAlaArgAlaCYsAsnAspLeu 20
 QY 411 CAGCCCAACCAAGCTGGCG 470
 DB 21 HisAlaThrIYsLeuAlaProGluYsGluYsGluProLeuIleSerGlnYrGluVal 40
 QY 471 GGGCGCTACTAGGGGAGCGCGCGCGCGCGCGCGCGCGCTTCACTACGAGATCCGCTCCGAC 530
 DB 41 GlyProLeuLeuGlySerIYrGlyPheGlySerValYrSerGlyIleArgValIserAsp 60
 QY 531 AACTTCGCGGTGCTCAACAACGCTGAGAGAACCGGATTTCCGACTGGGAGAGCTG 590
 DB 61 AsnLeuProValAlaIleYrHisValGluYsAspArgIleSerAspTrpGlyGluLeu 80
 QY 591 CCTAATGCACTGAGTGCCTATGGAAGTGTCTCTGGAAGAGGTGAGCTGGGTTTC 650
 DB 81 ProAsnGlyThrArgValIleProMetGluValIleLeuLeuYsValIserSerGlyPhe 100
 QY 651 TCCGGGCTGATTAGGCTCCGTCGAGCTGTTGAGAGGCCGAGAGTTTCGTCGATCTTG 710
 DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleLeu 120
 QY 711 GAGAGGCCGAGCGCGGTGCAAGATCTTTCGACTTCATCAACGAGAAAGGAGGCCCTGCA 770
 DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
 QY 771 GAGGAGCTGGCCGCGAGCTTCTTCTGCGAGGTGCTGAGAGGCCGTGGGCGACTGCCAAC 830
 DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValIleGluAlaValaArgHisCYsHisAsn 160
 QY 831 TGGCGGCTGTACACCGGACATCAAGACGAAAACATCTTATGACCTCAATCCGCGC 890
 DB 161 CYsGlyValLeuHisArgAspIleYsAspGluAsnIleLeuIleAspLeuAsnArgGly 180
 QY 891 GAGCTCAAGCTCATCGACTTCGGGTGCGGGCGCTGCTCAAGACACCGTCTACACGAC 950
 DB 181 GluLeuYrLeuIleAspPheGlySerGlyAlaLeuLeuYsAspThrValYrThrAsp 200
 QY 951 TTGATGGAGCCGAGTGTATAGCCCTCAAGATGATCGGTACCACTGCTACCAATGC 1010

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Db      201 PheAspGlyThrArgValTyrSerProProGluTrrIleArgTyrHisArgTyrHisGly 220
QY      1011 AGGTGGCGGGCACTCTGTCCTCCGGGATCTCTGTATATATGTTGTGTGAGATATT 1070
Db      221 ArgSerAlaIaIaValTrrPserLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
QY      1071 CCTTGGAGCATGACGAGAGATCATCAGGGGCGAGGTTTCTTTCAGGCGAGAGGTCTCT 1130
Db      241 ProPheGluHisAspGluGluIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
QY      1131 TCAGATGTCAGCATCTCATTAATGTCCTTGGCCCTGAGACCATCATGATGAGCCAAAC 1190
Db      261 SerGluCysGlnHisLeuIleArgTrrCysLeuAlaLeuArgProSerAspArgProtr 280
QY      1191 TTGAGAAATCCAGAACCATCATGAGATGATGATGTTCTCGCCGCCAGAAACGTGCT 1250
Db      281 PheGluGluIleGlnHisAsnHisProTrrPmetGlnAspValLeuLeuProGlnIuThrAla 300
QY      1251 GAGATCCACCTCCACAGCCTGTGCGCGGGGCCAGCAAA 1289
Db      301 GluIleHisLeuHisSerLeuSerProGlyProSerTyr 313

RESULT 9
US-09-237-543-8
; Sequence 8, Application US/09237543A
; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-237-543-8

Alignment Scores:
Pred. No.: 1,4e-114 Length: 313
Score: 1636.00 Matches: 304
Percent Similarity: 99.04% Conservative: 6
Best Local Similarity: 97.12% Mismatches: 3
Query Match: 34.16% Indels: 0
Gaps: 0

US-10-705-757-1 (1-2623) x US-09-237-543-8 (1-313)
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Db      1 MetLeuLeuSerTyrHisLeuAsnSerLeuAlaHisLeuTrrAlaIaProCysAsnAspLeu 20
QY      411 CAGGCCACAGACTGGCGCGCGCGCAAGAGAGAGAGCCCTGAGTGCAGTACAGAGTG 470
Db      21 HisAlaAsnLysLeuAlaIaProGlyLysGluLysGluProLeuGluSerGlnTrrGlnVal 40
QY      471 GGGCCGCTACTGGGACGGCGGCTTGGCTCGCTCACTCAGGCACTCGCGTCTCCGAC 530
Db      41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTrrSerGlyIleArgValAlaAsp 60
QY      531 AACTTGGCGGTGGCCATCAAAACAGTGGAGAGAGAGCCGATTTCCGATGGGAGAGCTG 590
Db      61 AsnLeuProValAlaIaIeLysHisValGluLysAspArgLieserAspTrrGlyGluLeu 80
QY      591 CCTAATGCACTGAGTGGCCCATGAGAGTGTCTCTGCTGAGAGAGAGTGGAGCTCGGGTTTC 650
Db      81 ProAsnGlyThrArgValProMetGlnValValLeuLeuLysValSerSerGlyPhe 100
QY      651 TCGGCGCTCATTAAGCTCTCGACTGGTTCGAGAGGCCGACGATTTCTGCTGATCTCTG 710

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Db      101 SerGlyValIleArgLeuLeuAspTrrPheGluArgProAspSerPheValLeuIleLeu 120
QY      711 GAGAGGCCCGACCGGTGGAAGATCTTTCGACTTCATCAAGGAAAGGGAGCCCTGCA 770
Db      121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGlnArgGlyAlaLeuGln 140
QY      771 GAGGAGTGGCCCGGAGCTTCTTTCGAGAGTGTGTGAGGCCGTGCGGCACTGCGCAAC 830
Db      141 GluGluLeuAlaIaArgSerPhePheTrrGlnValLeuGluAlaValArgHisCysHisAsn 160
QY      831 TCGGGGGTCTACACCGGCACATCAAGACGAAACATCTTATGACTTCATGCGCGC 890
Db      161 CysGlyValLeuHisArgAspIleLysAspGluAsnIleLeuIleAspLeuAsnArgGly 180
QY      891 GAGTCAAGCTCATGACTTCGGGTGGGGGGCGTGTCTCAAGACACGCTACAGCGAC 950
Db      181 GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTrrThrAsp 200
QY      951 TTGATGGGACCCGAGTGTATAGCCCTCCAGATGAGATCCGCTAACCATGCTACATGGC 1010
Db      201 PheAspGlyThrArgValTyrSerProProGluTrrIleArgTyrHisArgTyrHisGly 220
QY      1011 AGGTGGCGGGCACTCTGTCCTCCGGGATCTCTGTATATATGTTGTGTGAGATATT 1070
Db      221 ArgSerAlaIaIaValTrrPserLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
QY      1071 CCTTGGAGCATGACGAGAGATCATCAGGGGCGAGTTCCTTTCAGGCGAGGGTCTCT 1130
Db      241 ProPheGluHisAspGluGluIleValLysGlyGlnValTrrPheArgGlnArgValSer 260
QY      1131 TCAGATGTCAGCATCTCATTAATGTCCTTGGCCCTGAGACCATCATGATGAGCCAAAC 1190
Db      261 SerGluCysGlnHisLeuIleArgTrrCysLeuSerLeuArgProSerAspArgProser 280
QY      1191 TTGAGAAATCCAGAACCATCATGAGATGCAAGATTTCTCTGCGCCCGAGAACTGCT 1250
Db      281 PheGluGluIleGlnHisAsnHisProTrrPmetGlnAspValLeuLeuProGlnIaThrAla 300
QY      1251 GAGATCCACCTCCACAGCCTGTGCGCGGGGCCAGCAAA 1289
Db      301 GluIleHisLeuHisSerLeuSerProSerTrrLys 313

RESULT 10
US-09-644-450-8
; Sequence 8, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; CURRENT FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-644-450-8

Alignment Scores:
Pred. No.: 1,4e-114 Length: 313
Score: 1636.00 Matches: 304
Percent Similarity: 99.04% Conservative: 6
Best Local Similarity: 97.12% Mismatches: 3
Query Match: 34.16% Indels: 0
Gaps: 0

US-10-705-757-1 (1-2623) x US-09-644-450-8 (1-313)
QY      351 ATGCTCTTGTCCAAATCAACTCGCTTGGCCCACTGGCGCGCGCCCTTCGACGACTTG 410

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Db      1 MetLeuLeuSerLySIIeAsnSerLeuLhIstLeuRgIaIaIaProCySaAsnAspLeu 20
Qy      411 CAGCCCAACCAAGCTGGCGCGCCGCAAGAGAGAGAGCCCTGGAGTGGCAATCCAGGTG 470
Db      21 HIsAlaSnLySIIeAsnSerLeuLhIstLeuRgIaIaIaProCySaAsnAspLeu 40
Qy      471 GGCCCGCTACTGGGAGCGCGCGCTGGCTGGCTACTAGGCAATCCGCTCTCCGAC 530
Db      41 GlyProLeuLeuGlySerGlyIyPheGlySerValIySerGlyIleArgValAlaAsp 60
Qy      531 AACTTGGCGGTGGCCATCAACACGTGAGAGAGAGAGCCGATTTCCGATGGAGAGAGCTG 590
Db      61 AsnLeuProValAlaIleLySIIeAsnSerLeuLhIstLeuRgIaIaIaProCySaAsnAspLeu 80
Qy      591 CCTAATGCACTCGAGTGGCCATCAACACGTGAGAGAGAGCTGGTGGTGGTGGTGGTTC 650
Db      81 ProAsnGlyThrArgValIProMetGlyValIleuLeuLySIIeAsnSerGlyPhe 100
Qy      651 TCCGGCGCTCAATTAGGCTCTGGAGTGGTGGTGGAGAGCCGCAAGTTCCTGCTGATCTG 710
Db      101 SerGlyValIleArgLeuLeuAspTrpPheGlyArgProAspSerPheValIleuLeu 120
Qy      711 GAGAGCCCGAGCGCGGTGCAAGATCTCTGCACTTCAACAGAGAGAGAGAGCCCTGCA 770
Db      121 GluArgProGlyProValGlnAspLeuPheAspPheIleThrGlyArgGlyAlaLeuGln 140
Qy      771 GAGAGTGGCGCGCGCACTTCTTGGCAGGTGGTGGAGGCGGTGCGCACTGCGCACAC 830
Db      141 GluGlyLeuLeuAlaArgSerPhePheTrpGlnValIleuGlnAlaValArgHisCyHisAsn 160
Qy      831 TGGCGGCTGCTACACCCGCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 890
Db      161 CyGlyValIleuAlaArgSerPheIleAspGlyAsnIleuLeuLeuAsnArgGly 180
Qy      891 GAGCTCAAGCTCATCGACTTCGAGGTGGGCGCGCTGCAAGAGAGAGAGAGAGAGAGAGAG 950
Db      181 GluLeuLySIIeAsnSerLeuLhIstLeuRgIaIaIaProCySaAsnAspLeu 200
Qy      951 TTGAGTGGAGACCGAGTGTATAGCTTCCGAGTGGATCGGCTACCATCGCTACCATGAGC 1010
Db      201 PheAspGlyThrArgValIySerProProGlyTrpIleArgGlyHisArgGlyHisGly 220
Qy      1011 AGGTGGCGCGCACTGCTGCTGGAGATCTGCTGATGATGATGATGATGATGATGATGAT 1070
Db      221 ArgSerAlaIaValAlaTrpSerLeuGlyIleuLeuLySIIeAsnSerValCySgIyAspIle 240
Qy      1071 CCTTTCAGAGATGACGAGAGATCATCATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1130
Db      241 ProPheGlyHisAspGlyGlnIleValIySgIyGlnValIyTrpPheArgGlnArgValSer 260
Qy      1131 TCAGAGATGTCAGATCTCATTAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1190
Db      261 SerGlyCySgIyHisLeuIleuArgTrpCyLeuSerLeuArgProSerAspArgProSer 280
Qy      1191 TTGGAAGAAATCCGAACCATCCATGATGATGATGATGATGATGATGATGATGATGATG 1250
Db      281 PheGlyIleuIleGlnAsnHisProTrpMetGlnAspValIleuLeuProGlnAlaThrAla 300
Qy      1251 GAGATCCAGCTCCAGAGCTGTGGCGGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAG 1289
Db      301 GlnIleHisLeuHisSerLeuSerProSerProSerIys 313

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; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 313
; TYPE: PR
; ORGANISM: Mus musculus
US-09-237-543-7
Alignment Scores:
Pred. No.: 1,58e-110 Length: 313
Score: 1582.00 Matches: 294
Percent Similarity: 97.12% Conservative: 10
Best Local Similarity: 93.93% Mismatches: 9
Query Match: 33.03% Indels: 0
Gaps: 0
US-10-705-757-1 (1-2623) x US-09-237-543-7 (1-313)
Qy      351 ATGCTCTTGTCCAAATCAACTGCTTGGCCACTGCGCGCGCGCCCTTCGACAGACTG 410
Db      1 MetLeuLeuSerLySIIeAsnSerLeuLhIstLeuRgIaIaIaProCySaAsnAspLeu 20
Qy      411 CAGCCCAACCAAGCTGGCGCGCCGCAAGAGAGAGAGCCCTGGAGTGGCAATCCAGGTG 470
Db      21 HIsAlaThrLySIIeAsnSerLeuLhIstLeuRgIaIaIaProCySaAsnAspLeu 40
Qy      471 GGCCCGCTACTGGGAGCGCGCGCTGGCTGGCTACTAGGCAATCCGCTCTCCGAC 530
Db      41 GlyProLeuLeuGlySerGlyIyPheGlySerValIySerGlyIleArgValAlaAsp 60
Qy      531 AACTTGGCGGTGGCCATCAACACGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 590
Db      61 AsnLeuProValAlaIleLySIIeAsnSerLeuLhIstLeuRgIaIaIaProCySaAsnAspLeu 80
Qy      591 CCTAATGCACTCGAGTGGCCATCAACACGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 650
Db      81 ProAsnGlyThrArgValIProMetGlyValIleuLeuLySIIeAsnSerGlyPhe 100
Qy      651 TCCGGCGCTCAATTAGGCTCTGGAGTGGTGGTGGAGAGCCGCAAGTTCCTGCTGATCTG 710
Db      101 SerGlyValIleArgLeuLeuAspTrpPheGlyArgProAspSerPheValIleuLeu 120
Qy      711 GAGAGCCCGAGCGCGGTGCAAGATCTTCTGCACTTCAACAGAGAGAGAGAGAGAGAGAGAG 770
Db      121 GluArgProGlyProValGlnAspLeuPheAspPheIleThrGlyArgGlyAlaLeuGln 140
Qy      771 GAGAGTGGCGCGCGCACTTCTTGGCAGGTGGTGGAGGCGGTGCGCACTGCGCACAC 830
Db      141 GluAspLeuAlaArgGlyPhePheTrpGlnValIleuGlnAlaValArgHisCyHisAsn 160
Qy      831 TGGCGGCTGCTACACCCGCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 890
Db      161 CyGlyValIleuAlaArgSerPheIleAspGlyAsnIleuLeuLeuAsnArgGly 180
Qy      891 GAGCTCAAGCTCATCGACTTCGAGGTGGGCGCGCTGCAAGAGAGAGAGAGAGAGAGAGAG 950
Db      181 GlnIleLySIIeAsnSerLeuLhIstLeuRgIaIaIaProCySaAsnAspLeu 200
Qy      951 TTGAGTGGAGACCGAGTGTATAGCTTCCGAGTGGATCGGCTACCATCGCTACCATGAGC 1010
Db      201 PheAspGlyThrArgValIySerProProGlyTrpIleArgGlyHisArgGlyHisGly 220
Qy      1011 AGGTGGCGCGCACTGCTGCTGGAGATCTGCTGATGATGATGATGATGATGATGATGAT 1070
Db      221 ArgSerAlaIaValAlaTrpSerLeuGlyIleuLeuLySIIeAsnSerValCySgIyAspIle 240
Qy      1071 CCTTTCAGAGATGACGAGAGATCATCATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1130
Db      241 ProPheGlyHisAspGlyGlnIleValIySgIyGlnValIyTrpPheArgGlnArgValSer 260
Qy      1131 TCAGAGTGCAGATCTCATTAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1190

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; AUTHORS: Hunter, T.
; TITLE: The protein kinase family
; JOURNAL: Science
; VOLUME: 241
; PAGES: 42-52
; DATE: 1988
US-07-857-224B-41

Alignment Scores:
Pred. No.: 3,93e-89 Length: 257
Score: 1296.50 Matches: 242
Percent Similarity: 97.67% Conservative: 9
Best Local Similarity: 94.16% Mismatches: 3
Query Match: 27.07% Indels: 3
DB: Gaps: 2

US-10-705-757-1 (1-2623) x US-07-857-224B-41 (1-257)

QY 456 TCGCAGTACCAAGTGGGCGGCTACTGAGGAGCGGCGGCTTGGGCTGCTACTGAGGC 515
DB 1 SerGlnArgGlnValGlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGly 20
QY 516 ATCCGCGTCTCCGACAACTTGCCGCGTGCCTCAACACGTGAGAGAACCGGATTGCC 575
DB 21 IleArgValAlaAerAenLeuProValAlaIleIleYshIleValGluYbAerArgIleSer 40
QY 576 GACTGGGGAAGAGCTGCTTAATGCGACTGAGTGCCTGGAAGTGGTCTGCTGAGAGAG 635
DB 41 AepTrrpGlyGlu-----AangIyThrArgValProMetGluValIleuLeuYbLys 58
QY 636 GTGAGCGTGGGTTTCTCGGCGTCAATTAAGGCTCTGAGCTGGTTCCGAGGCGCGAAGT 695
DB 59 ValSerSerAerPheSerGlyValIleArgLeuLeuAerTrrpPheGluYbAerProAerSer 78
QY 696 TTCGCTCTGATCTCTGAGAGAGCGCGAGCCGAGTGCAGAGATCTTTCGACTTCATCAAGAA 755
DB 79 PheValIleuIleLeuGlnArgProGluProValGlnAerPheAerPheIleThrGlu 98
QY 756 AGGGAGACCTGCAAGAGAGAGTGGCCCGAGCTTCTTGGCAGAGTGGTGGAGCGCGT 815
DB 99 ArgGlyAlaLeuGlnGluAerPheLeuAlaArgIyPhePheTrrpGluValIleuGluAlaVal 118
QY 816 CGGCACTGCGCAACAATCGGGGGTGTACACCGCGACATCAAGAGCGAAACATCTTATC 875
DB 119 ArgHisGlyYshIleValAsnGlyValIleuHisArgAerPheIleYbAerGluAerIleLeuIle 138
QY 876 GACCTCAATCGCGCGAGCTCAAGCTCATGACTTCGGGTCGGGCGCTGCTCAAGAGC 935
DB 139 AepLeuSerArgIyGluIleYbLeuIleAerPheGlySerGlyAlaLeuLeuYbAer 158
QY 936 ACCGTTTACACGGAATTGATGGAGCCGAGTGTATAGCCCTTCAGAGTGAATCCGCTAC 995
DB 159 ThrValIyThrAerPheAerGlyThrArgValTyrSerProProGluTrrpIleArgTyr 178
QY 996 CATCGGACATGAGGAGTGGGCGGAGCTGTGGTCCCTGGGATCCGTCGTGTATGATG 1055
DB 179 HisArgGlyThrIleGlyArgSerAlaAlaValTrrpSerIleuGlyIleuLeuTyrAerPhe 198
QY 1056 GTGTGTGAGATATTCTCTTC-----GAGCATGACGAAGAGATCATCAGGCGCGAGTTTTC 1112
DB 199 ValCyseGlyAerPheProPheAerGluHisAerPheGluIleIleYbGlyGluValPhe 218
QY 1113 TTCAAGGCAAGAGGCTCTTCAAAATGTCAAGATCTCATTAAGATGGTGTCTGGCCCTGAGA 1172
DB 219 PheArgGlnThrValIleSerSerGlyCyGlnHisIleuIleYbTrrpCybLeuSerLeuYbArg 238
QY 1173 CCAATCGATGAGGCAACTTCGAAGAAATCCAGAAACATCAATCAGATGAGTGA 1223
DB 239 ProSerAerAerProSerPheGluGluIleArgHisHisProTrrpMetGln 255

RESULT 14
US-09-237-543-5
; Sequence 5, Application US/09237543A
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; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
; FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRF
; ORGANISM: Rattus norvegicus
US-09-237-543-5

Alignment Scores:
Pred. No.: 5,21e-78 Length: 455
Score: 1149.50 Matches: 240
Percent Similarity: 66.59% Conservative: 37
Best Local Similarity: 57.69% Mismatches: 66
Query Match: 24.00% Indels: 73
DB: Gaps: 10

US-10-705-757-1 (1-2623) x US-09-237-543-5 (1-455)

QY 43 CGGCGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 91
DB 58 ProArgGlyGluHisAlaIleGlyAlaCys-GluProLeuGlyGlnLeuProSerThrGlyPh 77
QY 92 -----GGGCGTTCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 147
DB 77 eArgAlaAlaThrGlyGlnLeuArgArgAlaAlaProLeu-----SerAlaAr 94
QY 148 ACCCGCGTGGC-----GGCGTCCGCGCG 171
DB 94 gProArg-GlyArgGlyIleArgArgAlaValCyseGlyGlnGluAerArgProProHis 114
QY 172 CAGTCCCGGAGCGGCTCAAGTGTCTCGACTCGGCTTCGCGCAGCGCAGCA 231
DB 114 eValProAerPheGlySerGlu----- 120
QY 232 CAGCGCGACGACCGCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 291
DB 121 -----AlaAlaProHisAlaArgProProAla-----SerAlaAr 129
QY 292 GCTCCGCGTCTCGGCGAGCTCTTGGCAGCGTCCCTGGCGCGACATTCGAGGTGGA 351
DB 130 -----M 130
QY 352 TGGCTTTGTCCAAATCAATCGCTTGGCCACTGGCGCGCGCGCC-----TGCAGCG 405
DB 130 eLeuLeuSerIleYbPheGlySerLeuAlaHisIleu-----CybGlyProGlyGlyValAerPh 149
QY 406 ACTGCAACCGCACCAAGCTGGCGCGCGAG--GAGAAAGAGCGCCCTGAGATCGCAGT 462
DB 149 IseLeuProValIleYbIleGlnProAlaIleYbAlaAerPheYbGlySerPheGluValT 169
QY 463 ACCAGGTGGGCGGCTACTGAGGAGCGGCGGCTTCGGTCCGCTCAAGGATCGCGG 522
DB 169 yGlnValGlyAlaValIleGlySerGlyGlyPheIleYbThrValTrrpAlaGlySerArgT 189
QY 523 TTCGCGAACATTCGCGGCGGCGCATCAACAGTGAAGAGACCGGATTCGAGTGGG 582
DB 189 IeAlaAerPheGlyLeuProValAlaValIleHisIleValIleYbGluArgValThrGluTrrp 209
QY 583 GAGAGTGCCTTAATGCACTCGAGTGCCTGAGTGAAGTGGTCTGCTGGAAGAGT----- 638
DB 209 IySerLeu-----GlyGlyMetAlaValProLeuGluValIleuLeuAerGlybValGlyA 228
QY 639 --AGTCCGGGTTTCTCGGCGTCAATTAAGCTCTGAGTGGTTCGAGAGCGCGACAGTT 696
DB 228 IAlaIleGlyAlaAerGlyValIleArgLeuLeuAerTrrpPheGluArgProAerPheGlyP 248
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Oy	657	TCGTCCTGATCTCTGAGAGAGCCCGGAGCCGCTGCAAGATCTCTTGACATTCATCAAGGAA	756
Db	248	heleuLeuValleuIduArgProGluProAlaGlnAspLeuPheAspHeleuTrgIua	268
Oy	757	GGGAGGCCCTCGAAGAAGAGCTGAGCCCGCAGGCTCTTCTTGCGAGGATGTGAGAGCCGTGC	816
Db	268	rgGIyAlIleuAspIuProIeuAlaIaIaGArgPhePheAlaGlnIvalIleuAlaIaVala	288
Oy	817	GGCACTGCCAACAATGTCGGGGGTGTCTAACACCGGACATCAAGAGAGGAAACATCTTATCG	876
Db	288	rgHleCyuHleAsnCyseGIyAlValHleArgDApIleIyAspIuIaAsnIleuVala	308
Oy	877	ACCTCAATCGGGGCGAGCTCAAGCTCAATCAATCTTGCGGTGGGGCGCGCTGCTCAAGACA	936
Db	308	spleuArgSetIyIuIeuIeuIeIuIleAspPheGlySetIyAlaIaIleuIyAspT	328
Oy	937	CCGTTCACACGCACTTCGATGGAGACCCGAGTGTATAGGCTTCAGAGTGTGATCCGCTACC	996
Db	328	hrValIyThrAspPheAspIuIyHTrArgValIySerProProIuIuIrpIleArgTyH	348
Oy	997	ATCGTACCAATGGCAGGTGCGGCGAGTGTGATCTCTTGCGGATCTGTGTATGATATGG	1056
Db	348	leArgTyHleGIyAspIeArgSerAlaTrHValIyTrpSerIeGIyAlIleuIeuTyAspMetv	368
Oy	1057	TGTGTGAGATATTCCTCTTTCAGAGTACGAAAGATATCATAGGGGCGAGGCTTCTTCA	1116
Db	368	alCyseGIyAspIleProPheGluGlnAspGIuIuIleuArgIuIyArgLeuPhePheA	388
Oy	1117	GGCAGAGGATCTCTTCAGATATGTCAAGATCTTCATAGATAGTGTGCTTGCCCTGAGACCAT	1176
Db	388	rgArgArgValserProGluCyseGlnIleuIleIeGIuIuIyIrpCyAsuSerIeIuArgProS	408
Oy	1177	CAGATAGGCCCAACTTCGAGAAGATCCAGAACATCCATGATG	1220
Db	408	ergIuArgProSerIeAspGlnIleAlaIaIaHleProIyMet	422
RESULT 15			
US-09-644-450-5			
; Sequence 5, Application US/09644450			
; Patent No. 6383791			
; GENERAL INFORMATION:			
; APPLICANT: Kapeller, Rosana			
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY			
; TITLE OF INVENTION: AND USES THEREOF			
; FILE REFERENCE: 035800/175631			
; CURRENT APPLICATION NUMBER: US/09/644,450			
; NUMBER OF FILING DATE: 2000-08-23			
; NUMBER OF SEQ ID NOS: 11			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 5			
; LENGTH: 455			
; TYPE: PRT			
; ORGANISM: Rattus norvegicus			
US-09-644-450-5			
Alignment Scores:			
Pred. No.:		5, 216-78	Length: 455
Score:		1149.50	Matches: 250
Percent Similarity:		66.59%	Conservative: 37
Best Local Similarity:		57.69%	Mismatches: 66
Query Match:		24.00%	Indels: 73
DB:		3	Gaps: 10
US-10-705-757-1 (1-2623) x US-09-644-450-5 (1-455)			
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Db	58	ProArgGIyGIuAlaIaIeGIyAlaCyS-cluProIeuGIyGIuIeuProSerThrGIyPh	77
Oy	92	---GCGGCGTTGCCAGACGCCCAAGAGCCGCTACCCCGCGGCTTCAGAGCGTCGCCG	147
Db	77	eArgIuAlaIaTrHrgIyGIuIleuArgArgIuAlaIaIaIaProIeu-----SerIaIa	94

QY	148	ACCCGCGTGGC-----GGGCTCCGCGCG	171
Db	94	gprkayr-glyAarglyTleargAargAlaValCysglyLeuIleuAraArgProProAlaAs	114
QY	172	CAGTCCCGCGGAGCGGCTCAAGTTGTCTCCGACTCCGCTCCGAGCTTCGCGGACGCGAGCA	231
Db	114	erValProAaRgPglySerGIu-----	120
QY	232	CAGCGCGACGCGACCGGACGACAGCAGCAGCGGCAATGACTTCGGGACAGCGCGG	291
Db	121	-----AlaAlaProHValAlaAargProProAla-----	129
QY	292	GCTCCGAGCTCTCGGCGGACGTCCTGTGGACAGTCCCTCGCGCGGACATTCGAGGTGGa	351
Db	130	-----M-----	130
QY	352	TGCTCTGTTCGAAATCAATCGCTGTGCCCACTCGCGCGCGCGCC-----TGCACG	405
Db	130	etLeuLeuSerTyrPhegIlySerLeuAlaHleu-----CysglyProglyIyAlaRph	149
QY	406	ACCTGCACGCGCACCAAGCTGGCGCGCGCGGCAAG---GAGAGGAGCGCCCTCGAGTGGCACT	462
Db	149	leuProVallyleTleuGlnProAlaValAlaAspArglySerPheGlyIyValT	169
QY	463	ACCAAGTGGGCGCGCTACTGTGGGACAGCGCGGCTTCGAGTCTACTCAAGGCAATCCGCG	522
Db	169	yrGlnValAlGlyAlaValLeuGlySerGIyIyPheGlyTyrValTyrAlaGlySerArgI	189
QY	523	TCTCCGACAACTTGGCGCGGCTGCATCAAAACAGCTGGAAGAAGACCGGATTCGACGTGG	582
Db	189	leAlaAspGIyLeuProValAlaValIyVhIAsValIyVallySerIuArgValITrGlyTTrG	209
QY	583	GAGAGCTGCTTAATATGCACTCGAGTGGCCCATGAGAGTGGTCTGTGTAAGAAGATG---	638
Db	209	lySerIu---GIyGIyMetAlaValProLeuGlnValValLeuLeuAarglyIyValGIyA	228
QY	639	--AGCTCGAGTTTCTCCGAGCTCATTTAGGCTCTCGAGTGGTTCGAGAGCGCCGACAGTT	696
Db	228	laAlaGlyGIyAlaArglyValIleArgLeuLeuAaPTrPheGlyIuArgProAspGIyP	248
QY	697	TGCTCTGTATCTGGAGAGCGCCGAGCGGTCGAGATCTCTCGACTTCATCAACGGAA	756
Db	248	heLeuLeuValIleuGIuArgProGlyIuProAlaGlnAspPheAaPheIleTrGlnA	268
QY	757	GCGGAGCCCTGCAGAGAGAGAGCTGGCGCGCAGCTTCTTGTGCGAGGTGTGAGGCGCGTGC	816
Db	268	rgGIyAlIleuAaRgPlyIuProLeuAlaIaArgRgPhePheIaGlnValIleuAlaIaValA	288
QY	817	GGCAATGGCAAACTGGCGGGGTGCTACACCGCGAATCAAGACGAAACATCCTTATAG	876
Db	288	rgHAsCyHhIAsVhIAsVgIyAlaValIhIAsAAspRlyleuAAspGIyAaPheLeuLeuValA	308
QY	877	ACCTCAATTCGCGGCGAGCTCAAGCTCATCTGCACTTGGGAGTGGGAGCGCTGCTCAAGACA	936
Db	308	spLeuAAspSerGIyIuLeuIySerIuIleAaRphGlySerGIyAlaValIleuIyAspR	328
QY	937	CCGTTCACACGAGCTTCGATGGAGACCCGAGGTATAGCTTCGACAGTGCATCCGCTACC	996
Db	328	hValIyTTrAspAaRphAspGIyTTrAArgValTyrSerProGlyIuTrpIleArgTyrH	348
QY	997	ATCGTACCAATGGAGAGTTCGCGCGGAGTGGCTCCCTGGGAGATCCGCTATGATATAG	105
Db	348	lAsArgTyrHleGIyAAspSerAlaTrValITrPserLeuGIyAlaLeuLeuTyrAspMeIy	368
QY	1057	TGTGTGAGATATTCCTTTTCGACATGACGAGATATCATCAGGGGACAGTTTTTCTCA	111
Db	368	AlCyGlyIyAspRlyleProPheGlnGlnIaRgIuGlnIleuAArgIyAlaArgLeuPheAa	388
QY	1117	GCGAAGAGGCTCTTCACAAATGTACGACATCTATTAAGATGAGTGGCGCTTCGACACAT	117
Db	388	rgArArgValAspSerProGIuCyGlnGlnIleuIleGIyIuTrpCyAspLeuSerIleuAArgPro	408

OY 1177 CAGATAGGCCAACCTTCCAGAAATCCAGATCCATCCATGSGATG 1220
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Db 408 exgiuArGProSerleuApeGinIleAlaAlaH1sProIrpMet 422

Search completed: September 22, 2005, 17:24:27
Job time : 87.9838 sec8

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: September 22, 2005, 16:17:56 ; Search time 85.9602 Seconds
(without alignments)
5871.937 Million cell updates/sec

Title: US-10-705-757-1

Perfect score: 4789

Sequence: 1 gagagagccgcagagagcgc.....aataaaacccttgcttc 2623

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-Q=/cgn2.1/USPTO.spool.p/US10705757/runat_22092005.115015.22141/app_query.fasta_1.5333

-DB=pir -OPMT=faetan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdt -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=pro-NOR=ext -HEAPSIZES=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10705757_@CCN_1_1_256_@runat_22092005.115015.22141 -NCPU=6 -ICPU=3
-NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -DEPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FCAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

pir_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB ID	Description
1	1670	34.9	313	1	TVHUP1
2	1636	34.2	313	1	S26298
3	1582	33.0	313	1	TYWSP1
4	918	19.2	370	1	S55333
5	620	12.9	363	2	T22255
6	486	10.1	409	2	T15435
7	402	8.4	1398	2	T13741
8	397.5	8.3	481	2	I49072
9	385.5	8.0	512	2	JC1446
10	378	7.9	504	2	T10449
11	376	7.9	1101	2	S66730
12	373	7.8	1192	2	T18611
13	369.5	7.7	512	2	T07788
14	367	7.7	1358	2	S33653

15	366.5	7.7	512	2	T52633	serine/threonine-s
16	364.5	7.6	511	1	A56009	serine/threonine-s
17	362.5	7.6	651	1	S52244	p69B3 protein - A
18	361	7.5	798	2	JC7500	gik protein - chic
19	348.5	7.3	887	2	T20941	hypothetical prote
20	348	7.3	469	2	B84644	probable protein k
21	348	7.3	472	2	B90100	SNF-related kinase
22	345	7.2	726	2	T33998	hypothetical prote
23	343.5	7.2	414	2	UN0323	Ca2+/calmodulin-de
24	342.5	7.2	489	2	T04862	probable serine/th
25	342.5	7.2	527	2	A53467	protein kinase SNF
26	342.5	7.2	1558	2	T29253	hypothetical prote
27	342	7.1	639	1	T02784	calcium-dependent
28	341	7.1	502	2	T02306	probable protein k
29	341	7.1	513	1	S60304	serine/threonine-s
30	340.5	7.1	1518	2	S37928	serine/threonine-s
31	340	7.1	745	2	G01025	serine/threonine p
32	339.5	7.1	504	2	T07415	probable serine/th
33	337.5	7.0	520	2	G86414	probable protein k
34	337	7.0	713	2	S27866	probable serine/th
35	336.5	7.0	445	2	T50802	serine/threonine p
36	336.5	7.0	891	2	A38903	protein kinase I -
37	336.5	7.0	891	2	T40503	calcium-dependent
38	332.5	6.9	553	1	T02139	calcium-dependent
39	331.5	6.9	513	1	S60303	serine/threonine-s
40	331.5	6.9	529	1	S71774	calcium-dependent
41	331.5	6.9	540	1	T01989	calcium-dependent
42	331.5	6.9	582	2	B84721	probable calcium-d
43	331.5	6.9	774	2	I46609	probable serine/th
44	331	6.9	435	2	B84707	probable protein k
45	330.5	6.9	339	2	S56719	serine/threonine-s

ALIGNMENTS

RESULT 1

protein kinase (EC 2.7.1.37) pim-1 - human

N/A:Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene prot

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1989 #sequence revision 07-Oct-1994 #ext_change 09-Jul-2004

C/Accession: J00327; A46554; A27476; I58412

R/Reviews: R.; Spies, G.A.; Kiefer, M.; Barr, P.J.; Power, M.

Gene 90, 303-307, 1990

A/Title: Primary structure of the putative human oncogene, pim-1.

A/Reference number: J00327; MUID:90382681; PMID:2205533

A/Accession: J00327

A/Molecule type: DNA

A/Residues: 1-313 <RES>

A/Cross-references: UNIPROT:P11309; GB:M27903; NID:G1066790; PID:AAA60090.1; PID:G38702.

R/Wecker, T.C.; Nagarajan, L.; ar-Rushdi, A.; Croce, C.M.

J. Cell. Biochem. 35, 105-112, 1987

A/Title: Cloning and characterization of the human pim-1 gene: a putative oncogene rela

A/Reference number: A46554; MUID:88115604; PMID:3429489

A/Accession: A46554

A/Molecule type: mRNA

A/Residues: 1-313 <RES>

A/Cross-references: GB:M24779; NID:G1066790; PID:AAA81553.1; PID:G1066791

R/Zakut-Houri, R.; Hazum, S.; Givol, D.; Teitelman, A.

Gene 54, 105-111, 1987

A/Title: The cDNA sequence and gene analysis of the human pim oncogene.

A/Reference number: A27476; MUID:87277423; PMID:3475233

A/Accession: A27476

A/Molecule type: mRNA

A/Residues: 1-14, 'RA', 17-313 <ZAK>

A/Cross-references: GB:M16750; NID:G189956; PID:AAA60089.1; PID:G189957

R/Domen, J.; Von Lindern, M.; Hermans, A.; Breuer, M.; Grosveld, G.; Berns, A.A.

Oncogene Res. 1, 103-112, 1987

A/Title: Comparison of the human and mouse PIM-1 cDNAs: Nucleotide sequence and immuno

A/Reference number: I58412; MUID:88217305; PMID:3329709

A/Accession: I58412

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

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 Db 101 SerGlyValIleAlaGlyLeuAlaSerPheGluArgProAspSerPheValIleLeu 120
 QY 711 GAGAGCCCGAGCCGATGCAAGATCTTCTGACTTCAACGAAAGGGAGCCCTGCA 770
 Db 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
 QY 771 GAGAGCTGGCCGCGAGCTTCTTGGAGAGGTGTGAGGCGCTGCGGACATGCGAC 830
 Db 141 GluGluLeuAlaArgSerPheThrGlnValIleuGluAlaValArgHisCysHisAsn 160
 QY 831 TGGGGGGTGGTACACCCGCGACATCAAGAGCAAAACAATCTTATCGACCTCAATCGGGC 890
 Db 161 CysGlyValLeuHisAlaArgAspIleLeuAspGluAsnIleLeuIleAspLeuAlaArgGly 180
 QY 891 GAGCTCAAGCTCATCGACTTCGAGGTGCGGGGCGCTGCAAGGACACCGTCTACACGAC 950
 Db 181 GluLeuLeuLeuIleAspPheGlySerGlyAlaLeuLeuLeuAspThrValTyrThrAsp 200
 QY 951 TTGAGTGAACCCGAGTGTATAGCTTCCAGAGTGAATCCGCTACATGCTACATGAC 1010
 Db 201 PheAspGlyThrArgValTyrSerProGluIleArgTyrHisArgTyrHisGly 220
 QY 1011 AGGTGGGCGGCACTGCTGCTCCCTGGGAGATCTGCTGTATGATATGCTGTGAGAAAT 1070
 Db 221 ArgSerAlaValAlaIlePheSerLeuGlyIleLeuLeuLeuAspMetValCysGlyAspIle 240
 QY 1071 CCTTTCAGAGTACGAAAGATCATCATGAGGAGGCGAGTTTCTTCAGGAGAGAGTCTCT 1130
 Db 241 ProPheGluIleHisArgGluGluIleValIleValGlyGlnValTyrPheArgGlnArgValSer 260
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 Db 281 PheGluGluIleGlnHisAspProTyrPheGlnAspValIleLeuProGlnAlaThrAla 300
 QY 1251 GAGATCCACCTCCACAGCTGTGCGCGGAGCCGACGAA 1289
 Db 301 GluIleHisLeuHisSerLeuSerProSerProSerLys 313
 RESULT 3
 TVMSPI
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 N/Alternate names: kinase-related transforming protein p1m-1; p1m-1 proto-oncogene proce
 C/Spectrum: Mus musculus (house mouse)
 C/Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
 C/Accession: A24169
 R/Selten, G.; Cuyper, H.T.; Boelens, W.; Robanus-Maandag, E.; Verbeek, J.; Domen, J.;
 Cell 46, 603-611, 1986
 A/Title: The primary structure of the putative oncogene p1m-1 shows extensive homology w
 A/Reference number: A24169; MUID:86272105; PMID:3015420
 A/Accession: A24169
 A/Molecule type: DNA
 A/Features: 1-313 <SEL>
 A/Cross-references: UNIPROT:P06803; GB:M13945; GB:M13946; NID:g200352; PIDN:AAA39930.1;
 C/Comment: P1m-1 autophosphorylates at unknown sites.
 C/Genetics:
 A/Gene: p1m-1
 A/Introns: 28/1; 63/3; 80/3; 203/1; 262/1
 C/Function:
 A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
 C/Keyword: ATP; autophosphorylation; phosphotransferase; proto-oncogene; serine/threonin
 P/36-220/Domain: protein kinase homology <KIN>
 P/44-52/Region: protein kinase ATP-binding motif
 P/67/Active site: Lys #status predicted

Pred. No.: 2,866-60 Length: 313
 Score: 1582.00 Matches: 294
 Percent Similarity: 97.12% Conservative: 10
 Best Local Similarity: 93.93% Mismatches: 9
 Query Match: 33.03% Indels: 0
 DB: 1 Gaps: 0
 US-10-705-757-1 (1-2623) x TVMSPI (1-313)
 QY 351 ATGCTTTGTCCAAATCAACTGCTTGGCCACCTGCGGCGCGCTTGCACGACTG 410
 Db 1 MetLeuLeuSerLysValIleAsnSerLeuAlaHisIleLeuArgAlaArgProCysAsnAspLeu 20
 QY 411 CAGGCCACCAAGCTGGCGCCCGGCAAGAGAGAGACCCCTGAGATGCGAGTACAGCTG 470
 Db 21 HisAlaThrLysLeuAlaProGluLysGluLysGluLysGluLysGluLysGluLysGluLys 40
 QY 471 GGCCTGCTACTGGGCGAGCGGCTTCCGCTCGGCTTACTCAGGACATCCGCTCCGAC 530
 Db 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValAlaAsp 60
 QY 531 AACTGCGGCTGACATCAACACGTCGAGAGAGACCGGATTTCCGACTGGGAGACTG 590
 Db 61 AsnLeuProValAlaIleLysHisValGluLysAspArgIleSerAspTyrGluLeu 80
 QY 591 CCTAATGCACTGAGTGCCTCATGAAAGTGTCTCTGTGAAGAGGTGAGCTGGCTTTC 650
 Db 81 ProAsnGlyThrArgValProMetGluValIleLeuLeuLysValIleSerSerAspPhe 100
 QY 651 TCGGCGCATTTAGGCTCTGGACTGGATTGAGAGGCCGACAGTTTGGTCTGATCTG 710
 Db 101 SerGlyValIleArgLeuLeuAlaSerPheGluArgProAspSerPheValIleLeu 120
 QY 711 GAGAGCCCGAGCCGATGCAAGATCTTCTGACTTCAACGAAAGGGAGCCCTGCA 770
 Db 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
 QY 771 GAGAGCTGGCCGCGAGCTTCTTGGAGAGGTGTGAGGCGCTGCGGACATGCGAC 830
 Db 141 GluGluLeuAlaArgSerPheThrGlnValIleuGluAlaValArgHisCysHisAsn 160
 QY 831 TGGGGGGTGGTACACCCGCGACATCAAGAGCAAAACAATCTTATCGACCTCAATCGGGC 890
 Db 161 CysGlyValLeuHisAlaArgAspIleLeuAspGluAsnIleLeuIleAspLeuAlaArgGly 180
 QY 891 GAGCTCAAGCTCATCGACTTCGAGGTGCGGGGCGCTGCAAGGACACCGTCTACACGAC 950
 Db 181 GluLeuLeuLeuIleAspPheGlySerGlyAlaLeuLeuLeuAspThrValTyrThrAsp 200
 QY 951 TTGAGTGAACCCGAGTGTATAGCTTCCAGAGTGAATCCGCTACATGCTACATGAC 1010
 Db 201 PheAspGlyThrArgValTyrSerProGluIleArgTyrHisArgTyrHisGly 220
 QY 1011 AGGTGGGCGGCACTGCTGCTCCCTGGGAGATCTGCTGTATGATATGCTGTGAGAAAT 1070
 Db 221 ArgSerAlaValAlaIlePheSerLeuGlyIleLeuLeuLeuAspMetValCysGlyAspIle 240
 QY 1071 CCTTTCAGAGTACGAAAGATCATCATGAGGAGGCGAGTTTCTTCAGGAGAGAGTCTCT 1130
 Db 241 ProPheGluIleHisArgGluGluIleValIleValGlyGlnValTyrPheArgGlnArgValSer 260
 QY 1131 TCAGATGTCAAGCATCTCATTTAGATGCTTGGCCCTGAGACCATCATGATAGGCCAAC 1190
 Db 261 SerGluCysGlnHisValIleArgTyrCysLeuSerLeuArgProSerAspArgProSer 280
 QY 1191 TTGGAAGAATCCAGAACCATCCATGATGATGATGATGATGATGATGATGATGATGAT 1250
 Db 281 PheGluGluIleGlnHisAspProTyrPheGlnAspValIleLeuProGlnAlaThrAla 300
 QY 1251 GAGATCCACCTCCACAGCTGTGCGCGGAGCCGACGAA 1289
 Db 301 GluIleHisLeuHisSerLeuSerProGlySerSerLys 313

Alignment Scores:

RESULT 4
S55333
protein kinase pim-2 (EC 2.7.1.-) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 10-Oct-1995 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C/Accession: S55333; A43093
R/Van der Lugt, N.M.T.; Domen, J.; Verhoeven, E.; Lindere, K.; van der Gulden, H.; Allen
EMBO J. 14, 2536-2544, 1995
A/Title: Proviral tagging in E-mu-myc transgenic mice lacking the Pim-1 proto-oncogene 1
A/Reference number: S55333; MUID:95300786; PMID:7781606
A/Accession: S55333
A/Molecule type: mRNA
A/Residues: 1-370 <V>
A/Cross-references: UNIPROT:Q62070; GB:L41495; NID:g765065; PIDN:AAA98922.1; PID:g765066
A/Note: 40K form
A/Accession: A43093
A/Molecule type: mRNA
A/Residues: 'M', 27-370 <V>
A/Cross-references: GB:L41495; NID:g765065; PIDN:AAA98922.1; PID:g765067
A/Note: 37K form
A/Accession: B43093
A/Molecule type: mRNA
A/Residues: 'M', 61-370 <V>
A/Cross-references: GB:L41495; NID:g765065; PIDN:AAA98922.1; PID:g765068
A/Note: 34K form
C/Comment: Pim-2 autophosphorylates at unknown sites.
C/Genetics:
A/Gene: Pim-2
A/Map position: X
A/Start codon: CTG
A/Note: locus between A-raf and Act-7, near Kv4.1
C/Function:
A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C/Superfamily: kinase-related transforming protein; protein kinase homology
C/Keywords: alternative initiators; ATP; autophosphorylation; phosphoprotein; phosphotransferase
F/89-345/Boman: protein kinase homology <KIN>
F/97-105/Region: protein kinase ATP-binding motif
F/120/Active site: Lys #status predicted

Alignment Scores:
Pred. No.: 3,89e-32 Length: 370
Score: 918.00 Matches: 195
Percent Similarity: 62.44% Conservative: 51
Best Local Similarity: 49.49% Mismatches: 104
Query Match: 19.17% Indels: 44
DB: 1 Gaps: 9

US-10-705-757-1 (1-2623) x S55333 (1-370)

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QY      153  GTGGGCGGCTCCCGCGAGTCCCGGCA-----GCGCTCAGTTGTCCTCGACTCG 206
DB      15  AIsSerGlyProIaSerPseSerLeuProSerThreuAlaProPro---SerProGlySer 33
QY      207  CCCTCGGCTTCGCGAGCGACGACGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 266
DB      34  ProAlaAlaLeuProAlaSerThr-----TCTGGC 320
QY      267  CAGGATAGCTTGGCGACAGCCCGGCTCGGCTCTCGGCGAGCTCC-----TCTGGC 320
DB      43  -----ProGlySerLeuSerGlyPheSerGly 51
QY      321  ACGTCCGCGCGGACATTCGAGAGTTGATGCTCTTGCAGAAATCAACTGCTTGC 380
DB      52  LeuAenIleArgSerThrSerSer-----MetLeuThrIys-----63
QY      381  CACCTGCGCGCGCGCTTCGACAGACTGACGCGCAGCAAGCTGCGCGCGCAAGAG 440
DB      64  ProLeuGlnGlnIylHisProSerProProValThrProThrGlnProProGlyGlyAsp 83
QY      441  AAGAGGCCCTGAGAGTGCAGTACAGATGGGCGCGCTTATGGGCGAGCGCGCTTGGC 500
DB      84  ArgAlaAlaPheGlnAlaGlnIylArgLeuGlyProLeuLeuGlnIylGlyGlyPheGly 103

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QY      501  TCGGTCTACTCAGAGCATCCGCTCTCCGACACTTGCAGGTCGAGCCATCAACAGTGGAG 560
DB      104  ThrValPheAlaGlyHisArgValThrPheArgAlaGlnValAlaIleValIleSer 123
QY      561  AAGACCGGATTTCCGACTGGGAGAGCTCGCTTAATGGCATTCGATGCTCCATGAGTG 620
DB      124  ArgAenArgValLeuGlyThrPseThrAlaSerPseValThrCysProLeuGlnVal 143
QY      621  GTCCTGCTGAAGAAGTG-----AGCTCGGCTTCTCCGGGCTATTAAGTCCCTGGAC 674
DB      144  AlaLeuLeuTrpIylValGlyGlyGlnGlyHisProGlyValIleArgLeuLeuAsp 163
QY      675  TGGTTCGAGAGCGCGGACAGTTCTGCTGATCTCTGAGAGCGCGGAGCGGTCGAGAT 734
DB      164  TrpPheGlnThrProGlnGlyPheMetLeuValLeuGlnIylArgProMetProAlaGlnAsp 183
QY      735  CTCTTGACTTCATCAACGAAAGGAGCGCTTCGACAGAGAGCTGGCCCGCAGCTTCTTC 794
DB      184  LeuPheAspTyrIleThrGlnIylGlyProLeuGlyGlnSerCysSerArgSerPhePhe 203
QY      795  TGGCAGGCTGCGAGCGCGCTGCGGACTGCGCAACTGCGGGGCTCTACACCGCGCATC 854
DB      204  ThrGlnValValAlaValAlaGlnHisCysHisAlaArgGlyValValHisArgAspIle 223
QY      855  AAGACGAAACATCTTATCGACTTCATCGCGCGGAGCTCAAGCTCATTCGACTTCGG 914
DB      224  LysAspGlnAenIleLeuIlePheLeuGlySerArgGlySerIleLeuLeuIleAspPheGly 243
QY      915  TCGGGGCGCTGCTCAAGACCGCTTCACAGCACTTCGATGGGACCCGAGTGTATAC 974
DB      244  SerGlyAlaLeuLeuHisAspIylProIylThrAspPheAspGlyThrArgValTyrSer 263
QY      975  CCTCCAGATGATCCGCTACCATGCTTCATTCGAGAGTTCGCGGAGCTGCTGCTCCG 1034
DB      264  ProProGlnIylTrpIleSerArgHisGlnIylHisAlaLeuProAlaThrValTrpSerLeu 283
QY      1035  GGGATCTGCTGATGATATGCTGTGTGGAGATATCTCTTGGAGCATGACGAAGATC 1094
DB      284  GlyValIleLeuLeuIylAspMetValCysGlyAspIleProPheGlnIylArgAspGlnIyl 303
QY      1095  ATCAGGGGCGAGTTTCTTCAGGCGAGGGTCTTCAGATTCACAGATCTCATTTAA 1154
DB      304  LeuGlnAlaGlnLeuHisPheProAlaHisValIleSerProAspCysValIleLeuIleArg 323
QY      1155  TGGTGTGGCGCTGACATCAGATAGTAGGCGCACTTGGAGAAATCCAGAAACATCA 1214
DB      324  ArgCysLeuAlaProIylProCysSerArgProSerLeuGlnGlnIleLeuLeuAspPro 343
QY      1215  TGAATGCAAGATGTTCTCTGCGCCGACGAAACTGTGAGATCCACCTCCAGCCTGTGC 1274
DB      344  TrpMetGlnSer-----ProAlaGlnIylIylProIleAsnSerSerIylGlySer 360
QY      1275  CCGGGGCCGACGAATAGCAGCTTTCGCGAGTCTTCCC 1316
DB      361  ProThrProLeuPro-----TrpSerLeuLeuPro 370

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RESULT 5
T22255
hypothetical protein F45H7.4 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T22255
R/Pericy, C.
submitted to the EMBL Data Library, June 1994
A/Reference number: Z19538
A/Accession: T22255
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-363 <WIL>
A/Cross-references: UNIPROT:Q20443; EMBL:Z14800; PIDN:CAA84323.1; GSPDB:GN00021; CESP:F
A/Experimental source: clone F45H7
A/Genes: CESP:F45H7.4

A,Map position: 3

A; Introns: 72/3; 160/3; 310/1

C/Superfamily: kinase-related transforming protein; protein kinase homology

Alignment Scores:

Pred. No.:	1.66e-19	Length:	364
Score:	620.00	Matches:	133
Percent Similarity:	59.49%	Conservative:	107
Best Local Similarity:	41.46%	Mismatches:	10
Query Match:	12.95%	Indels:	2
DB:	2	Gaps:	5

US-10-705-757-1 (1-2623) x T22255 (1-363)

[illegible]

QY 1302 TGGAGGTCTCCCTCTTGTTCAGATGCCCGAGGAGGGGAGGC 1347
 ||||| ||| ||| :||| |||||
 Db 324 uAspArgSerProThrSerSerValSerGlnGlnProGlySer 339

RESULT

T15435

hypothetical protein C06B8.3 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C:\Accession: T1543E
C:\Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:\Access810: 115435
R:\Fave110: A

submitted to the EMBL Data Library, February 1994

A;Description: The sequence of *C. elegans* cosmid

A;Reference number: Z18350

A;Accession: T15435

A/Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-409 <FAV>

A: Experimental source:

A/bayesianmethod source: brian dabbott in C:Genetics:

A;Gene: CESP:C06B8.3

A;Introns: 24/1; 76/3; 107/2; 145/3; 199/1; 307/1; 375/1

Alignment Scores:

Pred. No.:	7.85e-14	409
Score:	486.00	Matches:
Percent Similarity:	54.61%	Conservative:
Best local Similarity:	35.84%	Mismatches:
Query Match:	10.15%	Indels:
DB:	2	Gaps:
		5

US-10-705-757-1 (1-2623) X T15435 (1-409)

QY 351 ANSGCTTGTCCAAAATCAACTCGGTTCCGCACTCGCGCGCGCCCTGCAAGACATG 410

Db 1 MetTILuYarGyLeuLdlnAspLeuAlaValCySvSerrTgLnAlaIAspPheLeu 20

QY 411 CAGCCACCAACGCTGGCGCGCGCGCAAGAGAAAGAGCCCTCGAGTGGCACTACAGTG 470

Db 21 HisGluYbLys-----HisSerVallysgLunPheLybGlyTyrGluVal 36

QY 471 GGGCCGCTACTGGGCAAGCGCGGGCTTCGGCTCGGTTACTAGGC---ATCCGGTCTCC 522

Db 37 LeuAspGluILeGIYarGelyGelyPheGlyILeValYtrGluAlaThrThrArgGlnAsp 56

QY 528 GACAACTTCGCGGTGGCCATCAAAACAGCTGGAGAAAGACCGGATTTTCGACTGGGGAGAG 587

Db 57 GlyGlnGlnProValAlaValIysPheValGlnIlySvHsIAspSerTrr--Thr 75

QY 588 CTGCGCTAATGGACACTCGAGTCCCAATGGAACTGGCTCTGTAAGAAAGTGAAGCTCGGAT 647

Db 76 MetThrCyArgGlnLeuILeProSerGluValCySvHsIAsp---GluThrCyGluAsp 94

QY 648 TTCTCGGGGTATTAAGGCTCTGTGAACGTGTTCGAAGGCCCACTTCCTGCTGATC 707

Db 95 ILleProGlyValILeIyValLeuAspTrpPheAlaAsnSerIyGlyPheLeuILeVal 114

QY 708 CTGAGAGAGCCCGAGCCGGTCAAGATCTTTCGACTTCATCAGCGAAAGGGAGCCCTG 767

Db 115 MetGluAspProAlaAsnCyMetSerAspLeuPheAspMetValSerValILeGlyProLeu 134

QY 768 CAAGAGAGCTGGCCCGCAGCTTCTTCTGGAGAGTGTGAGAGCCGTGGCGACATGGCAC 827

Db 135 AsnGluAspMetGlyLysPheILePheYsgILeValILeThrThrValIAsnAspMetYr 154

QY 828 AAC---TGGGGGATGTACAACCGGACATCAAGAGCGAAACATCCTTAATCGACTCAAT 884

Db 155 SerLySvHsIGlyLeuLeuHsILeAspTrpILeYAspTrpILeAsnILeValIAsnMetAsn 174

QY 885 CGCGGAGACTCAAGCTCATGTGACTTCGGGATCGGGGGCGCTGCTCAAGACACCGTTTAC 944

Db 175 ThrGlyValValIysLeuValAspPheGlyAlaThrIleAlaTyrAlaGlyAlaThrIys 194

QY 945 ACGGACTTCGATGGGACCCGAGGTGTAAGCCCTCCAGAGTGATCCGCTACCATCGCTAC 1004

Db 195 LysGlnPheGlnGlyThrArgSerYxCysProProGluTyrPheArgAspGlnLeuYr 214

QY 1005 CATGGCAGAGTGGCGCGCAGATCGTGTCCCTGGGGATCCTGCTGATGATGATGGTGATGGA 1064

Db 215 LeuProLeuGluAlaThrSerTrpSerLeuGlyValLeuLeuPheIleLeuLeuThrGly 234

QY 1065 GATATTCCTTTCCGACATGACGAGAAGATCATCAGGGGCGCAGGTTTCTTTCAGCGCAGAG 1124

Db 235 LysLeuProPheArgAsnGluIleGlnIleCysLeuGlyAsnValLysPheProPheAsp 254

QY 1125 GTCTCTTCAGATGTCACGATCTCATAGATAGTGCCTGGCCCTGAGACCATCAGATAGT 1184

Db 255 LeuSerIysGluValCysGlnLeuValLysSerCysLeuThrThrSerThrSerIleArg 274

QY 1185 CCAACCTTCGAAGAATCCAGAACCATTCATGATGATGCA 1223

Db 275 AlaSerLeuAlaGlnIleAlaIleAlaHisProTrpMetGlu 287

RESULT 7

hypothetical protein 22B5.8 - fruit fly (*Drosophila melanogaster*)
 C|Species: *Drosophila melanogaster*
 C|Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
 C|Accession: T13741
 R|Murphy, L.; Harris, D.; Barrel, B.
 submitted to the EMBL Data Library, April 1999
 A|Description: Sequencing the distal X chromosome of *Drosophila melanogaster*.
 A|Reference number: Z17668
 A|Accession: T13741
 A|Status: preliminary; translated from GB/EMBL/DBJ
 A|Molecule type: DNA
 A|Residues: 1-1398 <MUR>
 A|Cross-references: UNIPROT:O77268; EMBL:AL031765; NID:e137523; PID:e1329905; PIDN:CAA2
 C|Genetic8:
 A|Cross-references: FlyBase:FBgn000067
 A|Introns: 205/3; 227/1; 322/3; 688/3; 782/3; 814/2; 1363/3
 ;Note: EG:22E5.8

Alignment Scores:

Pred. No.:	2,266-10	length:	1398
Score:	402.00	Matches:	123
Percent Similarity:	43.82%	Conservative:	72
Best Local Similarity:	27.64%	Mismatches:	154
Query Match:	8.39%	Indels:	96
DB:	2	Gaps:	17

US-10-705-757-1 (1-2623) X T13741 (1-1398)

[illegible]

Db	105	-----			107
QY	300	TCCTGCGCAGACTCTCTGGACAGCTCCCTGGCCGAGATTCCTGGAGTTGGATCTCTTG			359
Db	108	SerThrProGluProSerProThrSerSerAlaValGluAlaGlyGly-----			123
QY	360	TCCAAATCAACTGCTTGCCCACTGGCGCGCCCTCGAAGACCTGGACGCCAC			419
Db	123	-----			123
QY	420	AAGCTGGCGCCCGCAAGAG-----AAGAGCCCTGGAG---TCGACGATC			464
Db	124	-----IleSerGlyLeuValPheLeuLeuLeuValGluProMetArgValGlyPheTyr			141
QY	465	CAGGTGGCCCGCTACTATGGCGAGCGCGAGCTTCGGCTCGATC---TACTACGACATCCG			521
Db	142	Asp1LeuIleuArgThrIleGlyLeuGlyValAsnPheAlaValValValValMetAlaArgHisArg			161
QY	522	GTCCTCCGACAACTTGGCCGCTGGCCATCAACACCTGGAGAAAGACCGGATTTCCGACTGG			581
Db	162	IleThrIlyuAsn---GluValAlaIleLeuValIleLeuPheIlySerGlnLeu-----			177
QY	582	GGAAGACGCTGATATGGACATCGAGTCCCAATGGAAAGTGCCTCGAGAAAGATGAGC			641
Db	178	--AspGlnThrAsnLeuGlnValValTyrArgGluValGluIleMetLeuValPheLeuVal			196
QY	642	TCGGGTTTCTCCGCGCTATGAGCTCTGAGCTGGATCGATTGCAAGAGCCGACATTTGCTC			701
Db	197	-----HisProHisIleIleLeuLeuTyrGlnValMetGluThrIlyuAsnMetIleTyr			214
QY	702	CTGATCTCGAGAGAGCCCGGACCCGCTGCAAGATCTTTCGACTTCATCAGCAAAAGGGA			761
Db	215	IleValSerGlyTyrAlaSerGln---GlyGluIlePheAspTyrIleAlaLeuTyrGly			233
QY	762	GCCCTGCAAGAGAGAGCTGGCCCGGACGCTTCTTGGAGGAGTGGAGGCGCTGGCGGAC			821
Db	234	ArgPheSerSerGlnSerAlaAlaAspPheLeuPheThrGlnIleIleSerAlaValGluTyr			253
QY	822	TGCCCAACTGCGGGGTGCTACACCGGACATCAAGACGAAACATCTTTATGCACTC			881
Db	254	CysHisIleuValuValGlyIleValHisArgPheLeuValAlaGluAsnLeuLeuAspLeu			273
QY	882	AATCGCGCGAGCTCAAGACTCATGACTTCGGG---TCGGGGGCGCTGCTCAAGACACC			938
Db	274	AsnMet---AsnIleLeuValIleAlaAspPheGlyPheSerAsnHisPheIlyProGlyGlu			292
QY	939	GTCACACAGCACTCGATGGGACCCGAGATGATACCTCCAGAGTGGATCCGCTACAT			998
Db	293	LeuLeuAlaThrTyrCysGlySerProProTyrAlaAlaProGluValPheGluGlyLeu			312
QY	999	CGCTACACATGCGAGGATGGCGCGGACCTGTGCTCCCTGGGACATCGCTGATATGATGATG			1058
Db	313	GlnTyrThrGlyProGluIleAspIleThrSerLeuGlyValIleValLeuTyrValLeuVal			332
QY	1059	TGTGGAGATATCTCTTTCGAGCATGAC-----GAAGACATCATCAGG			1100
Db	333	CysGlyAlaIleuProPheAspGlySerThrLeuGlnSerLeuArgAspArgValIleuSer			352
QY	1101	GGCCAGGTTTCTTCAAGCAGAGGCTCTTTCAGAAATGTCAGCATTCATTAATGAGTGC			1166
Db	353	GlyArgPheArgIleProPhePheMetSerSerGlnCysGlyHisIleuValIleArgArgMet			372
QY	1161	TTGGCCCTCGAGACATCATGATAGGCAACCTTCGAGAAATCCAGAACATCATCATGATG			1220
Db	373	LeuValLeuGluProHisArgTyrThrIleAspGlnIleuValArgHisIleArgTyrMet			392
QY	1221	CAAGATGTTCTCTG			1235
Db	393	CysProGluLeuLeu			397

protein kinase mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Aug-2004
C:Accession: I49072
R:Ruiz, J.C.; Conlon, F.L.; Robertson, E.J.
Mech. Dev. 48, 153-164, 1994
A:Title: Identification of novel protein kinases expressed in the myocardium of the developing mouse heart
A:Reference number: I49071; MUID:95200798; PMID:7893599
A:Accession: I49072
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-481 <RBS>
A:Cross-references: EMBL:U11494; NID:G595420; PIDN:AAA67926.1; PID:G595421
C:Superfamily: protein kinase homology
C:Keywords: ATP
E:71-324/Domain: protein kinase homology <KIN>
E:79-87/Region: protein kinase ATP-binding motif

Alignment Scores:

Pred. No.:	4.29e-10	Length:	488
Score:	397.50	Matches:	139
Percent Similarity:	42.17%	Conservative:	79
Best Local Similarity:	26.89%	Mismatches:	166
Query Match:	8.30%	Indels:	113
DB:	2	Gaps:	21

US-10-705-757-1 (1-2623) X I49072 (1-481)

Qy	15	GCATGGGCGCGCTCCGCGCGAGTCCGCGAGGCGCTGACGTTGGCTCCGACTGCGCCCTCG	212
Db	5	AlaArgAlaValAlaAlaAlaLeuAlaAlaAlaAlaAlaGlyThrAlaGlyThrGlyAlaGlu	24
Qy	213	GCCTTCGCGAGCGGAGCAcAGCCGCGACCGGAGCAcAGCAcAGCAcAGCCAGCCAGCA	272
Db	25	LeuAlaAlaGluThrGlyAlaValAlaAlaSerArgVal	35
Qy	273	TACCTTCGAGCAcAGCCCGGCTCCGAGCTTCGCGAGCTCCTTCGCAcCTCCCTCGC	332
Db	36	-----GlySerArgArgAlaAlaGluValArg	44
Qy	333	CGACATTCGAGGTTGATGCTTCGTTCcAAATTCATCTGATCGCTGCCACTGCGGCGC	392
Db	45	ProGluAla-----MetValIle-----MetSerGluPheArgAla	56
Qy	393	GCGCCCTCGCAcGACTGCAcCGCAcCAAGCTGGCGCCCGGAGAGAAcAGACCCCTG	452
Db	57	ValProSer-----GlyThrGlyArgSerGlnIlyProIeu	68
Qy	453	GAG---TCCGAGTACcAGTGGGCGCCGCTACCTGGGAGCGCGGCTTCGCTCGCTC---	506
Db	69	ArgValGlyPheIlyAspAlaGluThrGlnLeuGlyIlyGlyAlaPheAlaValAlaLys	88
Qy	507	TACTCAGGcATCCGCGCTTCcCGACAACTTCGCGGTGCATCAAAcAGTGAAGAAcAG	566
Db	89	LeuArgGlyHisArgValThr---LysThrGlnValAlaIleIlyIleIleAspIlyThr	107
Qy	567	CGGATTTCCGACTCGGGAGAGcTGCCTTAATGCGACTCGAGTGCcCCATGAAGTGTCTG	626
Db	108	ArgIleu-----AspSerSerIleuGlnIlyIlyTyrArgGluValGlnIleu	123
Qy	627	CTGAAGAGGTGAGCTCGGATTTCCTCCGCGCTATTAGAGTTCcCGGACTGGTTCGAGAGG	686
Db	124	MetIlyLeuIleuAsn-----HisProAlaIleIleIlyIlyIleuIlyArgIleValMetGluThr	141
Qy	687	CCCGACAGTTTCGTCTGATCTCGAGAGAGCCCGAGCCGAGTGCAGATCTTCCTGACTTC	746
Db	142	LysAspMetLeuIlyTrIleValThrGluPheAlaIlyAsn---GlyGluMetPheAspTyr	160
Qy	747	ATACCGGAAGGAGGAGCCCTCGMAAGAGAGcTGTGGCCGCGCAcGTTCTTCCTGCAAGTCTG	806
Db	161	LeuThrSerArgGlnIlyHisLeuSerGlnIlyuGlnIlyAlaIlyGlnIlyIlyPheTTPGlnIleIeu	180
Qy	807	GAGGCGGTGCGGAGCTGCGCAcATCTCGGGGTGTCAcCGCGCACTcAGAGCAAAAC	866

[illegible]

A:Cross-references: UNIPROT:Q38997; GB:M93023; NID:gl66599; PIDN:AAA32736.1; PID:gl66600
R:Thummler, F.; Kirchner, M.; Teuber, R.; Ditttrich, P.
Submitted to the EMBL Data Library, May 1995
A:Description: Differential accumulation of the transcripts of 22 novel protein kinase g
A:Reference number: S58256
A:Accession: S58256
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 144-198 <THU>
A:Cross-references: EMBL:X86966; NID:g928909; PIDN:CAAG0529.1; PID:g928910
R:Thummler, F.; Kirchner, M.; Teuber, R.; Ditttrich, P.
Plant Mol. Biol. 29, 551-565, 1995
A:Title: Differential accumulation of the transcripts of 22 novel protein kinase genes i
A:Reference number: S66314; MUID:96123233; PMID:8534852
A:Accession: S66314
A:Molecule type: DNA
A:Residues: 144-198 <TH2>
A:Cross-references: EMBL:X86966; NID:g928909; PIDN:CAAG0529.1; PID:g928910
C:Comment: This enzyme plays an important role in a signal transduction cascade regulat
C:Gene(s):
A:Gene: AK1n10; AK21
A:Introns: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3
C:Function:
A:Description: catalyzes the formation of peptidyl-L-serine-phosphate or peptidyl-L-threonin
C:Superfamily: AMP-activated protein kinase; protein kinase homology
C:Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F:1-7-271/Domain: protein kinase homology <KIN>
F:25-33/Region: protein kinase ATP-binding motif
F:48,67,142,144/Active site: Lys, Glu, Asp, Lys status predicted
F:147,151/Binding site: magnesium (Asn, Asp) status predicted

Alignment Scores:

Pred. No.:	1.37e-09	Length:	512
Score:	385.50	Matches:	138
Percent Similarity:	46.15%	Conservative:	78
Best Local Similarity:	29.49%	Mismatches:	182
Query Match:	8.05%	Indels:	70
DB:	1	Gaps:	19

US-10-705-757-1 (1-2623) x JC1446 (1-512)

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425 GCGCGCCGGCAGAGAGAGAGAGCCCTTGAAAGTCCGATACCAAGTGGGCCCGCATCTGGG 484
426 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
427 GlySerAlaArgSerGly-ValGluSerIleLeuProAsnIleTyrLeuGluValArgThrLeuGI 26
485 CAGCGGCGCGCTTCGGCTCGCTCTACTACGAGCATCCGCTCCGCAACAATTGCGGGTGGC 544
486 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
487 yIleGlySerHeGlyArgValIleAlaGluHisAlaLeuThrArgIleValValAl 46
545 CATCAACAACGTGAGAGAGACCGGATTTCCGATCGGAGAGACTGCTTAATGCGACTCG 604
546 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
547 aIleLeysIleLeuAsnArgValGlyIleLeuAsn-----MetGluMetGluGluTly 63
605 AGTGCCCATGGAAGTGTCTCGTGAAGAGAGGTGACTCGGGATTTCTCCGGCGTCAATTAG 664
606 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
607 bValArgArgGluIleIleValIleLeuArgLeuPheMet-----HisProHisIleIleArg 81
665 GCTCTCTGACTGGTTCCGAGAGGCCCGACAGTTTCGTCCTGATCCTGAGAGAGCCCGAGCC 724
666 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
667 gLeuTyrIleValIleGluIleThrProThrAspIleTyrLeuValMetGluTyrValAlaAsn 101
725 GGTGCAAGATCTCTTCGACTTCATACAGAAAGAGGCCCTTGAGAGAGAGCTGGCCCG 784
726 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
727 r--GlyIleuLeuPheAspTyrIleValGluIleValArgLeuGluGluAspGluAlaAsr 120
785 CAGCTTCTTCTGGCAGGTGCTGAGAGCCGTGCGGCACTGCCACAACCTCGGGGTGCTACA 844
786 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
787 gAsnHehGluGluGluGluIleIleSerGlyValGluTyrGlySerHisValArgAsnMetValValHis 140
845 CCGCGACATCAAGACGAGAAACATCTTATGACTTCAATGCGCGGAGCTCAAGCTCAT 904
846 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
847 sArgSerPheuIysProGluAsnIleuLeuIleuAsp---SerIysCysAsnValIleValAl 159
140 sArgSerPheuIysProGluAsnIleuLeuIleuAsp---SerIysCysAsnValIleValAl 159

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QY	CGACCTTCGGGTCGGGGGGCGCTGCCTACAGGACACCGCTCCACCGACTTCGAT---GGGAC	961
Db	159 AAsPPhEiLYeuSerAEnIIMeCAtAgARGLYnIbHeuLYnThrSerCYGSLYSe	179
QY	CGAGATGATAGCGCCCTCCAGATGAGATCCGCTACATCGCTACCATGGCAGAGTGGCGGCG	1021
Db	179 rProAenThrAlaAlaProGluValIIeSerGlyLYbLeuThrAlaGlyProGluValAa	199
QY	1022 AGTCTGGTCCCTGGGGATCTGCTGTATGATATGATGATGTGTGGAGATATCTTTCCAGCA	1081
Db	199 pValTrpSerCYbSLYValIIeLeuThrAlAlaLeuLYcYbSLYThrLeuProPhaAep--	218
QY	1082 TGAGGAAGAGTCT-----ATCAGGGGCGCAGGTTTTTC---TTCAGGCA	1120
Db	219 -AspGLuAEnIIeProAEnLeuPhElybLYbLYbGLYGLYLeuThrLeuProSe	238
QY	1121 GAGGGTCTCTTCAGAAATGTCAGACTTCATTAGATGGTGTCTGGCCCTGAGACCATCAGA	1180
Db	238 rHisLeuSerProGlyAlaArgARbLeuIIeProArgMeLeuValValARProMeuLY	258
QY	1181 TAGGCCAACTTTCAGAAATATCCAAACCATCCATGATGACAGATGTTCTCTGCCCA	1240
Db	258 sArgValThrIIeProGluIIeArgGlnARProThrPhEgIn--AlaHisLeuProAR	277
QY	1241 GGAAATGCTGAGATTCACCTCCACAGCGTCTGCCCGGGCGCCGCAAAATAGACGCTTT	1300
Db	277 gTyrLeuAlaVal--ProProARbARbThrValGlnGlnAlaLYbLYbIIe-AspGLu--	295
QY	1301 CTGGCAGGCTCTCCCTCTCTTGTTCAGATGCCAGGAGGAGGAAAGTTCTGTCTCCAGC	1360
Db	296 ----GluIleLeuGlnGluValIIeAEnMeGlyPhaAspArgAEnIIbLYbIIeGluSe	314
QY	1361 TTCGGAGTACCAAGTACACGCTCTGCCAGACAGACAGTGGTGTATACAGAAACAACAT	1420
Db	314 rLeuArg-----AsnArgThrGlnAAsnARbGLYThrValThrTyrrLeuIIeLe	331
QY	1421 TTACAACTCATTCACAGATCCAGAGCCCTGAGAGCTGCTCCCAACAGTGGG-----	1472
Db	331 nAspARbARbPhEArg-----AlaSerSerGlyTyrrLeuG1	343
QY	1473 -----GAGAGTGACTCTCCAGGGGCTTAGCGCTCAACTCTCCCATAGATACT	1522
Db	343 yAlaGluPhEgInGlnThrMetGluGlyThrProArgMeHisProAlaGluSerValAl	363
QY	1523 CTCTTCT---TCTCATAGTGTCCAGCAATTCGATGAGATATTCGCGGGGTGGG	1579
Db	363 aSerProValSerHisARGLeupProGlyLeuMeGluThrGln-----G1	378
QY	1580 GGTGGGGGTGGGCGAAGACCTGCCCAATGAACTCTTCTTATCATGATGTTCTGTGAAT	1639
Db	378 yValGlyLeuArgSerGlnTyrrProValGln-----	388
QY	1640 GCCGGAAATGGGTCAAGTACGGGGGGAACAAGSTTGGAGTGGATAGAGTACACACTTTTA	1699
Db	389 -ArgLYsTrpAla-----LeuGlyLeuGln--SerArgAlaHis-----	400
QY	1700 AGTCCCTGTCACTCTTCCGACTCTTCTGAGTGCCTT-----CTGCGGAGACTCCGCGC	1753
Db	401 -----ProArgGluIurLeuMetThrGluValIIeLYbAlAlaLeuGlnARbLeuAEnV	417
QY	1754 TGTGCTGGAGAA 1767	
Db	417 aLYcTrpLYbLYbSe 421	

RESULT 10

16-01-1999 #text_change 09-Jul-2004
 C:Accession: F10449
 C:Date: 16-01-1999 #sequence_revision
 N:Alternate names: Sucni-related protein kinase
 C:Species: Cucumis sativus (cucumber)
 R:Gumpel, N.J.
 submitted to the EMBL Data Library, December 1996


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Db      859  ILEHLEASNAHrgLunHtIeTylleVallelleYMeIlePhelyeGLunHrgIleLeu 878
QY      573  ---TCCGATGGGGAAGAGCTTAATGGACATCGAGTCCCATGGAAGTGGCTGGG 629
Db      879  ValAspThrTrpValArgAspArgLysLeuGlyThrtIleProSerGluIleGlnIleMet 898
QY      630  AAGAAAGTGAGC---TCGGGTTTCTCCGGCTCATTAAGCTCTCGAGCTGTTCGAGAG 686
Db      899  AlathleuAsnLysAsnSerGlnGluAsnIleLeuLysLeuAspPhePheGluAsp 918
QY      687  CCCGACAGTTTCCTCTGATCTCGAGAGGCGCCGAGCCGGTGCAG-----731
Db      919  AspAspTyrTrpTyrIle-----GluThrProValHISglYgluThrGlySer 934
QY      732  ---GATCTTCGATCTTCATCGAGAAAGGGAGCCCTCGAAGAGAGCTGGCCCGCAC 788
Db      935  IleAspLeuPheAspAlaIleGluPheLysLysAspMetValGluValAlaLysLeu 954
QY      789  TTCCTTGGCAGAGTGGTGGAGCGCGGACATCGACAACTGCGGGTGTCAACCGC 848
Db      955  ValPheLysGlnValValAlaSerIleLysHISleuHISAspGlnGlyIleValHISArg 974
QY      849  GACATCAAGAGCAAGAAACATCTTATCGACCTCATCGCGGAGCTCAAGCTCATGAC 908
Db      975  AspIleLysAspGluAsnValIleValAsp---SerHISglYpHeValLysLeuIleAsp 993
QY      909  TTCGGGTGGGGGCGGTGCTCAAGAGACCGCTGTACAGGACTTCATGAGGACCGAGTG 968
Db      994  PheGlySerAlaAlaTyrIleLysSerGlyProPheAspValPheValGlyThrMetAsp 1013
QY      969  TATAGCCCTTCAGAGTGATCCGCTACATCGCTCAATCGAGCGAGCTGGCGAGTCTG 1028
Db      1014  TyrAlaAlaProIleValLeuGlyLysSerSerTyrLysArgProGlnAspIleTrp 1033
QY      1029  TCCCTGGGAGATCTCTGTATGATATAGTGTGTGGAGATTTCTTCCAGCATGACGA 1088
Db      1034  AlaLeuGlyValLeuLeuTyrTrpIleLysGluAsnProTyrTrpAsnIleAsp 1053
QY      1089  GAGTATCATGAGGGCGGAGTTTCTTC-----AGCGAGAGGCTCTTCAGAAATGTCAG 1142
Db      1054  GluIleLeuGluIleGluLeuAspPheAspLysSerGluIleValSerGluGlySile 1073
QY      1143  CATCTATAGATAGTGTGCTTGGCCCTGAGACATCATGATCGAGCAACTTCGAGAAATTC 1202
Db      1074  SerLeuIleLysArgIleLeuThrArgGluValAspLysArgProThrIleAspGluIle 1093
QY      1203  CAGAACCATTCATGATGCAA 1223
Db      1094  TyrGluAspLysTrpLeuLys 1100

RESULT 12
T18611
Probable serine/threonine-specific protein kinase (EC 2.7.1.-), long splice form - Caen
N:Contains: Probable serine/threonine kinase, short splice form
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18611; T18610; T23144; T23143
R:McMurray, A.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z18997
A:Accession: T18611
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Cross-references: UNIPROT:Q9TW45; EMBL:Z81027; PDB: CAB54179.1; GSPDB:GN00023; CESP:H3
A:Status: translated from GB/EMBL/DBJ
A:Accession: T18610
A:Molecule type: DNA
A:Residues: 1487,536-1192 <W112>
A:Cross-references: EMBL:Z81027; PDB: CAB54178.1; GSPDB:GN00023; CESP:H39E23.1b
R:McMurray, A.

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submitted to the EMBL Data Library, June 1997
A:Reference number: Z18996
A:Accession: T23144
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1192 <W113>
A:Cross-references: EMBL:Z96102; PDB: CAB54263.1; GSPDB:GN00023; CESP:H39E23.1a
A:Experimental source: clone H39E23
A:Accession: T23143
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-487,536-1192 <W114>
A:Cross-references: EMBL:Z96102; PDB: CAB54262.1; GSPDB:GN00023; CESP:H39E23.1b
A:Experimental source: clone H39E23
A:GeneticS:
A:Gene: CESP:H39E23.1a; CESP:H39E23.1b
A:Map position: 5
A:Intron: 10/3; 33/3; 67/3; 139/2; 183/3; 451/3; 535/3; 631/1; 825/2; 914/3; 992
C:Keywords: alternative splicing; ATP; phosphotransferase; serine/threonine-specific pr
F:1-1192/Product: Probable serine/threonine-specific protein kinase, long splice form #
F:1-487,536-1192/Product: Probable serine/threonine-specific protein kinase, short spli

Alignment Scores:
Pred. No.: 3,94e-09 Length: 1192
Score: 373.00 Matches: 116
Percent Similarity: 44.91% Conservative: 78
Best Local Similarity: 26.85% Mismatches: 166
Query Match: 7,79% Indels: 72
DB: Gaps: 14

US-10-705-757-1 (1-2623) x T18611 (1-1192)
QY      6  GGCCGAGAGAGTGGTGGCAGCGGC-----GGCGCGGG 41
Db      52  GlyThrArgLysSerSerGlySerGlyLeuYsrThrAlaAsnLeuYsrProAlaArg 71
QY      42  ACCGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 101
Db      72  ProSerThrGluSerSerThrSerSerSerHISArgArgProAla-----87
QY      102  GACGAGCCCAAGAGCCGCTACCCCGCTTCAGCGCTGCCGAGCCCGCTGGCGGG 161
Db      88  GlnGluMetAsnGlyThrSerThrAlaThrAlaThrGlyGlyGlyThrSerGlyAla 107
QY      162  CTTCCCGCGAGTCCCGGCGGCTCAGTTGCTCTCCGAGTCCGCGCTTCGGCG 221
Db      108  ThrThrAlaSerSerGlyAlaProAlaAlaSerSerGlyLysSer-----Ala 125
QY      222  CAGCGCAGCAGCAGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 281
Db      126  ArgTyrSerSerSerGlyArgSer-----HisProThrSerGlySerSerSerSer 142
QY      282  CACAGCCCGGCTCCGGCTCTCGCGAGCTCTCTGGACACTCTCGGCGGACACTTCT 341
Db      143  HisAlaArgSerThrGlyGlnSerGlyMetSerSerSerAlaAlaArgArgAsnAsp 162
QY      342  GAGAGTGGATGCTCTTGGCAAAATCAACTGCTTGCACCTGGCGCGCGCCCTGC 401
Db      162  -----162
QY      402  AAGACCTTGACAGCAGCAGCAGAGTGGCGCGCGGCAAGAGAGAGCCCTGAGTGCAG 461
Db      163  GlnAspValHISValGlyLys-----169
QY      462  TACCAAGTGGCGCCCTACTGGGCGAGCGCGGCTTCGGCTCGGTACTCAGGACTCCG 521
Db      170  TyrLysLeuLeuLysThrIleGlyLysGlyAsnPheAlaLysValLysLeuAlaLys 189
QY      522  GTTCCGACAACTTGGCCGGTCCCATCAACAGTGAAGAGAGACCGGATTTCCGACTG 581
Db      190  ValIleThrGlyHISGluValAlaIleLysIleIleAspLysThrAlaLeuAsn-----207
QY      582  GGAGAGTGGCTTAATGCG---ACTGAGTGGCCATGAGAGAGTGGTCTGTGAAGAGTGG 638

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Db      208  -----ProSerSerLeuGlnLysLeuPheArgIleValLysIleMetLysGlnLeu 224
QY      639  AGCTGGGTTTCTCCGGCGTCATTTAGGCTCTGGAGCTGGTTCGAGAGCCCGACAGTTTC
Db      225  Asp-----HisProAsnIleValLysLeuTyrGlnValMetGlnThrGlnThrLeu 242
QY      699  GTCCATGCTGGAGAGCCCGGAGCGGTGCAGATCTCTTCATCTTCATCAGGAAAG 758
Db      243  TyrLeuValLeuGlnTyrAlaSerGly--GlyGlnValPheAspTyrLeuValAlaHis 261
QY      759  GAGACCTGCAAGAGAGAGCTGGCCCGGAGCTTTCTGGAGAGCTGGAGGCGGTGG 818
Db      262  GlyArgMetLysGlnLysGlnAlaArgAlaLysPheArgGlnIleValSerAlaValGln 281
QY      819  CACTGCCACAACTGGCGGGTGTACACCGGACATCAAGAGACGAAACATCTTATGAC 878
Db      282  TyrLeuHisSerLysAsnIleIleHisArgAspLeuLysAlaGlnAsnLeuLeuAsp 301
QY      879  CTGAATGGGGGCGAGCTCAAGCTCATGAGCTTCGGG--TCGGGGGGCGCTCAAGAG 935
Db      302  GlnAspMet--AsnIleLysIleAlaAspPheGlyPheSerAsnThrPheSerLeuGly 320
QY      936  ACCGTCACACGAGACTTCGATGGGACCCGAGTGAATGAGCCCTCAGAGTGAATCCGCTAC 995
Db      321  AsnLysLeuAspThrPheCysGlySerProProTyrAlaAlaProGlnLeuPheSerGly 340
QY      996  CATCGCTACCATGGGAGAGTGGCGGCGAGTGTGCTCCCTGGGAGATCTGCTATGATG 1055
Db      341  LysLysTyrAspGlyProGlnValAspValIlePheSerLeuGlyValIleLeuTyrThrLeu 360
QY      1056  GTCTGTGAGATATTCCTTTC-----GAGCATGACGAAAGATCATC 1097
Db      361  ValSerLysSerLeuProPheAspGlyGlnAsnLeuLysGlnLysGlnValLeu 380
QY      1098  AGGCGACAGGTTTCTTTCAGAGGACAGGCTCTTCGAAATGTCAGCATCTTAATGATG 1157
Db      381  ArgGlyLysTyrArgIleProPheTyrMetSerThrAspCysGlnAsnLeuLysLys 400
QY      1158  TGGTTGGCCCTGAGACCATCATAGGCCCACTTCGAGAAATCCAGAACCATTCATG 1217
Db      401  PheLeuValIleAsnProGlnArgArgSerSerLeuAspAsnIleMetLysAspArgTyr 420
QY      1218  ATG-----CAAGATGTTCTCTGCTCC 1238
Db      421  MetAsnValGlyTyrGlnAspAspGlnLeuLysPro 432

RESULT 13
T07788
probable serine/threonine-specific protein kinase (EC 2.7.1.1-) SNF1 - potato
N:Alternate names: ScdSNF1 protein
C:Species: Solanum tuberosum (potato)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C:Accession: T07788
R:Lakatos, L.; Banfalvi, Z.
submitted to the EMBL Data Library, January 1997
A:Reference number: Z16133
A:Accession: T07788
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-512 <LAK>
A:Cross-references: UNIPROT:O04122; EMBL:U03797; NID:G1935915; PIDN:AAB52224.1; PID:G193
C:Genetic:
A:Gene: SNF1
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C:Superfamily: AMP-activated protein kinase; protein kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
P:17-271/Domain: protein kinase homology <KIN>

Alignment Scores:
Pred. No.: 6.53e-09 Length: 512
Score: 369.50 Matches: 124

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Percent Similarity: 44.62% Conservative: 79
Best Local Similarity: 27.25% Mismatches: 180
Query Match: 7.72% Indels: 72
DB: 2 Gaps: 18

US-10-705-757-1 (1-2623) x T07788 (1-512)

QY      462  TACCAGTGGGCGCCGCTCATGGGACGCGGCTTGGCTCGGTCACTACGACATCCG 521
Db      19  TyrLeuLeuGlyLysThrLeuGlyIleGlySerPheGlyLysValLysIleAlaGlnHis 38
QY      522  GTCTCCGACAACTTGGCCGATCAACACAGTGGAGAAAGGACCGGATTTCCAGTGG 581
Db      39  ThrLeuIleGlyHisLysValAlaValLysIleLeuAsnArgLysIleAlaGlnHis 57
QY      582  GAGAGCTGCTTAATGACATCGAGTGCCTGAGAGAGTGGCTCTGCTGAGAAAGTGA 641
Db      58  -----MetAspMetGlnGlnLysValSerArgGlnIleLysIleLeuArgLeuPheMet 75
QY      642  TCGGTTTCTCCGGCGTCATTTAGGCTCTGAGCTGTGAGAGGCCGACATTCGCTC 701
Db      76  HisGlyHis-----IleSerArgLeuTyrGlnValIleGlnThrProSerAspIleTyr 93
QY      702  CTGATCTGGAGAGGCGCGGCGGCGGAGGACGAAAGATCTTCGAGCTTCATCCAGAAAGGGA 761
Db      94  ValValMetGlnTyrValLysSer--GlyGlnLeuPheAspTyrIleValGlnLysGly 112
QY      762  GCCCTGCAAGAGAGAGCTGGCCGAGCTTCTTGGCAGAGTGGAGGCGGTGGCGGAC 821
Db      113  ArgLeuGlnGlnAspGlnAlaArgAsnPhePheGlnGlnIleIleSerGlyValGlnTyr 132
QY      822  TGGCACAACTGGCGGGTGTCTACACCGGACATCAAGAGACGAAACATCTTATGACCTC 881
Db      133  CysHisIleAsnMetValValHisArgAspLeuLysProGlnAsnLeuLeuAsp--- 151
QY      882  AATCGGGGAGAGTCAAGCTTCAGCTTCGAGTGGGGGCGGTGTCMAAGACACGCTC 941
Db      152  SerLysTyrAsnAlaLysIleIleAlaAspPheGlyLeuSerAsnIleCysArgAspGlyHis 171
QY      942  TACACGCACTTCGAT--GAGACCCGAGTGTATAGCCCTCAGAGTGAATCCGCTACAT 998
Db      172  PheLeuLysThrSerCysGlySerProAsnTyrAlaAlaProGlnValIleSerGlyLys 191
QY      999  CGCTACATGGCAGAGTGGCGGCGAGTGTGCTCCCTGGGAGATCTGCTGATGATGATG 1058
Db      192  LeuTyrAlaGlyProGlnValAspValTyrSerCysGlyValIleLeuTyrAlaLeuLeu 211
QY      1059  TGTGAGATATCTCTTTCGAGCATGAC-----CAAGATCATCAAG 1100
Db      212  CysGlyThrLeuProPheAspAspGlnAlaIleProAsnLeuPheLysIleLysGly 231
QY      1101  GGCAGAGTTTCTTTCAGGAGAGAGTCTCTTTCAGATGTCACAGATCTTATGATGATG 1160
Db      232  GlyTyrIleThrLeuProSerHisLeuSerAlaGlyAlaArgAspLeuLeuProAspMet 251
QY      1161  TTGGCCCTGAGACCATCATAGGCCCACTTCGAAAGAAATCCAGAAACATTCATGATG 1220
Db      252  LeuIleValAspProMetLysArgMetThrIleProGlnIleArgLeuHisProTyrPhe 271
QY      1221  CAAGATGTTCTCTGCGCCAGGAAACATGTCAGATCCACCTCAACAGCTTCGCGGGG 1280
Db      272  Gln-----AlaHisLeuProArgTyrLeuAlaValProPro 283
QY      1281  CCCAGCAATATGACAGCTTTCTGGAGAGGCTCCCTCTTTCAGATGCCCCGAGGAG 1340
Db      284  ProAspThrMetGln-----Gln 289
QY      1341  GGAAGCTTCTGCTTCAGCTTCCGAGTACAGTGAACAGTCTGCGCAAGAGACAGT 1400
Db      290  AlaLysLysIleAspGlnGlnIleLeuGlnGlnValIleValMetGlyPheAsp----- 307
QY      1401  GCTTATATCAGGAAACAATTACATTCATCCAGATCCGAGGCGCCCTGAGAGCTGCT 1460

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Db 308 -----ArgAsnAsnLeuThrGluSerLeu-ArgAsnArgValGln----- 320
QY 1461 CCCAAGAGGGGAAAGAGGACTCTCCAGGGGCTCCAGGCCCTCAACTCTCCCATGATA 1520
Db 321 -----AangLuglyThrValProlyrTyrlleuLeuAspAsnArgHisArgVala 337
QY 1521 CTCTCTTCTTCATGATGCTGTCGACATTGCTGACACTGMAATATATCCGGGGGTGGGG 1580
Db 337 lserThrGlyrTyrlleuGlyAlaGluPheGlnGlnGlnSerMetGluTy-----G 353
QY 1581 GTGGGGGTGGGCAAA-----CCCTGCCAATGACACTCTTTC---TT 1619
Db 353 yTyraAsnArglLeaAsnSerAsnGluProleuLeuProCyS---TrpGlnArgPheProG 372
QY 1620 CATCATGAGATTCTGCTGAAATGCCGCGATGGGTGAGGTAGGGGGAAACAAGTTGGGATG 1679
Db 372 ylleMetAspTyrlleGlnGlnAlaArgGlnPheProLleGlnArgLysrTrp---Al 391
QY 1680 GATAGGACTA-----GCACATTTTAAATCCCTGTCGACCTCTTCCGACTCTTCTGA 1730
Db 391 aleuGlyLeuGlnSerArgAlaHis-----ProArgGlnLleMetThrG 406
QY 1731 GTGCTT-----CTGTGGGACTCCGGGCTGTGCTGGAGAAA 1767
Db 406 vAlleuLysAlaLeuGlnGlnLeuAsnValCystrIlySlys 420
RESULT 14
S33653
probable serine/threonine protein kinase (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
N/Alternate names: protein YAL0102; protein YAL017w; secretory protein SSP138
C/Species: Saccharomyces cerevisiae
C/Date: 30-Sep-1993 #sequence revision 02-Aug-1994 #text_change 16-Aug-2004
C/Accession: S33653; S36717; S36732; JH0486
R/Clark, M.W.; Zhong, W.W.; Keng, T.; Storme, R.K.; Ouellette, B.F.F.; Barton, A.; Kabac
Yeast 9, 543-549, 1993
A/Title: The YAL017 gene on the left arm of chromosome I of Saccharomyces cerevisiae enc
A/Reference number: S33653; WUID:93311122; PMID:8322517
A/Accession: S33653
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-1358 <CL>
A/Cross-references: UNIPROT:P31374; EMBL:L05146
R/Ouellette, B.F.; Clark, M.W.; Keng, T.; Storme, R.K.; Zhong, W.; Zeng, B.; Fortin, N.; D
submitted to the EMBL Data Library, January 1993
A/Description: Sequencing of Chromosome I from Saccharomyces cerevisiae: analysis of a 3
A/Reference number: S36711
A/Accession: S36717
A/Molecule type: DNA
A/Residues: 1-864,867-1358 <QOE>
A/Cross-references: EMBL:L05146; NID:G171851; PIDN:AAC04940.1; PID:G171858; MIPS:YAL017W
R/Clark, M.W.; Zhong, W.W.; Keng, T.; Storme, R.K.; Barton, A.; Kaback, D.B.; Bussey, H.
Yeast 8, 133-145, 1992
A/Title: Identification of a Saccharomyces cerevisiae homolog of the SNF2 transcriptions
A/Reference number: S22266; WUID:92221690; PMID:1561836
A/Accession: S36732
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-862 <CL>
A/Cross-references: EMBL:S93805
R/Sidhu, R.S.; Mathew, S.; Bollon, A.P.
Gene 107, 111-118, 1991
A/Title: Selection of secretory protein-encoding genes by fusion with PHO5 in Saccharomy
A/Reference number: JH0483; WUID:92077420; PMID:1743509
A/Accession: JH0486
A/Molecule type: DNA
A/Residues: 1-72, 'E', 74-154 <SID>
C/Genetics:
A/Genes: SGD:FUN31; SSP138
A/Cross-references: SGD:S0000015; MIPS:YAL017W
C/Map position: 1L
C/Superfamily: protein kinase homology
C/Keywords: ATP; glycoprotein; phosphotransferase; serine/threonine-specific protein kin
P1096-1356/Domain: protein kinase homology <KIN>

F1104-1112/Region: protein kinase ATP-binding motif
F18,128/Binding site: carbohydrate (Asn) (covalent) #status predicted
F1123/Active site: Asp Metacis predicted
Alignment Scores:
Pred. No.: 6,91e-09 Length: 1358
Score: 367.00 Matches: 87
Percent Similarity: 54.26% Conservative: 53
Best Local Similarity: 33.72% Mismatches: 102
Query Match: 7.66% Indels: 16
Gaps: 6
US-10-705-757-1 (1-2623) x S33653 (1-1358)
QY 480 CTGGCAGCGGGGCTGCTGGCTCGCTCACTGAGCATCCGCTCCGACAACTTGGCCG 539
Db 1104 MetGlyGlnGlyAlaTyrlleYylsValAsnLeuCySllleHlyblybAsnArgTyrlle 1123
QY 540 GTGGCATCAAAACAGCTGGAAGAAGACCGGATT-----TCGACCTGGGAGAGCTGCT 593
Db 1124 ValValLleTyMetLlePheTySgluArgLleValAspThrTrpValArgAspArg 1143
QY 594 AATGGCACTCGAGTCCCATGGAAGTGTCTGCTGGAAGAGTACG---TCGGGTTTC 650
Db 1144 lylleuGlyThrLleProSerGlnLleGlnLleMetAlaThrLeuAsnLysbProHis 1163
QY 651 TCCGGCTCATAGGCTCCTGAGCTGTGAGAGGCCGACAGTTTCCTGATCTTG 710
Db 1164 GluAsnLleLeuAlaTyrlleLeuAspPhePheGlnAspAspTyrlleTyrlle----- 1181
QY 711 GAGAGCCCGAGCCGCTGCA-----GATCTCTTGACCTTCATCAG 752
Db 1182 -----GluThrProValHleGlylulThrGlyCySllleAspLeuPheAspLeuLleGlu 1199
QY 753 GAAAGGAGACCCCTCAAGAGAGAGCTGCCGCCGACCTTCTTGAGAGCTGCGAGGCG 812
Db 1200 PheTyThrAsnMetThrGlnPheGlnAlaTyrlleLysLlePheLysGlnAlaGly 1219
QY 813 GTGGGCACTGCGCAACTGCGGGGTGTACACCGGACATCAAGACGAAACATCTT 872
Db 1220 lleybHlybLeuHleAspGlnGlyllevAlaHleAspPheLleTyAspGlnValle 1239
QY 873 ATGCACTCAATCGGGGCGAGCTCAAGCTCATGCACTTGGGCTGGGGCGCTGCTCAAG 932
Db 1240 ValAsp---SerTyGlyPheValLysLlelleAspPheGlySerAlaLayrVallys 1258
QY 933 GACACCGCTACACGAGCTTCGATGAGACCCGAGTGTACGCTCCGAGTGGATCCGC 992
Db 1259 SerGlyProPheAspValPheValGlyThrLleAspTyrlleAlaAlaProGlnValleuGly 1278
QY 993 TACCATCGCTTACCATGAGAGCTGCGGCGAGCTGTGCTCCCTGGGATCTGCTATGAT 1052
Db 1279 GlyAsnProTyrlleGlnGlyllevProGlnAspLleTrpAlaLleGlyllevleuLeuTyrlle 1298
QY 1053 ATGTGTGTGAGATATTCCTTTCAGACATGACGAAGAGATCATCAGGGGCCAGTTTTC 1112
Db 1299 ValValPheTyGlnAspPheProPheTyrlleAsnLleAspGlnLleLeuGlnLysbLeuLys 1318
QY 1113 TTCAGG-----CAGAGGCTCTTCAGATGATGACGATCATTTAGATGCTGGCC 1166
Db 1319 PheAsnAsnAlaGlnGlnValSerGlnAspCySllleGlnLleLysSerLleLeuAsn 1338
QY 1167 CTGAGCAGCATCAGATGAGCCCACTTCGAAGAAATTCAGAACATTCATGATG 1220
Db 1339 ArgCySValProLysArgProThrLleAspAspLleAsnAsnAspLysrTrpLeu 1356
RESULT 15
T52633
serine/threonine-specific protein kinase (EC 2.7.1.-) AKIN11 [validated] - Arabidopsis
N/Alternate names: SNF1 protein kinase omolog AKIN11
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
C/Accession: T52633

R/Bhalerao, R.P.; Saichert, K.; Bako, L.; Okresz, L.; Szabados, L.; Muranaka, T.; Machida
Proc. Natl. Acad. Sci. U.S.A. 96, 5322-7, 1999
A/Title: Regulatory interaction of PRL1 WD protein with Arabidopsis SNF1-like protein K1
A/Reference number: Z25116; MUID:99238528; PMID:10220464
A/Accession: T52633

A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA

A/Residues: 1-512 <BHA>

A/Cross-reference: UNIPROT:P92958; EMBL:X99279; PTDN:CAA67671.1

A/Experimental source: cultivar Columbia

C/Genetic:

A/Function:

A/Description: EC 2.7.1.-; serine/threonine-specific protein kinase AKIN1 [validated, N
completeness SNF1 mutations in yeast
C/Superfamily: AMP-activated protein kinase; protein kinase homology
C/Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

Alignment Scores:

Pred. No.:	8.75e-09	Length:	512
Score:	366.50	Matches:	130
Percent Similarity:	44.02%	Conservative:	76
Best Local Similarity:	27.78%	Mismatches:	178
Query Match:	7.65%	Indels:	84
DB:	2	Gaps:	19

US-10-705-757-1 (1-2623) x T52633 (1-512)

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QY 444 GAGCCCTGAGTGCAGTACAGAGTGGCCGCTACTGAGCGGCGGCTGCGGCTG 503
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DB 14 G|u|s|e|r|l|e|u|p|r|o|a|n|t|y|r|y|b|l|e|u|g|l|y|e|r|t|h|r|e|u|s|i|l|e|g|s|e|r|p|h|e|g|l|y|l|y|e 33
QY 504 G|T|T|A|C|T|G|A|G|C|A|T|C|C|G|G|T|T|C|C|G|A|C|A|C|T|G|C|C|G|T|G|C|C|A|A|C|A|G|T|G|A|G|A|G 563
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 34 V|a|l|l|e|y|l|e|a|l|u|n|l|a|l|u|n|l|a|l|t|h|r|g|l|u|n|l|e|y|v|a|l|a|l|l|e|y|v|l|e|u|a|n|a|x 53
QY 564 G|A|C|C|G|A|T|T|C|C|A|C|T|G|G|G|A|G|C|T|G|C|A|T|G|G|C|A|T|G|C|C|A|G|A|G|T|G|C 623
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 54 A|g|l|y|v|l|e|y|a|n|-----M|e|t|G|l|u|e|l|u|n|l|y|v|a|l|A|r|g|a|t|g|l|u|l|e|y 70
QY 624 C|T|G|T|G|A|G|A|G|T|G|A|G|C|T|G|G|T|T|C|C|G|G|C|A|T|T|A|G|C|T|G|C|T|G|A|G|T|G|C|A|G 683
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 71 I|l|e|u|n|l|e|y|u|e|h|e|t|-----H|a|r|o|h|i|a|l|e|l|e|a|r|g|l|n|t|y|r|g|l|u|n|l|e|g|l 88
QY 684 A|G|C|C|G|A|C|A|G|T|T|C|G|T|C|G|A|T|C|T|G|A|G|A|G|C|C|G|G|C|G|T|G|A|G|A|G|T|T|C|T|G|A|C 743
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 89 T|h|r|S|e|r|a|p|l|e|t|y|r|v|a|l|a|l|e|t|g|l|u|t|y|r|v|a|l|l|e|y|S|e|r|---G|l|y|c|l|u|e|p|h|e|a|r 107
QY 744 T|T|C|A|T|C|A|G|G|A|A|G|G|G|A|G|C|C|T|G|C|A|A|G|A|G|T|G|C|C|G|G|A|G|C|T|T|C|T|G|C|A|G|T|G 803
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QY 804 C|T|G|A|G|C|C|T|G|C|G|C|A|C|T|G|C|C|A|A|C|T|G|C|G|G|T|G|C|T|A|C|C|G|A|C|A|G|A|G|A|G|A 863
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 128 I|l|e|s|e|r|c|l|y|a|l|g|l|u|t|y|r|c|y|h|i|a|r|g|a|n|e|t|v|a|l|a|h|i|a|r|g|a|b|l|e|u|l|y|p|r|o|g|l 147
QY 864 A|A|C|A|T|C|T|T|A|T|G|A|C|C|T|G|A|T|G|C|G|G|A|G|C|A|A|G|C|T|A|T|G|C|A|T|T|C|G|G|T|G|C|G|G|G|C 923
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 148 A|s|n|l|e|u|l|e|u|n|e|r|p|---S|e|r|a|r|g|c|y|a|n|i|l|e|y|e|i|l|e|a|h|a|r|p|h|e|g|l|y|e|u|s|e|r|a|h 166
QY 924 C|T|G|C|T|A|A|G|A|C|A|C|C|G|T|A|C|A|G|G|A|C|T|T|G|A|T|---G|G|A|C|C|G|A|G|T|T|A|G|C|C|T|C|C|A 980
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 167 V|a|l|e|t|a|r|g|a|p|l|y|h|a|r|p|h|e|u|l|y|e|r|h|S|e|r|C|y|e|l|y|S|e|r|p|r|o|a|n|t|y|r|a|l|a|a|p|r|o 186
QY 981 G|A|G|T|G|A|T|C|G|T|A|C|A|C|T|G|T|A|C|A|T|G|C|A|G|G|T|G|C|G|G|A|G|C|A|T|G|T|G|T|C|C|T|G|G|A|G|A|T 1040
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 187 G|l|u|v|a|l|l|e|s|e|r|c|l|y|u|s|l|e|u|t|y|r|a|l|a|g|l|y|p|r|o|g|l|u|v|a|l|a|r|p|y|a|l|t|r|p|s|e|r|C|y|e|l|y|v|a|l 206
QY 1041 C|T|G|C|T|A|T|A|T|G|T|G|T|G|A|G|A|T|T|C|T|T|T|G|A|G|A|T|A|C|A|G|A|G|A|G|A|T|C|----- 1094
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 207 I|l|e|u|t|y|r|a|l|e|u|l|e|u|C|y|e|l|y|T|h|r|e|u|p|r|h|e|r|p|---A|e|r|g|l|u|a|n|i|l|e|p|r|o|a|n 225
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 1095 -----A|T|C|A|G|G|G|C|A|G|T|T|T|C|---T|T|C|A|G|G|A|G|G|G|T|C|T|T|C|A|G|A|A|T|G 1139

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DB 226 l|e|u|p|h|e|l|y|e|l|l|e|y|s|e|l|y|e|l|y|e|t|y|r|h|r|e|u|p|r|o|S|e|r|h|i|s|l|e|u|e|r|S|e|r|g|l|u|a|l 245
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 1140 C|A|G|C|A|T|C|A|T|T|A|G|A|T|G|T|G|T|G|C|T|G|G|C|T|G|A|G|C|A|T|G|A|T|G|G|C|A|A|C|T|T|G|A|G|A|A 1199
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 246 A|s|r|p|h|e|l|u|l|e|r|p|r|o|a|r|g|u|e|l|e|u|i|l|e|v|a|l|a|r|p|r|o|v|a|l|y|a|r|g|i|l|e|h|r|i|l|e|p|r|o|g|l 265
QY 1200 A|T|C|A|A|A|C|A|T|T|C|A|T|G|A|T|G|C|A|A|G|T|-----G|T|T|C|C|G|C|C|C|C|A|G 1241
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 266 I|l|e|a|r|g|l|h|i|a|r|t|r|p|h|e|g|i|n|h|r|h|i|l|e|u|p|r|o|a|r|g|t|y|r|e|u|a|l|a|v|a|l|S|e|r|p|r|o| 285
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 1242 G|A|A|C|T|G|C|T|-----G|A|G|A|C|C|T|C|C|A|G|C|C|T|G|C|G|C|G 1277
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 286 A|s|r|p|h|t|v|a|l|g|l|u|n|l|a|l|u|y|v|l|e|a|n|g|l|u|n|l|e|v|a|l|g|l|u|n|l|a|l|a|n|e|t 305
QY 1278 G|G|G|C|C|A|G|A|A|T|A|G|A|G|C|T|T|T|G|C|A|G|T|C|T|C|C|T|G|T|T|G|C|A|G|T|G|C|C|G|A|G 1337
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 306 G|l|y|h|e|a|r|a|x|-----A|e|r|g|i|n|v|a|l|e|u|g|l|u|s|e|r|e|u|----- 316
QY 1338 G|A|G|G|A|G|A|C|T|T|G|T|C|C|A|G|C|T|C|C|G|A|G|T|A|C|A|G|T|A|C|A|S|G|T|C|C|G|C|A|A|G|A|G|A|C 1397
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 317 -----A|r|g|a|n|h|x|t|h|r|g|i|n|a|n|a|r|a|a| 324
QY 1398 A|G|T|G|T|A|T|A|C|A|A|A|A|A|T|T|A|C|A|T|G|A|T|T|C|A|A|T|C|C|A|G|C|C|G|G|A|G|C|G 1457
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 325 T|h|r|v|a|l|t|h|r|t|y|r|t|y|r|e|u|e|u|a|r|a|n|h|x|p|h|e|a|r|v|a|l|p|r|o|S|e|r|c|l|y|t|y|r|e|u|--- 343
QY 1458 C|T|C|C|A|A|C|A|T|G|G|G|A|A|G|A|G|T|A|C|T|T|C|A|G|G|G|T|C|T|A|G|G|C|T|A|C|T|C|C|C|A|T|A|G 1517
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 344 ---G|l|u|s|e|r|c|l|y|h|e|g|i|n|l|u|h|r|h|r|a|r|p|S|e|r|h|a|r|p|r|o|k|e|t|a|r|g|h|r|p|r|o|g|l 362
QY 1518 A|T|A|G|C|T|T|C|T|-----T|C|A|T|A|G|T|G|T|C|A|G|A|T|T|C|G|A|C|T|T|G|A|T|A|T|A|T|A|T|C|C|G|G 1571
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 363 A|l|a|g|l|a|l|S|e|r|e|r|o|v|a|l|g|l|u|n|i|s|t|r|i|l|e|r|o|l|a|h|i|v|a|l|a|r|h|i|s|----- 378
QY 1572 G|G|T|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G 1631
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 379 ---T|y|r|g|l|u|e|l|y|a|l|a|r|g|e|r|g|i|n|v|a|l|p|r|o|v|a|l|a|r|p|----- 390
QY 1632 T|G|C|T|A|A|T|C|C|G|G|A|T|G|G|T|C|A|G|T|A|G|G|G|G|G|A|A|C|A|G|T|T|G|G|A|T|G|G|A|T|G|A|G|A|C|A|G 1691
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 391 -----A|r|g|l|y|e|r|t|r|a|l|a|-----L|e|u|g|l|y|e|u|g|i|n|---S|e|r|h|i|v|a|l| 401
QY 1692 A|C|A|T|T|T|A|A|G|C|C|T|G|C|A|C|C|T|T|C|C|A|C|A|C|T|T|T|G|A|G|T|G|C|T|-----C|T|G|G|G|G 1745
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 401 a|h|i|s|-----P|r|o|a|r|g|l|u|i|l|e|e|t|e|r|g|i|n|v|a|l|e|u|l|y|a|l|e|u|g|i|n|l 416
QY 1746 A|C|T|C|G|G|C|T|G|T|G|C|T|G|G|A|A|A 1767
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 416 u|l|e|u|a|n|v|a|l|C|y|t|r|p|l|y|e|l|y|s 423

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Search completed: September 22, 2005, 17:20:15
Job time : 115.96 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: September 22, 2005, 15:59:25 ; Search time 433.035 Seconds
(without alignments)
6203.583 Million cell updates/sec

Title: US-10-705-757-1

Perfect score: 4789

Sequence: 1 gaggagagccgagagagc.....aataaaacccttgcttc 2623

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODE=frame+np.model -DEV=xlp
-Q/cgnt_1/USPTO.spool_p/US10705757/runat_22092005_115015_22129/app_query.faeca_1.5333

-DB=uniprot -QFMT=fasta -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=psco -NOR=ext -HEAPSIZES=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10705757_QCGN_1_1_980 @runat_22092005_115015_22129 -NCP=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

uniprot_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1670	34.9	313	1	P1M1_HUMAN
2	1659	34.6	313	1	P1M1_PELCA
3	1656	34.6	313	1	P1M1_BOVIN
4	1636	34.2	313	1	P1M1_RAT
5	1587	33.1	313	2	O8CFN8
6	1582	33.0	313	1	P1M1_MOUSE
7	1140	23.7	313	1	P1M1_COTJA
8	1133	23.6	313	1	P1M1_HUMAN
9	1129.5	23.6	313	1	P1M1_MOUSE
10	1128.5	23.6	313	1	P1M1_MOUSE
11	1116	23.3	313	2	O811X8
12	1105	23.1	313	1	P1M1_XENLA
13	1101	23.0	318	2	O66111
14	918	19.2	310	1	P1M1_MOUSE
15	889.5	18.6	311	2	O8R2P0
16	877.5	18.3	311	1	P1M2_HUMAN

17	854	17.8	310	2	O7ZVJ5	O7ZVJ5 brachydanio
18	851	17.8	310	2	O8JFW9	O8JFW9 brachydanio
19	846	17.7	310	1	P1M1_BRARE	O9Y125 brachydanio
20	844	17.6	310	2	O6D152	O6D152 brachydanio
21	724.5	15.1	221	2	O8R1Z0	O8R1Z0 mus musculus
22	620	12.9	441	2	O20443	O20443 caenorhabditis
23	486	10.1	378	2	O8T3P1	O8T3P1 caenorhabditis
24	486	10.1	566	2	O17737	O17737 caenorhabditis
25	423	8.8	1383	1	PASK_MOUSE	O8EE66 mus musculus
26	421.5	8.8	134	2	O6P2J9	O6P2J9 homo sapien
27	403	8.4	125	2	O6Q2K5	O6Q2K5 canis fami
28	402	8.4	628	2	O9H093	O9H093 homo sapien
29	402	8.4	1398	2	O77268	O77268 drosophila
30	402	8.4	1398	2	O9W532	O9W532 drosophila
31	398	8.3	1107	2	O6C310	O6C310 yarrowia
32	397	8.3	661	1	ARK5_HUMAN	O60285 homo sapien
33	393.5	8.2	832	2	O963B6	O963B6 drosophila
34	391.5	8.2	658	2	O641K5	O641K5 mus musculus
35	391.5	8.2	1033	2	O8MLJ7	O8MLJ7 drosophila
36	391.5	8.2	1060	2	O9VBW0	O9VBW0 drosophila
37	391.5	8.2	1098	2	O7KRX7	O7KRX7 drosophila
38	391.5	8.2	1138	2	O7KRX3	O7KRX3 drosophila
39	390.5	8.2	950	2	O8CIC0	O8CIC0 mus musculus
40	390.5	8.2	950	2	O6NPA6	O6NPA6 drosophila
41	389	8.1	833	2	O7KRX5	O7KRX5 drosophila
42	389	8.1	905	2	O7KRX5	O7KRX5 drosophila
43	389	8.1	938	2	O9VBW8	O9VBW8 drosophila
44	389	8.1	1323	1	PASK_HUMAN	O96192 homo sapien
45	388	8.1	1075	2	O95U75	O95U75 drosophila

ALIGNMENTS

RESULT 1
P1M1_HUMAN
ID P1M1_HUMAN STANDARD; PRT; 313 AA.
AC P11309; O96RG3;
DT 01-UTR-1989 (Rel. 11, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Proto-oncogene serine/threonine-protein kinase Pim-1 (BC 2.7.1.37).
GN Name=PIM1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90182681; PubMed=2205533; DOI=10.1016/0378-1119(90)90195-W;
RA Zukut-Houri R., Hazum S., Givoli D., Telexman A.;
RT "Primary structure of the putative human oncogene, pim-1.";
RT Gene 90:303-307(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86727423; PubMed=3475233; DOI=10.1016/0378-1119(87)90352-0;
RA Zukut-Houri R., Hazum S., Givoli D., Telexman A.;
RT "The cDNA sequence and gene analysis of the human pim oncogene.";
RT Gene 54:105-111(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88217305; PubMed=3329709;
RA Domen J., von Lindern M., Hermans A., Breuer M., Grosfeld G., Berns A.;
RT "Comparison of the human and mouse PIM-1 CDNA: nucleotide sequence and immunological identification of the in vitro synthesized PIM-1 protein.";
RT Oncogene Res. 1:103-112(1987).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=88115604; PubMed=3429489;
RA Meeker T.C., Nagarajan L., Ar-Rushdi A., Croce C.M.;
RT "Cloning and characterization of the human PIM-1 gene: a putative oncogene related to the protein kinases.";
RT

RL J. Cell. Biochem. 35:105-112(1987).
 [5]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schaller G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Tohivukki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millar S.J.,
 RA Bosak S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodighiero S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.W., Maier M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [6]
 RN SEQUENCE OF 1-302 FROM N.A.
 RX MEDLINE=21354098; PubMed=11460166; DOI=10.1038/35085588;
 RA Pasqualucci L., Neumeister P., Goossens T., Nannjand G.,
 RA Chaganti R.S.K., Kupper R., Dalla-Favera R.,
 RT "Hypermutation of multiple proto-oncogenes in B-cell diffuse large-
 cell lymphomas.";
 RL Nature 412:341-346(2001).
 RN [7]
 RP CHARACTERIZATION.
 RX MEDLINE=88246418; PubMed=2837645;
 RA "Telerman A., Amson R., Zakut-Houri R., Givoli D.,
 RT "Identification of the human p14 gene product as a 33-kilodalton
 cytoplasmic protein with tyrosine kinase activity.";
 RL Mol. Cell. Biol. 8:1498-1503(1988).
 RN [8]
 RP FUNCTION.
 RX MEDLINE=20130009; PubMed=10664448; DOI=10.1016/S0014-5793(00)01105-4;
 RA Koike N., Maiba H., Taira T., Ariga H., Iguchi-Ariga S.M.M.,
 RT "Identification of heterochromatin protein 1 (HP1) as a
 phosphorylation target by Pim-1 kinase and the effect of
 phosphorylation on the transcriptional repression function of
 HP1(1).";
 RL FEBS Lett. 467:17-21(2000).
 RN [9]
 RP SUBCELLULAR LOCATION.
 RX MEDLINE=22567470; PubMed=12680209;
 RA Ionov Y., Le X., Tunquist B.J., Sweetenham J., Sachs T., Ryder J.,
 RA Johnson T., Lilly M.B., Kraft A.S.,
 RT "Pim-1 protein kinase is nuclear in Burkitt's lymphoma: nuclear
 localization is necessary for its biologic effects.";
 RL Anticancer Res. 23:167-178(2003).
 CC -1- FUNCTION: Thought to play a role in signal transduction in blood
 cells. May affect the structure or silencing of chromatin by
 phosphorylating HP1 gamma/CBX3.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SUBUNIT: Binds to Rpg (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
 CC -1- TISSUE SPECIFICITY: Expressed primarily in cells of the
 hematopoietic and germ line lineages.
 CC -1- PTM: Autophosphorylated on tyrosine residues.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
 subfamily.
 CC -1- DATABASE: NMR-Atlas Genet. Cytogenet. Oncol. Haematol.;
 WWW="http://www.infobiogen.fr/services/chronocancer/Genes/PIM1ID261.html".
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 CC -----

CC EMBL; M27903; AAA0090.1; -
 DR EMBL; M16750; AAA0089.1; -
 DR EMBL; M54915; AAA6447.1; -
 DR EMBL; M24791; AAA81553.1; -
 DR EMBL; BC020224; AAH20224.1; -
 DR EMBL; AF386792; AAK0871.1; -
 DR PIR; J0327; TVHUP1.
 DR Genew; HGNC:8986; PIM1.
 DR H-InvDB; HIX0005835; -
 DR MIM; 164960; -
 DR GO; GO:0005737; Cytoplasm; TAS.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
 DR GO; GO:0007275; P:development; TAS.
 DR GO; GO:0004668; P:protein amino acid phosphorylation; TAS.
 DR InterPro; IPR011009; Kinase-like.
 DR InterPro; IPR000719; Prot. kinase.
 DR InterPro; IPR008271; Ser. Thr. kin. AS.
 DR Pfam; PF00069; Kinase; 1.
 DR ProDom; PD000001; Prot. kinase; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Nuclear protein; Phosphorylation; Proto-oncogene;
 Serine/threonine-protein kinase; Transferase.
 FT DOMAIN 38 290
 FT NP BIND 44 52 ATP (By similarity).
 FT BINDING 67 67 ATP (By similarity).
 FT ACT SITE 167 167 Proton acceptor (By similarity).
 FT CONFLICT 15 16 AE -> RA (in Ref. 2).
 FT SEQUENCE 313 AA; 35685 MW; 35BA76D3688B9A3 CRC64;

Alignment Scores:

Align. No.:	5,436-83	Length:	313
Score:	1670.00	Matches:	313
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	34.87%	Indels:	0
DB:	1	Gaps:	0

US-10-705-757-1 (1-2623) x PIM1_HUMAN (1-313)

QY 351 ATGCTCTGTGCAAAATCACTGCTTGGCCACCTGCGCGCGCTGCAACGACTG 410
 DB 1 MetLeuSerLysIleHisSerLeuAlaHisLeuAlaAlaProCysAsnAspLeu 20
 QY 411 CACGCCACCAACACTGCGCGCGCGCAAGAGAGAGCGCGCGAGTCCGAGTACCAAGCG 470
 DB 21 HisAlaThrLysLeuAlaProGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 40
 QY 471 GGCCTGCTACTGGGCGCGCGCTTGGCTGCTGCTACTGAGGACTCGCGCTTCCGAC 530
 DB 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValSerAsp 60
 QY 531 AACTTGGCGTGGGCGCATCAACACGTGAGAGAGACCGGATTTCCGACTGGGAGAGCTG 590
 DB 61 AsnLeuProValAlaIleHisValGlyGlyAspArgIleSerAspTyrGlyGlyLeu 80
 QY 591 CCTAATGAGCTCGAGTCCGCTGAGAGTGGTCCGCTGCAAGAGTGGAGTTCG 650
 DB 81 ProAsnGlyThrArgValProMetGlyValValLeuLeuLysValSerSerGlyPhe 100
 QY 651 TCCGGGCTATTAGGCTCTGAGCTGTTGAGAGGCGCGAGAGTTCGCTGATCTG 710
 DB 101 SerGlyValIleArgLeuLeuSerTyrPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120
 QY 711 GAGAGCGCGAGCGCGGTGAGATGCTCTTGCATTCATCAAGAGAGGAGGCGCTGCA 770

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Db      121  GluArgProGluProValGlnAspLeuPheAspHeilerThrguArgValAlaLeuGln 140
Qy      771  GAGAGACTGGCCCGCCACTTCTTTGGCAGGTGCTGGAGGCCGCTGGCCGCACTGGCCAAAC 830
Db      141  GluGluLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgHisCysHisAsn 160
Qy      831  TGGCGGGTGTCTACACCCGCAATCAAGAGAGAAAACCTCTTATCGACCTCAATCGCGGC 890
Db      161  CysGlyValLeuHisAspGlyLeuAspGlnAsnLeuLeuLeuLeuLeuLeuLeuLeuLeu 180
Qy      891  GAGCTCAAGCTCATCGACTTCGGGTCCGGGGCGCTGCTCAAGACACCGTCTACACGAC 950
Db      181  GluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 200
Qy      951  TTGCGATGGGACCCGAGCTGTATAGCCCTCCAGAGTGGATCCGCTACCTACCATGGC 1010
Db      201  PheAspGlyThrArgValValTyrSerProGluLeuTrpIleArgTyrHisAspGlyHisGly 220
Qy      1011  AGGTGGCGGCGAGCTGTGCTCCGTGGGGATCCGTGATGATATAGTGTGGAGATATT 1070
Db      221  ArgSerAlaAlaValTrpSerLeuGlyIleLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 240
Qy      1071  CCTTCGAGCATGACGAAGATCATCAGAGGCGCCAGGTTTCTTCAAGCGAGAGGTTCT 1130
Db      241  ProPheGluHisAspGluGluIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
Qy      1131  TCGAATGTACGATCTCATTAAGATGGTCTTGGCCCTGAGACCATAGATAGGCCAAC 1190
Db      261  SerGlyCysGlnHisLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 280
Qy      1191  TTGCAAGAAATCCGAAACATCATCATGATGATGATGATGATGATGATGATGATGATGAT 1250
Db      281  PheGluGluIleGlnHisAsnHisAspTrpPheGlnHisAspValLeuLeuProGluGlnHis 300
Qy      1251  GAGATCCACCTCCAGACGCTGTGCGCGCGGCCCAAGCAA 1289
Db      301  GluIleHisLeuHisSerLeuSerProGlyProSerIys 313

RESULT 2
PIM1_FELCA
ID      PIM1_FELCA      STANDARD;      PRT;      313 AA.
AC      095LTD;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
GN      Name=PIM1;
OS      Felis silvestris catus (Cat).
OC      Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Carnivora; Placentalia; Felidae; Felis.
OX      NCBI_TaxID=9685;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Fujino Y., Satch H., Hiseue M., Maeda K., Ohno K., Tsujimoto H.;
RT      "The cDNA sequence of the feline pim-1 oncogene.";
RL      Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC      -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC      -1- SUBUNIT: Binds to Rps (By similarity).
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC      -1- PTM: Autophosphorylated (By similarity).
CC      -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC      subfamily.
CC      -----
CC      This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      or send an email to license@emb-sib.ch).
CC      -----
CC      EMBL; AB073748; BAB71752.1; -.
CC      InterPro; IPR011009; Kinase_like.

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DR      InterPro; IPR000719; Prot kinase.
DR      InterPro; IPR008271; Ser_Thr_kin_AS.
DR      Pfam; PF00069; Pkinase; 1.
DR      ProDom; PD000001; Prot_kinase; 1.
DR      PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR      PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW      ATP-binding; Nuclear protein; Phosphorylation; Proto-oncogene;
KW      Serine/threonine-protein kinase; transferase.
FT      DOMAIN      38      290      Protein kinase.
FT      NP_BIND      44      52      ATP (By similarity).
FT      BINDING      67      67      ATP (By similarity).
FT      ACT_SITE      167      167      Protein acceptor (By similarity).
SQ      SEQUENCE      313 AA; 35685 MW; C0BE26BD63BE6967 CRC64;

Alignment Scores:
Pred. No.:      2,16e-82      Length:      313
Score:      1659.00      Matches:      310
Percent Similarity:      99.68%      Conservative:      2
Best Local Similarity:      99.04%      Mismatches:      1
Query Match:      34.64%      Indels:      0
DB:      Gaps:      0

US-10-705-757-1 (1-2623) x PIM1_FELCA (1-313)

Qy      351  ATGCTCTTGTCCAAATCAACTGCTGCCACTCGCGCGCGCCCTGCACAGACTTG 410
Db      1  MetLeuLeuSerIysIleAsnSerLeuAlaHisLeuArgThrAlaProCysAsnAspLeu 20
Qy      411  CAGCCACCAAGCTGCGCGCGCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 470
Db      21  HisAlaThrIleLeuAlaProGlyIleGluLeuGluLeuLeuLeuLeuLeuLeuLeuLeu 40
Qy      471  GCGCCGCTACTGCGGAGCGCGCGCTTCCGCTCGGTCTACTCAGAGATCCGCTTCGAC 530
Db      41  GlyProLeuLeuGlySerGlyIlePheGlySerValTyrSerGlyIleArgValAlaAsp 60
Qy      531  AACTCCCGCGTGGCCATCAAAACGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 590
Db      61  AsnLeuProValAlaIleIleHisValGluIleAspArgIleSerAspTrpGlyGluLeu 80
Qy      591  CCTAATGAGCAGCTGAGTGGCCATGGAAGGTGCTCTGTGAAGAGAGAGAGAGAGAGAG 650
Db      81  ProAsnGlyThrArgValAlaProMetGluValIleLeuLeuLeuLeuLeuLeuLeuLeu 100
Qy      651  TCGCGGCTATTAGGCTCTGTGACGAGGCTGAGAGGCGCGACAGTTCTGCTGATCTTG 710
Db      101  SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleLeu 120
Qy      711  GAGAGCGCGAGCGCGGTGCAAGATCTTTCGACTTCATCAAGAGAGAGAGAGAGAGAGAG 770
Db      121  GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
Qy      771  GAGGAGCTGGCCCGGAGCTTCTTGGGAGGTGCTGAGGCGGTGGGAGCTGGCCAAAC 830
Db      141  GluGluLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgHisCysHisAsn 160
Qy      831  TGGCGGGTGTCTACACCCGCAATCAAGAGAGAAAACCTCTTATCGACCTCAATCGCGGC 890
Db      161  CysGlyValLeuHisAspGlyLeuAspGlnAsnLeuLeuLeuLeuLeuLeuLeuLeuLeu 180
Qy      891  GAGCTCAAGCTCATCGACTTCGGGTCCGGGGCGCTGCTCAAGACACCGTCTACACGAC 950
Db      181  GluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 200
Qy      951  TTGCGATGGGACCCGAGTGTATAGCCCTCCAGAGTGGATCCGCTACCTACCATGGC 1010
Db      201  PheAspGlyThrArgValValTyrSerProGluLeuTrpIleArgTyrHisAspGlyHisGly 220
Qy      1011  AGGTGGCGGAGCTGTGCTCCGTGGGGATCCGTGATGATATAGTGTGGAGATATT 1070
Db      221  ArgSerAlaAlaValTrpSerLeuGlyIleLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 240

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AC P26794;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Proto-oncogene serine/threonine-protein kinase Pim-1 (EC 2.7.1.37).
GN Name=Pim1; Synonym=Pim-1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Testis;
RX MEDLINE=92319652; PubMed=1620615;
RA Kingett D., Reeves R., Magnuson N.S.;
RT "Characterization of the testes-specific pim-1 transcript in rat.";
RL Nucleic Acids Res. 20:3183-3189(1992).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBUNIT: Binds to Rp9 (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC -1- PTM: Autophosphorylated (By similarity).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, X63675; CAA45214.1; --
DR PIR, S26298; S26298.
DR RGD, 3330; Pim1.
DR InterPro, IPR011009; Kinase like.
DR InterPro, IPR000719; Prot kinase.
DR InterPro, IPR008271; Ser_Thr_kin_AS.
DR Pfam, PF00069; Pkinase; 1.
DR ProDom, PD000001; Prot_kinase; 1.
DR PROSITE, PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE, PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE, PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Nuclear protein; Phosphorylation; Proto-oncogene;
KW Serine/threonine-protein kinase; Transferase.
FT DOMAIN 38 290
FT NP_BIND 44 52
FT BINDING 67 67
FT ACT_SITE 167 167
FT ACT_SITE 167 167
SQ SEQUENCE 313 AA; 35630 MW; D5757DA9F1821BP9 CRC64;
Alignment Scores:
Pred. No.: 3, 87e-81 Length: 313
Score: 1636.00 Matches: 304
Percent Similarity: 99.04% Conservative: 6
Best Local Similarity: 97.12% Mismatches: 3
Query Match: 34.16% Indels: 0
Gaps: 0
US-10-705-757-1 (1-2623) x PIM1_RAT (1-313)
QY 351 ATGCTCTTTCACAAATCAACTGCTTGGCCACCTGCGCGCGCGCTTCAGACGACTG 410
DB 1 MetLeuLeuSerIysIleAsnSerIleuAlaIleLeuAlaIleProCysAsnAspLeu 20
QY 411 CAGCCACCAAGCTGGCGCGCGCGCAAGAGAGAGCGCTGAGTTCGACGTCAGGTC 470
DB 21 HisAlaAsnIleuAlaIleProGlyIleGluIleGluIleProLeuIleuSerGlnIleVal 40
QY 471 GGGCGGCTACTGGGACGCGCGCGCTTTCGCTCGCTTACTCAGGACATCCGCTTCGAC 530
DB 41 GlyProLeuLeuIleuSerGlyIleGlyIleGlySerValIleuSerGlyIleAlaValAlaAsp 60

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QY 531 AACTGCGCGGTGACCATCAACAGTGAAGAGACCGGATTTCCGACTGGGAGAGCTG 590
DB AsnLeuProValAlaIleuAlaIleuValGluIleuAspArgIleSerAspTrpGlyIleuLeu 80
QY 591 CCTAATGACACTGAGTGGCCATGAGAGTGGTCTCTGTAAGAGAGTGAAGCTCGGGTTTC 650
DB ProAsnGlyThrArgValProMetGluValIleuLeuIleuIleuValSerSerGlyPhe 100
QY 651 TCCGGGCTCATTTAGCTCTCTGACCTGGTTCGAGAGCCGACAGCTTTCTGTAATCTTG 710
DB SerGlyValIleuAlaIleuArgLeuAsnAspTrpPheGluArgProAspSerPheValIleuLeu 120
QY 711 GAGAGCGCGAGCGCGGTGCAAGATCTTCTGACTTCATCAACGGAAGGGAGCGCTGCAC 770
DB GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyIleValGln 140
QY 771 GAGAGCTGGCGCGCGCACTTCTTCTGCGAGTGGTCTGAGAGCCGTCGCGGCACTCCACAC 830
DB GluGluLeuAlaIleuArgSerPhePheTrpGlnValIleuGluAlaValArgHisCysHisAsn 160
QY 831 TCGCGGGTCTACACCGGACATCAAGACGAAACATCTTATGCACTCAATCCGCGC 890
DB CysGlyValIleuAlaIleuArgAspIleuIleuAspGluAsnIleuIleuAspLeuAsnArgGly 180
QY 891 GAGCTCAAGCTCATGCACTTTCGGTGGGGCGCTGCTCAAGACACCGCTTACAGGAC 950
DB GluLeuIleuAlaIleuAlaIleuArgSerGlySerGlyAlaLeuIleuIleuAspThrValIleuAsp 200
QY 951 TTCGATGAGACCGGAGTATGAGCCCTCCAGAGTGGATCCGCTACATGCTTACATGGC 1010
DB PheAspGlyThrArgValIleuSerProProGluIleuIleuArgTrpHisArgTrpHisGly 220
QY 1011 AGGTGCGCGGCACTGCTGCTTCTGCGGAGATCTGCTGATGATATGGTGTGAGATATT 1070
DB ArgSerAlaAlaValIleuPheLeuGlyIleLeuLeuIleuIleuIleuValCysGlyAspIle 240
QY 1071 CCTTGACACATGACCAAGATCATCAAGAGCGCGGCTTTCTTTCAGGAGGGTCTCT 1130
DB ProPheGluIleuAspIleuGluIleuValIleuValGlyGlnValIleuIleuValArgGlnValSer 260
QY 1131 TCAGATGTCAGCATCTCATTTAGATGTCCTTGGCCCTGAGACCATCAATAGAGCCACAC 1190
DB SerGluCysGlnIleuIleuAlaIleuArgTrpCysIleuSerLeuArgProSerAspArgProSer 280
QY 1191 TTCGAAGAATTCAGACCATCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1250
DB PheGluGluIleuGlnIleuAsnHisProIleuMetGlnAspValIleuLeuProGlnIleuAla 300
QY 1251 GAGATCCACCTCCACAGCGCTGTCGCGCGGCGCCAGCAAA 1289
DB 301 GluIleuIleuAlaIleuIleuSerLeuSerProSerProSerLys 313
RESULT 5
Q8CFN8 PRELIMINARY; PRT; 313 AA.
ID Q8CFN8;
AC Q8CFN8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 23, Last annotation update)
DE Proximal integration site 1.
GN Name=Pim1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain, and Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grove L.H., Derge J.G.,
Klauser R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Tohilyuki S., Garinai P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mallary S.J.,
 RA Bosak S.A., Mcwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richard S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
 RA Krzywiński M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RA Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL: BC042885; AAH42885.1; -;
 DR EMBL: BC053019; AAH53019.1; -;
 DR EMBL: BC055316; AAH55316.1; -;
 DR MGI: 97584; PIML.
 DR GO: GO:0005524; P:ATP binding; IEA.
 DR GO: GO:0004674; P:Protein serine/threonine kinase activity; IEA.
 DR GO: GO:0016740; P:transferase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR011009; Kinase_like.
 DR InterPro: IPR000719; Prot_Kinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR008271; Ser_thr_pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SO SEQUENCE 313 AA; 35451 MW; 1294F16A03B7CD7 CRC64;

Alignment Scores:
 Pred. No.: 1,81e-78 Length: 313
 Score: 1587.00 Matches: 295
 Percent Similarity: 97.44% Conservative: 10
 Best Local Similarity: 94.25% Mismatches: 8
 Query Match: 33.14% Indels: 0
 DB: 2 Gaps: 0

US-10-705-757-1 (1-2623) x Q8CFN8 (1-313)

QY 351 ATGCTCTGTCGAATTCACATGCTTGCACCTGCGCGCGCTTCGAACGACCTG 410
 Db 1 MetLeuLeuSerYylleaaSerLeuAlahleuArgAlaAlaProCysaaNapLeu 20
 QY 411 CAGGCCCAAGCTGCGCGCGCGCAAGAGAGAGAGCGCTGAGTGCAGTACGAGT 470
 Db 21 HieAlaThrIleuAlaProGlyIyglulYgluProleuAluSerGlnIyrglnVal 40
 QY 471 GGGCCGCTACTGGGAGCGGCGGCTTGGCTCGGCTCTACTCAGGCAATCGCGTCTCCGAC 530
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Db 41 GlyProLeuIleuGlySerGlyIyPheGlySerValIySerGlyIyIleArgValAlaAsp 60
 QY 531 AACTGCGCGGTGGCCATCAACAGCTGGAGAGAGCCGATTTCCGACTGGGAGAGCTG 590
 Db 61 AenLeuProValAlaIleIyehIleValIglulYaaPahIleSerAapIyIyIleu 80
 QY 591 CCTAATGGCACTCGAGTGCCTCCATGGAAGTGTCTCTGTAAGAGAGTGAAGTTCG 650
 Db 81 ProaNgIyIyIleArgValProMetGlnValIleuLeuIyIyValSerSerAapPhe 100
 QY 651 TCCGCGCTCATTAAGCTCTCTGAGCTGTTCCAGAGAGCCCGACAGTTTGTCTGATCT 710
 Db 101 SerGlyValIleArgLeuLeuAapIyPheGluArgProAapSerPheValIleuIleu 120
 QY 711 GAGAGCCCGAGCGGCTGAGATGCTTCCATTCATCAGGAAGAGGAGCCGCTGCA 770
 Db 121 GluArgProGluProValGlnAapPheAapPheIleIyGluArgGlyIyAlaGln 140
 QY 771 GAGAGCTGGCCGAGCTTCTTCTGAGAGTGTGAGGCGGCTGCGCACTGCGACAC 830
 Db 141 GluAapLeuAlaArgGlyPhePheIyIyGlnValIleuGlnAlaValArgIleCysHlaaen 160
 QY 831 TCGGGGCTGCTACCGCGGACATCAAGAGCAAAACATCTTATGACCTCAATGCGGCG 890
 Db 161 CysGlyValIleuHlaArgAapIleIyAapGluAenIleuIleAapLeuSerAargly 180
 QY 891 GAGCTCAAGCTCATGAGCTTGGGAGTGGGAGGCGCTCAAGAGACCGCTACAGCGAC 950
 Db 181 GluIleIyIyIleuIleAapPheIySerGlyAlaLeuLeuIyAapThrValIyIyIyIyIy 200
 QY 951 TTGATGGGAGCCGAGTATATAGCCCTCAGAGTGAATCCGCTACATGCTACATGAGC 1010
 Db 201 PheAapGlyIyIleArgValIySerProProGluIyIyIyIyIyIyIyIyIyIyIyIy 220
 QY 1011 AGCTGGCGGCGCTGCTGCTTCCGAGATCCCTGCTGATGATGATGATGATGATGAT 1070
 Db 221 ArgSerAlaAlaValIyIySerIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 240
 QY 1071 CCTTTCAGCATGAGAGAGATCATCATGAGGCGCAGTTTCTTTCAGGAGAGGCTCT 1130
 Db 241 PropheGluHlaAapGluIy 260
 QY 1131 TCAGATGTCAGCATCTATTAGATGTGCTTGGCCCTGAGACCATCAGATAGGCCAAC 1190
 Db 261 SerGluCysGlnHlaIleuIleIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 280
 QY 1191 TTCGAAGAATTCAGAACCATCATCATGATGAGCAAGATGTTCTCTGCGCCAGAACTG 1250
 Db 281 PheGluGluIleArgAapIy 300
 QY 1251 GAGATCCACCTCCACAGCTGTCGCGGAGGCCAGCAAA 1289
 Db 301 GluIleHlaIleuHlaSerIleuSerProGlyIySerIyIy 313

RESULT 6
 PIM1 MOUSE
 ID PIM1 MOUSE STANDARD; PRT; 313 AA.
 AC P06803;
 DT 01-JAN-1988 (rel. 06, Created)
 DT 01-JAN-1988 (rel. 06, Last sequence update)
 DT 05-JUL-2004 (rel. 44, Last annotation update)
 DE Proto-oncogene serine/threonine-protein kinase Pim-1 (BC 2.7.1.37).
 GN Name=Pim1; Synonyms=Pim-1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86272109; PubMed=3015420; DOI=10.1016/0092-8674(86)90886-X;
 RA Selen G., Cuyper H.T., Boelens W., Robanus-Maandag E., Verbeek J.,
 RA Domen J., van Beveren C., Berns A.;
 RT "The primary structure of the putative oncogene pim-1 shows extensive


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RT  homology with protein kinases."
RL  Cell 46:603-611(1986).
RN  [2]
RP  INTERACTION WITH RP9.
RX  MEDLINE=20369540; PubMed=10931201;
RA  Maita H., Harada Y., Nagakubo D., Kiteaura H., Ikeda M., Tamai K.,
RA  Takahashi K., Ariga H., Iguchi-Ariga S.M.M.;
RT  "RAP-1, a novel target protein of phosphorylation by Pim-1 kinase."
RL  Eur. J. Biochem. 257:5168-5178(2000).
CC  -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC  -1- SUBUNIT: Binds to RP9.
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC  -1- PTM: Autophosphorylated (By similarity).
CC  -1- DISEASE: Frequently activated by provirus insertion in murine
CC  leukemia virus-induced T-cell lymphomas.
CC  -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC  subfamily.
CC  -----
CC  This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC  or send an email to license@ebi.ac.uk).
CC  -----
DR  EMBL, M13945; AAA39930.1; -.
DR  PIR, A24169; TVMSPL.
DR  HSSP, Q63450; 1A06.
DR  MGD, MG1:97584; Pim1.
DR  InterPro, IPR011009; Kinase like.
DR  InterPro, IPR000719; Prot. kinase.
DR  InterPro, IPR008271; Ser_Thr_kin_AS.
DR  Pfam, PF00069; Kinase; 1.
DR  ProDom, PD000001; Prot. kinase; 1.
DR  PROSITE, PS00107; PROTEIN KINASE ATP; 1.
DR  PROSITE, PS0011; PROTEIN KINASE DOM; 1.
DR  PROSITE, PS00108; PROTEIN_KINASE_ST; 1.
KM  ATP-binding; Nuclear protein; Phosphorylation; Proto-oncogene;
KM  Serine/threonine-protein kinase; transferase.
FT  DOMAIN 38 290
FT  NP BIND 44 52
FT  BINDING 67 67
FT  ACT SITE 167 167
SQ  SEQUENCE 313 AA, 35536 MW, 799477959DCBDC16 CRC64;
Alignment Scores:
Pred. No.: 3,39e-78 Length: 313
Score: 1582.00 Matches: 294
Percent Similarity: 97.12% Conservative: 10
Best Local Similarity: 93.93% Mismatches: 9
Query Match: 33.03% Indels: 0
DB: 1 Gaps: 0
US-10-705-757-1 (1-2623) x PIM1_MOUSE (1-313)
QY 351 ATGCTCTTGCAAAATCAACTGCTTGCCACCTGCGCGCGCCCTGCAAGACCTG 410
DB 1 MetLeuLeuSerIySIIeaSenSerLeuAlhIleuArgIlaArgProCySaAnaPLeu 20
QY 411 CAGGCACCAAGCTGGCGCGCGCGCAAGAGAGAGCCCTTGAGTGCAGTCCAGAGT 470
DB 21 HlaAlaIthIyLeuAlaPArgIyLvgIuLySgluProLeuGluSerGlnIyVal 40
QY 471 GGGCCGCTACTGGGAGCGCGCGCTTGCTGCTGCTACTCAGACATCCGCTCCGAC 530
DB 41 G1yProLeuLeuG1ySerG1yPheG1ySerValIySerG1yIleArgValAlaAsp 60
QY 531 AACTGCGCGGTGGCCATCAAAACAGCTGAGAGAGACCGGATTTCCGACTGGGAGAGCTG 590
DB 61 AaIleuProValAlaIleIyVhIleValGluIyAaAspArgIleSerAspTrpG1yGluLeu 80
QY 591 CCAATAGGACCTGAGAGTCCCATGGAAGTGTCTCTGTAAGAAAGTGAAGCTGGGTTTC 650

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DB 81 ProaenGIyThrArgIyAlaProMetGluValValLeuLeuIySylSerSerAspPhe 100
QY 651 TCCGCGCTCAATAGCTCTCTGACCTGAGAGCGCCGACAGTTTCTGCTGATCTTG 710
DB 101 SerGIyValIleArgIleuLeuAaPTrpPheGluArgProAspSerPheValLeuLeu 120
QY 711 GAGAGCCCGAGCGCGGTGCAAGATCTTCTGACTTCATGACGGAAGGAGGAGCTGCA 770
DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgG1yAlaLeuGln 140
QY 771 GAGAGCTGGCGCGCAGCTTCTTCTGAGCTGCTGAGAGCGCTGCGGACCTGCAAC 830
DB 141 GluAspLeuAlaIArgG1yPhePheTrpGlnValLeuGluAlaValArgHisCyHisAsn 160
QY 831 TGGCGAGGTGTACACCGCGACATCAAGAGAGAAACATCTTATGACCTCAATCGCGC 890
DB 161 CyGglYValLeuHisArgAspIleIySAspGluAsnIleuIleAspLeuSerArgG1y 180
QY 891 GAGCTCAAGCTATCGACTTCCGGTGGGGGCGCTGTCAGAGACCCGCTACAGCGAC 950
DB 181 GluIleIySLeuIleAspPheG1ySerG1yAlaLeuLeuIyAspThrValIyThrAsp 200
QY 951 TTGATAGGAGCCGAGTGTATAGCTTCCAGAGTGGATCCGATCCGCTACCATCGCTA 1010
DB 201 PheAspG1yThrArgIyValIySerProProGluTrpIleArgIyHisArgIyThIleG1y 220
QY 1011 AGGTGCGCGGACGTGTGCTCTGAGAGATCTCTGTATGATATGTTGTGAGATATT 1070
DB 221 ArgSerAlaIaIaValIrpSerIleuG1yIleLeuLeuIyTrAspMetValCySglYAspIle 240
QY 1071 CCTTTCAGAGATACGAAGAGATCATCAGGGGCGAGTTTCTTTCAGGCGAGAGTCT 1130
DB 241 ProPheGluHisAspGluGluIleIySglYGlnValPheAspArgGlnThrValSer 260
QY 1131 TCAGAAATGTCAGCATCTCATTAAGATGATGATGATGATGATGATGATGATGATG 1190
DB 261 SerGluCySglHisIleuIleIyStrpCySleSerIleuArgProSerAspArgProSer 280
QY 1191 TTGGAAGAAATTCAGAACCATTCATGATGATGATGATGATGATGATGATGATG 1250
DB 281 PheGluGluIleIyArgHisIrpTrpMetGlnG1yAspLeuLeuProGlnAlaIaSer 300
QY 1251 GAGATTCACCTTCACAGCTGTGCGCGCGCGCCAGCAAA 1289
DB 301 GluIleHisIleuHisSerLeuSerProG1ySerSerIyS 313
RESULT 7
PIM3_COTJA STANDARD; PRT; 323 AA.
ID PIM3_COTJA
AC G9P085;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (pdim).
GN Name=PIM3; Synonym=PIM-3;
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OC NCBI_TaxID=93934;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=20180111; PubMed=10713710; DOI=10.1038/nj.onc.1203355;
RA Eichmann A., Yuan L., Breant C., Alitalo K., Koehlihan P.J.;
RT "Developmental expression of Pim kinases suggests functions also
RT outside of the hematopoietic system."
RL Oncogene 19:1215-1224(2000).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- PTM: Autophosphorylated.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC subfamily.

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CC or send an email to license@sb-sib.ch).

DR EMBL; AJ130845; CAB62386.1; -
DR HSSP; Q63450; 1A06;
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR Prodom; PD000001; Prot_kinase; 1.

DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KM ATP-binding; Phosphorylation; Serine/threonine-protein kinase;

FT DOMAIN 40 291 Protein kinase.
FT NP_BIND 46 54 ATP (By similarity).
FT BINDING 69 69 ATP (By similarity).
FT ACT_SITE 168 168 Proton acceptor (By similarity).
SQ SEQUENCE 323 AA; 36597 MW; E2A4FA20B6F6396C CRC64;

Alignment Scores:

Pred. No.: 4.17e-54 Length: 323
Score: 1140.00 Matches: 209
Percent Similarity: 81.94% Conservative: 45
Best Local Similarity: 67.42% Mismatches: 52
Query Match: 23.80% Indels: 4
DB: 1 Gaps: 3

US-10-705-757-1 (1-2623) x PIM3_COTUA (1-323)

QY 351 ATGCTCTTGGCAAAATCAACTGCGCTTGGCCAGCGCGCGCTGCAACGACCTG 410
DB 1 MetLeuLeuSerIysPheGlySerLeuAlaHisIleCysSerProAlaSerMetAspHis 20
QY 411 CACGCCACCAAGCTGGCGCC-----GGCAGAGAGAGAGCCCTCGAGTGCAGTAC 464
DB 21 LeuProValIysIleLeuProProValIysValGluIleuProPheAspIysValTyr 40
QY 465 CAGCTGGGCGCGCTACTGGGCGACCGCGGCTTGGCGCTCTACTACAGGATCCCGCTC 524
DB 41 GluValGlySerValIleuGlySerGlyGlyPheGlyThrValTyrIleGlySerArgThr 60
QY 525 TCCGACAACTTGGCGGTGGCGCATCAACGATGAGAGAGAGCCGAGATTTCGACGGAGA 584
DB 61 AlaAspGlyLeuProValAlaValIysHisValIalIysGluTyrValThrGluTyrPgly 80
QY 585 GAGCTGCTTAATGGCATCTGAGTGGCCAGGAAAGGTGCTTGTGTAAGAAAGTGAAGCTGC 644
DB 81 ThrIle---GlyGlyValMetValProLeuGluIleValLeuLeuIysIysValGlySer 99
QY 645 GGTTCCTCGGCGCTCATTAAGGCTCTCGGACTGCTGAGAGGCGCCGACAGTTCCGCTCG 704
DB 100 GlyPheArgGlyValIleValIleuLeuAspTyrTyrIleuArgProAspGlyPheLeuIle 119
QY 705 ATCTGGAGAGGCGCGGAGCGGAGGACGATCTTGCAGCTTCAACGAGAAAGGAGGCC 764
DB 120 ValMetGluArgProGluLeuValIysAspLeuPheAspPheIleThrGluIysGlyAla 139
QY 765 CTGCAAGAGAGAGCTGGCGCGCGACCTTCTTGGCAGGTGCTGAGAGCGCGTGGCGCATGC 824
DB 140 LeuAspGluArgPheThrAlaArgGlyPhePheArgGluValIleuGluAlaValArgHisCys 159
QY 825 CACAACTGGCGGGGTGCTACACCGCGACATCAAGAGAGAAACATCTTATCAACCTCAAT 884
DB 160 TyrGlyCysGlyValValIleArgAspIleIysAspGluValbndLeuValAspLeuArg 179

QY 885 CCGCGCAGACTCAAGCTCATCTTGGGTCGGGGCGCTGCTCAAGACACCGTCTAC 944
DB 180 ThrGlyGluLeuIysLeuIleAspPheGlySerGlyAlaLeuLeuIysAspThrValTyr 199
QY 945 ACGGACTTGCATGGAGACCGCGAGTGTATAGCCCTCCAGACTGCATCCGATCGCTAC 1004
DB 200 ThrAspPheAspGlyThrArgValTyrSerProProGluTyrIleArgTyrHisArgTyr 219
QY 1005 CATGGCAGGTGGCGGCGAGCTGTGGTCCCGGGAGATCGCTGATATGATGTGGGTGGA 1064
DB 220 HisGlyArgSerAlaThrValTyrSerLeuGlyValLeuLeuTyrAspMetValCysGly 239
QY 1065 GATATTCCTTTTGCAGCATGACCAAGAGATCATCAAGGCGCGCGATTTCTTCAGCAGAG 1124
DB 240 AspIleProPheGluGluAspGluIleuArgGlyArgLeuTyrPheArgArgArg 259
QY 1125 GTCTCTTCAAGATGTCAGCATCTCATTAATGTGTGCTTGGCGCTGAGACCATCATATAG 1184
DB 260 IleSerProGluCysGluGlnIleuLeuIysTyrCysLeuSerLeuArgProSerArgArg 279
QY 1185 CCACTCTGAGAGAAATCCAGAACCATCATCATGATG---CAGATGTTCTCGCGCCAG 1241
DB 280 ProTrnLeuGluGlnIlePheAspHisGlnTrpMetHisIysSerGluValIysSer 299
QY 1242 GAAACTGTGAGATCCACTCCACAGCGCTG 1271
DB 300 GluAspCysAspIleArgLeuArgThrLeu 309

RESULT 8
PIM3_HUMAN STANDARD; PRT; 326 AA.

ID PIM3_HUMAN STANDARD; PRT; 326 AA.

AC 086V6;
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
GN Name=PIM3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klauener R.D., Collins F.S., Wagner L., Scheiner C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.B.,
RA Scherach A., Schein J.B., Jones S.J.M., Maris M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN (2)
RP IDENTIFICATION FROM ESTS.
RX MEDLINE=22682943; PubMed=12798037; DOI=10.1016/S1476-9271(02)00095-6;
RA Chichester C., Nikitin F., Ravarini J.-C., Lisacek F.,
RT "Consistency checks for characterizing protein forms";
RL Comput. Biol. Chem. 27:29-35 (2003).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

```

CC - SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ch/announce/
CC or send an email to license@ebi-eb.ch).
CC -----
DR EMBL; BC052239; AAH52239.1; ALT INIT.
DR InterPro; IPR011009; Kinase_lke.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_kin_AS.
DR Pfam; PF00659; PKinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Phosphorylation; Serine/threonine-protein kinase;
KW transferase.
FT DOMAIN 40 293 protein kinase.
FT NE BIND 46 54 ATP (By similarity).
FT BINDING 69 69 ATP (By similarity).
FT ACT SITE 170 170 Proton acceptor (By similarity).
SQ SEQUENCE 326 AA; 35863 MW; 41FD9DD2467A162 CRC64;

Alignment Scores:
Pred. No.: 1.01e-53 Length: 326
Score: 1133.00 Matches: 219
Percent Similarity: 80.38% Conservative: 35
Best Local Similarity: 69.30% Mismatches: 52
Query Match: 23.66% Indels: 10
Gaps: 7

US-10-705-757-1 (1-2623) x PIM3_HUMAN (1-326)
QY 351 ATGCTCTTGTCCAAATCACTGGCTTGGCCACTGCGCCGCCGCC-----TGCAAC 404
DB 1 MetLeuLeuSerLysPheGlySerLeuAlaHisLeu---CyGlyProGlyGlyValAsp 19
QY 405 GACCTGCAGCCGCAACGAGCTGGCGCCGCCGAG---GAGAAAGAGCCCTCGAGTGCAG 461
DB 20 HisLeuProValIleValIleLeuGlnProAlaIleValAspLysGluSerPheGlyValAla 39
QY 462 TACCAAGTGGCCCGCTACTGGGAGCGCGCGCTTCGGCTCGGCTACTACAGGCATCCGC 521
DB 40 TyrGlnValGlyIleValIleValIleGlySerGlyPheGlyThrValTyrAlaGlySerArg 59
QY 522 GTCTCCGACAACTTGGCCGCTGGCCGATCAACAGCTGGAGAGAGACCGGATTTCCGACTG 581
DB 60 IleAlaAspIleLeuProValAlaValIleHisIleValIleValIleGluValIleArgValIle 79
QY 582 GGAGAGTGGCTTAAAGCACTGAGTGGCCAGTGGCCAGTGGCTTCGCTGAGAGAGTGG--- 638
DB 80 GlySerLeu---GlyGlyAlaIleThrValProLeuGluValValIleuValArgIleValGly 98
QY 639 ---AGCTCGGAGTTTCTCCGCGCTCATTAAGGCTCTGAGTCTGAGAGCGCCGACAGT 695
DB 99 AlaAlaGlyIleValAlaArgIleValIleArgLeuLeuAspIlePheGluValArgProAspGly 118
QY 696 TTTCGCTGATCTCTGGAGAGAGCCGAGCCGAGCTTCCTTCCGAGAGCGCCGACAGT 755
DB 119 PheLeuLeuValIleuGluValArgProGluProGluAlaGlnAspPheAspPheIleThrGln 138
QY 756 AGGAGAGCCCTCGAGAGAGAGCGCCGCGAGCTTCTTCCGAGAGCGCCGAGCGCG 815
DB 139 ArgGlyAlaLeuAspIleuProLeuAlaArgArgPhePheAlaGlnValIleuAlaAlaVal 158
QY 816 CGGCACTGCCCAACTGCGGGGTGTACTACCGGAGCATCAAGAGCAAAACATCTTATC 875
DB 159 ArgHisCysHisSerCysGlyValValIleHisArgAspIleuValAspIleuLeuVal 178

```

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QY 876 GACCTCAATCCGCGGAGAGCTCAAGCTCATCATCTTGGGAGCGCGCTCTCAAGCA 935
DB 179 AspleuArgSerIleGlyIleuValIleAspPheGlySerIleValAlaLeuLeuValAsp 198
QY 936 ACGGTCTACACGAGCTTCGATGGAGCCGAGTATAGCCCTTCACAGTGCATCCGCTAC 995
DB 199 ThrValTyrThrAspPheAspGlyThrArgValTyrSerProGluIleAspGlyTyr 218
QY 996 CATGCTTACCATGAGAGAGTGGCGGAGCTTGGCTCCCTGGGAGTCTGTATGATATG 1055
DB 219 HisArgTyrHisGlyIleTyrSerIleAlaThrValTyrSerLeuGlyValLeuLeuTyrAspMet 238
QY 1056 GTGTGTCGAGATATTTCTTTCGACATGACAGAGAGATCATCGGGGCCAGGTTTCTTC 1115
DB 239 ValCysGlyAspIleProPheGluGlnAspGluGlnIleLeuArgIleValTyrGlyLeuPhe 258
QY 1116 AGGCAAGAGGTCCTCTTCAGATATGACATCTCATATGATGGTGTGGCCCTGAGACCA 1175
DB 259 ArgArgArgValSerProGluCysGlnGlnIleuAlaArgTyrCysLeuSerLeuArgPro 278
QY 1176 TCAGATAGGCCCAACTTCGAGAAATCCAGAACCATTCATGTATG-----CAAGATGTT 1229
DB 279 SerGluArgProSerLeuAspGlnIleAlaHisProTyrPheTyrLeuGlyAlaAspGly 298
QY 1230 CTCTCTCCCGCCAGGAACCTGTCAGATCCACCTTCACAGCTGTGCGCG 1277
DB 299 GlyAlaPro---GluSerCysAspLeuArgLeuCysThrLeuAspPro 313

RESULT 9
PIM3_MOUSE
ID PIM3_MOUSE STANDARD; PRT; 326 AA.
AC P58750;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
GN Name=Pim3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon, and Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
RA Klausner R.D.; Collins F.S.; Wagner L.; Shennan C.M.; Schuler G.D.;
RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;
RA Hopkins R.F.; Jordan H.; Moore T.; Wax S.I.; Wang J.; Hsieh F.;
RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
RA Stapleton M.; Soares M.B.; Bonaldi M.F.; Casavant T.L.; Schetz T.E.;
RA Brownstein M.T.; Ueda T.B.; Toshlyuk S.; Carninci P.; Prange C.;
RA Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullaly S.J.;
RA Bosak S.A.; McKernan P.J.; McKernan K.J.; Malek J.A.; Gamarine P.H.;
RA Richards S.; Morley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;
RA Villalón D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
RA Fahy J.; Helton B.; Kettelman M.; Madan A.; Rodrigues S.; Sanchez A.;
RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;
RA Blakesley A.C.; Grimwood J.; Schmutz J.; Myers R.M.;
RA Butterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smalins D.E.;
RA Scherch A.; Schein J.E.; Jones S.J.M.; Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC subfamily.
CC -----
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DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; Pkinase_I.
DR ProDom: PD000001; Prot_Kinase_1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Phosphorylation; Serine/threonine-protein kinase;
KW Transferase.
FT DOMAIN 40 293 Protein kinase.
FT NP_BIND 46 54 ATP (By similarity).
FT BINDING 69 69 ATP (By similarity).
FT ACT_SITE 170 170 Proton acceptor (By similarity).
SQ SEQUENCE 326 AA; 36002 MW; DD6CBF4635F851B CRC64;

Alignment Scores:
Pred. No.: 1,77e-53 Length: 326
Score: 1128.50 Matches: 213
Percent Similarity: 82.71% Conservative: 31
Best Local Similarity: 72.20% Mismatches: 44
Query Match: 23.56% Indels: 7
DB: Gaps: 5

US-10-705-757-1 (1-2623) x PIM3_RAT (1-326)

QY 351 ATGCTCTTTCGCAAAATCAACTGCTGGCCCACTGGCGCGCGCC-----TGCAAC 404
DB 1 MetLeuLeuSerIlybPheglYSerLeuAlaHisLeu---CyeglYProglYglYValAsp 19
QY 405 GACCTGCACGCCCAACCAAGCTGGCGCGCGCGCAAG---GAGAAGAGACCCCTGAGTCGCAG 461
DB 20 HisLeuProValIlybIleLeuGlnProAlaIlyAlaAspIlybIlySerPheglYbVal 39
QY 462 TACCAAGTGGCGCGCTACTGGCGAGCGCGCGCTTCGCTCGCTTCACTCAAGCATCCGC 521
DB 40 TygIlnValIglYAlaValIleuGlYSerIglYglYbPheglYThrValIlyAlaIglYSerArg 59
QY 522 GTCTCCGACAACTTGGCGGTGGCCATCAACACGTGAGAGAGACCGGATTTCCGACTCG 581
DB 60 IleAlaAspIlyleuProValAlaValIlybIleValIlybValIlybValIlybValIlybVal 79
QY 582 GGAAGAGTGCCTAATGCACTGAGTGCCTGAGTGCCTGAGTGCCTGAGTGCCTGAGTGCCT 638
DB 80 GlYSerLeu---GlYglYMetAlaValIProLeuGlnValIlyLeuLeuAlYglYbValIglY 98
QY 639 ---AGTCCGGGTTTCTCCGGCGTCAATTAGGCTCTCGACTCGTTCGAGAGCCCGACAGT 695
DB 99 AlaIlaGlYglYAlaArgIlyValIleArgLeuLeuAspTrpPheglYbArgProAspGlY 118
QY 696 TTGCTCTGATCTCTGGAGAGAGCCCGGAGCGGTCGAGATCTTTCATCTTCACTCAAGCA 755
DB 119 PheLeuLeuValIleuGlnArgProGlnProAlaIglAlaAspPheIleTrpGln 138
QY 756 AGGAGAGCCCTGCAAGAGAGTGGCGCGCGCTTCTTTCGCGAGGTCGAGAGCGCGT 815
DB 139 ArgGlYAlaIleuAspIlybIleuAlaArgPheAlaIglAlaIleuAlaIlaVal 158
QY 816 CGGCACTGCCCAACTGCGGGGTGTACACCGCGACATCAAGAGCAAAAATCTTATTC 875
DB 159 ArgHisCybHisbAncYbGlYValIlaHisbArgAspIleIlybAspIlybAsnLeuVal 178
QY 876 GACCTCAATCGCGCGAGCTCAAGCTTCAAGTTCGGGTCGGGGGCGCTGCAAGAG 935
DB 179 AspLeuArgSerIglYIleuLeuIlybLeuIleAspPheIlySerIglYAlaValIleuIlybAsp 198
QY 936 ACCGTCTACACGAGCTTCAATGGGAGCCGAGTGTATGAGCCCTCAAGAGTGCATCCGCTAC 995
DB 199 ThrValIlyThrAspPheAspIlyThrArgValIlySerProGlnIlybIleArgIlyr 218
QY 996 CATCGCTACACGAGAGTGGCGCGCGAGTGTGCTCCCTGGGAGATCCGTGTATGATATG 1055
DB 219 HisArgIlyrHisbIglYArgSerAlaThrValIlyrPheLeuIlyValIleuLeuIlyrAspMet 238

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QY 1056 GTGTGTGAGATATATCTTTCGAGCATGACGAAGATCATCAGGCGCGGCTTCTTC 1115
DB 239 ValCyeglYAspIleProPheglYbGlnArgIleGlnIleuArgIglYbAspPhePhe 258
QY 1116 AGCAGAGGCTCTTTCAGAAATGTCAGACTCATTAAGATAGTGTGGCCCTGAGACCA 1175
DB 259 ArgArgbArgIlySerProGlnIlybGlnIleuIleIglYbTrpCybLeuSerLeuAspPro 278
QY 1176 TCAGATAGGCCCAACTTCGAGAAATTCAGAACCATTCATGATG 1220
DB 279 SerGlnArgProSerLeuAspGlnIleAlaIlaHisbProTrpMet 293

RESULT 11
Q811X8 PRELIMINARY; PRT; 325 AA.
ID Q811X8;
AC Q811X8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE KID1.
GN Name=Pim3; Synonym=Kidl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Yu L.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL: AY026239; AKL1606.1; -.
DR HSSP: Q03656; 1Q99.
DR MGD: MGI:1355297; Pim3.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004674; F:Protein serine/threonine kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0004688; F:protein amino acid phosphorylation; IEA.
DR InterPro: IPR011009; Kinase_like.
DR InterPro: IPR000719; Prot_Kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_Kinase; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 325 AA; 35931 MW; 77DBF8E20F41E3F4 CRC64;

Alignment Scores:
Pred. No.: 8.49e-53 Length: 325
Score: 1116.00 Matches: 212
Percent Similarity: 82.71% Conservative: 32
Best Local Similarity: 71.86% Mismatches: 43
Query Match: 23.30% Indels: 8
DB: Gaps: 6

US-10-705-757-1 (1-2623) x Q811X8 (1-325)

QY 351 ATGCTCTTTCGCAAAATCAACTGCTGGCCCACTGGCGCGCGCC-----TGCAAC 404
DB 1 MetLeuLeuSerIlybPheglYSerLeuAlaHisLeu---CyeglYProglYglYValAsp 19
QY 405 GACCTGCACGCCCAACCAAGCTGGCGCGCGCGCAAG---GAGAAGAGACCCCTGAGTCGCAG 461
DB 20 HisLeuProValIlybIleLeuGlnProAlaIlyAlaAspIlybIlySerPheglYbVal 39
QY 462 TACCAAGTGGCGCGCTACTGGCGAGCGCGCGCTTCGCTCGCTTCACTCAAGCATCCGC 521
DB 40 TygIlnValIglYAlaValIleuGlYSerIglYglYbPheglYThrValIlyAlaIglYSerArg 59
QY 522 GTCTCCGACAACTTGGCGGTGGCCATCAACACGTGAGAGAGACCGGATTTCCGACTCG 581
DB 60 IleAlaAspIlyleuProValAlaValIlybIleValIlybValIlybValIlybValIlybVal 79

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QY 582 GAGAGAGCTGCTTAATGCACTGAGAGTCCCATGAGAGTGTCTGCTGAGAGAGTGG---- 638
DB 80 GlySerLeu---GlyGlyValAlaValProLeuGlnValValLeuLeuArgGlyValGly 98
QY 639 ---AGCTCGGGTTTCTCCGGCTCATTTAGGCTCTGAGCTGTTTCAGAGGCCGCAAGT 695
DB 99 AlaAlaGlyGlyAlaArgGlyValIleArgLeuLeuAspTrpPheGlnArgProAspGly 118
QY 696 TTTCGCTCTGATCTCTGAGAGAGGCCGCGAGTCTTCTGCAATCTTCATCTCAGGAA 755
DB 119 PheLeuLeuValLeuGlnArgProGlnProAlaGlnAspLeuPheAspPheIleTrpGln 138
QY 756 AGGGAGGCCCTGCAAGAGAGAGCTGGGCGCGAGCTTCTTGGAGAGTGGCGAGGCGTG 815
DB 139 ArgGlyAlaLeuLeuArgLysProLeuAlaArgArgPhePheAlaGlnValLeuAlaVal 158
QY 816 CGGCACTGCGCAACTGCGGGGTGTACACCGGACATCAAGGACGAAACATCTTATTC 875
DB 159 ArgHisCysHisValMetCysGlyValValHisArgAspIleLeuAspArgLysLeuLeuVal 178
QY 876 GACCTCAATCGCGGCGAGCTCAAGCTCATGATCTTGGGGTGGGGCGCTGCTCAAGAC 935
DB 179 AspLeuArgSerGlyGlyLeuLeuValLeuAspPheGlySerGlyAlaValLeuLeuAsp 198
QY 936 ACCGCTCAACGAGACTTCGATGGAGCCGAGTATAGCCCTGACAGATGGATCGGCTAC 995
DB 199 ThrValValThrAspPheAspGlyThrAspValValSerProGlnTrpIleArgGly 218
QY 996 CATCGCTACCATGAGCAAGTGGCGGCGAGTGTGCTGCTGCGAGATCTGTATGATATG 1055
DB 219 HisArgGlyTrpHisGlyArgSerGlyAlaTrpValTrpSerLeuGlyValLeuLeuTrpAspMet 238
QY 1056 GTGTGTGAGATATTTCTTTCAGCATGACGAAAGATATCATCGGGCGCGAGGTTTCTTC 1115
DB 239 ValCysGlyAspIleProPheGlnGlnAspGlnGlnIleLeuArgGlyArgLeuPhePhe 258
QY 1116 AGGAGAGGGGTCTCTTCAGAAATGTCAGCATCTCATTAAGATGGATGGCGCTGAGACCA 1175
DB 259 ArgArgArgValSerProGlnCysGlnGlnIleLeuIleGlnTrpCysLeuSerLeuAspPro 278
QY 1176 TCAGATAGGCCCACTTCGAGAAATTCAGAACATTCATGATGATG 1220
DB 279 SerGlnArgProSerLeuAspLeuLeu---CysHisProTrpMet 292
RESULT 12
PIM3_XENLA STANDARD; PRT; 323 AA.
AC 091822;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (Pim-1).
GN Name=PIM3; Synonyms=PTM1;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN 11;
RP SEQUENCE FROM N.A., AND PHOSPHORYLATION SITES.
RA MEDLINE=9726766; Pubmed=909695; DOI=10.1074/jbc.272.16.10514;
RA Palaty C.K., Kaimar G., Tai G., Oh S., Amankwa L., Affolter M.,
RA Aebersold R., Pelech S.L.;
RT Identification of the autophosphorylation sites of the Xenopus laevis
RT Pim-1 proto-oncogene-encoded protein kinase."
RL J. Biol. Chem. 272:10514-10521(1997).
CC 1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC 1- PIM: Autophosphorylated.
CC 1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC subfamily.
CC 1- CAUTION: Was originally (Ref.1) called Pim-1 but seems to
CC represent the pim-3 isoform.

```

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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: L29495; AAA85389.1; -.
CC InterPro: IPR011009; Kinase_1like.
CC InterPro: IPR000719; Prot Kinase.
CC InterPro: IPR008271; Ser thr_pkin_AS.
CC Pfam: PF00069; Pkinase; 1.
CC ProDom: PD000001; Prot Kinase; 1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC ATP-binding; Phosphorylation; Serine/threonine-protein kinase;
CC Transferase.
CC DOMAIN
CC FT NP_BIND 40 291 Protein kinase.
CC FT BINDING 46 54 ATP (By similarity).
CC FT ACT_SITE 69 69 ATP (By similarity).
CC FT ACT_SITE 168 168 Proton acceptor (By similarity).
CC FT MOD_RES 4 4 Phosphoserine (by autocatalysis)
CC FT MOD_RES 190 190 Phosphoserine (by autocatalysis).
CC FT MOD_RES 205 205 Phosphothreonine (by autocatalysis)
CC FT SEQUENCE 323 AA; 36964 MW; AB4DD61E7A9A38F CRC64;
SQ
Alignment Scores:
Pred. No.: 3,37e-52 Length: 323
Score: 1105.00 Matches: 205
Percent Similarity: 80.25% Conservative: 47
Best Local Similarity: 65.29% Mismatches: 50
Query Match: 23.07% Indels: 12
DB: 1 Gaps: 5
US-10-705-757-1 (1-2623) x PIM3_XENLA (1-323)
QY 351 ATGCTCTGTTCCAAATATCACTGCTGGCCACTGCGCGCGCGCTCGAAC----- 404
DB 1 MetLeuLeuSerLeuPheGlySerLeuAlaHisIle-----CysAspProSer 16
QY 405 -----GACCTGACGCGCACCAAGCTGGGCGCGCGCGAG---GAGAAAGAGCCCGT 452
DB 17 AsnMetGlnHisLeuProValLysIleLeuGlnProValLysValAspLysGlnProPhe 36
QY 453 GAGTGCAGATACCAAGTGGGCGCGCTACTGCGAGCGGCGCTCGGCTCACTCA 512
DB 37 GlyLysValLysGlnValGlySerValAlaAspArgGlyPheGlyThrValTyrSer 56
QY 513 GGCATCCGCGTCTCCGACCACTTGCCCGGTGCCATCAACACGTGAGAAAGACCGGATT 572
DB 57 AspSerArgIleAlaAspArgLysGlnProValAlaValLysValAlaValArgVal 76
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DB 116 AlaPheLeuIleValMetGlnArgProGlnProValLysAspLeuPheAspTrpIleThr 135
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Qy	873	ATCGAAGCTCAATCCGGCGGAGACTCAAGCTCAAGCTTCCGGGTCCGGGCGCTGCTCAAG	932
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Qy	933	GACACCGGCTTACACGGAATTGATGATGGGACCGGAGGTATACCCCTCCAGATGGATCCGC	992
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Db	216	TyrHisArgIyPheIyGlyArgSerHisLeuThrValIyPheSerLeuGlyValLeuLeuIyTrAsp	235
Qy	1053	ATGGTGTGTGAGATATATCTTTTCAGACATACAGAGATCATCAGGGGCGAGATTTTC	1112
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DT	25-OCT-2004 (TEMBLrel. 28, Last annotation update)			
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OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;			
OC	Xenopodinae; Xenopus.			
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RA	Klausner R.D., Collins F.S., Wagner N., Shemen G.M., Schuler G.D.,			
RA	Altschul S.P., Zeeberg B., Bucow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H.I., Moore T., Wax S.I., Wang Y., Hsieh F.,			
RA	Diatchenko L., Marubina K., Farmer A.A., Rubin G.M., Hong L.,			
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RA	Beak S.A., McEwan P.J., McEwan K.J., Malek J.A., Gunaratne P.H.,			
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RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywnicki M.I., Skalka U., Smalins D.E., Scherch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
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RC	TISSUE=Embryo;			
RA	Klein S., Gerhard D.S.;			

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 DR InterPro: IPR000719; Ser Thr_kinase.
 DR InterPro: IPR002290; Ser Thr_kinase.
 DR InterPro: IPR0068271; Ser Thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc_1.
 DR SMART: SM00219; TyrKc; 1.
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 DR PROSITE: PSS0108; PROTEIN_KINASE_ST; 1.
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DB	208	ProGluTrpIleArgPheHisLysTyrHisIleLysArgSerAlaThrValTrpSerLeuGly	227
QY	1038	ATCTGCTGTATGATATGAGTGTGGAGATATTCTTTCCAGGATGACGAAAGATCATC	1097

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 AC Q62070; Q62071; Q62072;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
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 RX MEDLINE=95300786; PubMed=7781606;
 RA van der Lugt N.M., Domen J., Verhoeven E., Linders K.,
 RA van der Gulden N.M., Allen J., Berns A.;
 RT "Proviral tagging in E. mu-myc transgenic mice lacking the Pim-1 proto-
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 RL EMBL J. 14:2536-2544(1995).
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 CC -1- ALTERNATIVE PRODUCTS:
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 CC Comment=3 isoforms, 1 (shown here), 2 and 3, are produced by
 CC alternative initiation. Isoform 1 and isoform 2 initiate from
 CC CDS codons;
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
 subfamily.
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 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
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 CC HSSP; Q63450; LA06.
 CC MGD; MGI:97587; Pim2.
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 CC GO; GO:0004674; F-protein serine/threonine kinase activity; IDA.
 CC GO; GO:0006916; P-anti-apoptosis; IDA.
 CC GO; GO:0008637; P-apoptotic mitochondrial changes; IDA.
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KW Serine/threonine-protein kinase; Transferase.
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 FT CHAIN 60 370 isoform 2.
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GenCore version 5.1.6
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Run on: September 22, 2005, 16:26:26 ; Search time 356.236 Seconds

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Searched: 1826521 seqs, 407012169 residues

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	1670	34.9	313	16	US-10-664-421-1
6	1670	34.9	313	16	US-10-664-421-150
7	1670	34.9	313	16	US-10-377-268-9
8	1670	34.9	313	17	US-10-951-389-18
9	1670	34.9	313	17	US-10-951-406-18
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ALIGNMENTS

RESULT 1
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; Sequence 9, Application US/09971791
; Patent No. US20020115120A1
; GENERAL INFORMATION:
; APPLICANT: Rosanna Kapeller-Libermann
; APPLICANT: Laura A. Rudolph-Owen
; APPLICANT: Kyle MacBeth
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 35800/238856
; CURRENT APPLICATION NUMBER: US/09/971, 791
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/644, 450
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/237, 543
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 313

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-971-791-9

Alignment Scores:
Pred. No.:      2,42e-94      Length:      313
Score:          1670.00      Matches:      313
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      34.87%      Indels:      0
DB:               9          Gaps:      0

US-10-705-757-1 (1-2623) x US-09-971-791-9 (1-313)

QY      351  ATGCTCTGTCCAAATCAACTGCTTGGCCCACTGCGCGCGCCCTGCAACGACTG  410
      |||
Db      1  MetLeuLeuSerLysIleAsnSerLeuAlaHisLeuArgAlaIleProCysAsnAspLeu  20

QY      411  CACGCCACCAAGCTGGGCGCGCGCAAGAGAGAGAGCCCTGGAGTCCGAGTACCAAGTG  470
      |||
Db      21  HisAlaThrIleuLeuAlaProGlyLysGlyLysGlyProLeuLeuSerGlnIlyrGlnVal  40

QY      471  GGGCCGCTACTGGGCAAGCGCGGCTTCGCTCGTCTACTCAGGCAATCCGCGTCTCGAC  530
      |||
Db      41  GlyProLeuLeuGlySerGlyIlyPheGlySerValIlySerGlyIleArgValSerAsp  60

QY      531  AACTGCGCGTGGCCATCAAAACGTTGAGAGAGACCGGATTTCCGACTGGGAGAGCTG  590
      |||
Db      61  AsnLeuProValAlaIleLysHisValGlnLysAspArgIleSerAspTrpGlyLysLeu  80

QY      591  CCTAATGCACTGAGTGGCCCATGAGAGTGGTCTGCTGGAAGAGGAGTGGGTTTC  650
      |||
Db      81  ProAsnGlyThrArgValIleProMetGlyValValLeuLeuLysValSerSerGlyPhe  100

QY      651  TCGGGGCTCATTAAGCTCTGGAAGTGGTTCGAGAGCGCGCAAGTTTCCTGATCTCG  710
      |||
Db      101  SerGlyValIleArgLeuLeuAspTrpPheGlyArgProAspSerPheValLeuIleLeu  120

QY      711  GAGAGCGCGAGCGCGGTGCAAGATCTTTCGACTTATCAACGGAAGGGAGCGCTGCA  770
      |||
Db      121  GlnArgProGlnProValGlnAspLeuPheAspPheIleThrGlnArgGlyAlaLeuGln  140

QY      771  GAGGACTGGCGCGCGAGCTTCTTGGCAGAGTCTGAGAGCGCGTGGCGCACTGCCA  830
      |||
Db      141  GlnGlnLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgHisCysHisAsn  160

QY      831  TGGGGGCTGTACACCGGCATCAAGAGAGCAAAACCTTATTCGACTCAATCGCGCG  890
      |||
Db      161  CysGlyValIleuHisArgAspIleLysAspGlyAsnIleLeuIleAspLeuAsnArgGly  180

QY      891  GAGCTCAAGCTCATTCGACTTGGGGTGGGGGCGCTGCTCAAGGACCGGCTACAGGAC  950
      |||
Db      181  GlnLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValIlyTrnAsp  200

QY      951  TTGAGTGGGACCGGAGTGTATAGCCCTCGAGTGTATCCGTAACATCCGCTCAATG  1010
      |||
Db      201  PheAspGlyThrArgValIlyrSerProProGlnTrpIleArgIlyrHisArgIlyrHisGly  220

QY      1011  AGGTGGGCGGCACTGTGCTCGTGGGAGTCTGCTGTATGATATAGTGTGGAGATATT  1070
      |||
Db      221  ArgSerAlaIleValIleTrpSerLeuGlyIleLeuLeuIlyrAspMetValCysGlyAspIle  240

QY      1071  CCTTTGAGAGATACCAAGAGATCATACAGGGGCCAGGTTTCTTTCAGGCGAGAGGCT  1130
      |||
Db      241  ProPheGlnHisAspGlnGlnIleIleArgGlyGlnValPhePheArgGlnAspValSer  260

QY      1131  TCAGAAATGTCAGATCTCATTTAGATGGTGTGGTGGCCCTGAGACCATACAGATAG  1190
      |||
Db      261  SerGlnCysGlnHisIleuIleArgTrpCysLeuAlaLeuArgProSerAspArgProTrn  280

QY      1191  TTGGAAGAAATCCAGAACCATTCATGAGTCAAGATGTTCTCTGCGCCAGAGAACTG  1250
      |||
Db      281  PheGlnGlnIleGlnHisIleAsnHisProTrpMetGlnAspValLeuLeuProGlnGlnTrnAla  300
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QY      1251  GAGATCAACTTCACAGCGCTGTGCGCGGCGCCAGCAAA  1289
      |||
Db      301  GlnIleHisLeuHisSerLeuSerProGlyProSerLys  313

RESULT 2
US-10-081-119-18
; Sequence 18, Application US/1008119
; Publication No. US20030045491A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-081-119-18

Alignment Scores:
Pred. No.:      2,42e-94      Length:      313
Score:          1670.00      Matches:      313
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      34.87%      Indels:      0
DB:               14          Gaps:      0

US-10-705-757-1 (1-2623) x US-10-081-119-18 (1-313)

QY      351  ATGCTCTGTCCAAATCAACTGCTTGGCCCACTGCGCGCGCCCTGCAACGACTG  410
      |||
Db      1  MetLeuLeuSerLysIleAsnSerLeuAlaHisLeuArgAlaIleProCysAsnAspLeu  20

QY      411  CACGCCACCAAGCTGGGCGCGCGCAAGAGAGAGAGCCCTGGAGTCCGAGTACCAAGTG  470
      |||
Db      21  HisAlaThrIleuLeuAlaProGlyLysGlyLysGlyProLeuLeuSerGlnIlyrGlnVal  40

QY      471  GGGCCGCTACTGGGCAAGCGCGGCTTCGCTCGTCTACTCAGGCAATCCGCGTCTCGAC  530
      |||
Db      41  GlyProLeuLeuGlySerGlyIlyPheGlySerValIlySerGlyIleArgValSerAsp  60

QY      531  AACTGCGCGTGGCCATCAAAACGTTGAGAGAGACCGGATTTCCGACTGGGAGAGCTG  590
      |||
Db      61  AsnLeuProValAlaIleLysHisValGlnLysAspArgIleSerAspTrpGlyLysLeu  80

QY      591  CCTAATGCACTGAGTGGCCCATGAGAGTGGTCTGCTGGAAGAGGAGTGGGTTTC  650
      |||
Db      81  ProAsnGlyThrArgValIleProMetGlyValValLeuLeuLysValSerSerGlyPhe  100

QY      651  TCGGGGCTCATTAAGCTCTGGAAGTGGTTCGAGAGCGCGCAAGTTTCCTGATCTCG  710
      |||
Db      101  SerGlyValIleArgLeuLeuAspTrpPheGlyArgProAspSerPheValLeuIleLeu  120

QY      711  GAGAGCGCGAGCGCGGTGCAAGATCTTTCGACTTATCAACGGAAGGGAGCGCTGCA  770
      |||
Db      121  GlnArgProGlnProValGlnAspLeuPheAspPheIleThrGlnArgGlyAlaLeuGln  140

QY      771  GAGGACTGGCGCGCGAGCTTCTTGGCAGAGTCTGAGAGCGCGTGGCGCACTGCCA  830
      |||
Db      141  GlnGlnLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgHisCysHisAsn  160

QY      831  TGGGGGCTGTACACCGGCATCAAGAGAGCAAAACCTTATTCGACTCAATCGCGCG  890
      |||
Db      161  CysGlyValIleuHisArgAspIleLysAspGlyAsnIleLeuIleAspLeuAsnArgGly  180
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QY 891 GAGCTCAAGCTCATGACCTTCGGGTCGGGGCGCTGCTCAAGACACCGTCTACAGCGAC 950
|||
DB 181 G|u|e|u|y|s|e|u|l|e|a|s|p|h|e|g|l|y|s|e|r|g|l|a|l|e|u|e|u|y|s|a|s|p|h|r|v|a|l|y|r|h|n|a|s|p 200
|||
QY 951 TTCGATGGGACCCGAGTGTATAGCCCTTCAGAGTGTATCCGCTACATCGCTACCATAGGC 1010
|||
DB 201 Phe|a|s|p|g|l|y|h|r|a|g|v|a|l|y|r|s|e|r|p|r|o|b|o|l|u|t|r|p|l|e|a|r|g|y|r|h|s|a|r|g|y|r|h|s|g|l|y 220
|||
QY 1011 AGGTGGCGGCGAGTCTGGTCCCTGGGAGATCCTGCTGTATGTATGTGTGTGTGAAGATATT 1070
|||
DB 221 A|r|g|s|e|r|l|a|l|a|v|a|l|t|r|p|s|e|r|l|e|u|g|l|y|l|e|u|e|u|y|r|a|s|p|h|e|v|a|l|c|y|s|g|l|y|a|s|p|h|e 240
|||
QY 1071 CCTTCGAGCATGACGAGAGATCATGAGGCGCGGCTTTCTTCAGAGAGAGGTCTCT 1130
|||
DB 241 P|r|o|p|h|e|l|u|n|h|s|a|s|p|h|e|g|l|u|l|e|l|e|a|r|g|y|g|l|n|a|l|p|h|e|r|a|r|g|l|n|a|g|v|a|l|s|e|r 260
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QY 1131 TCAGATGTGACGATCTCATTTAGATGGTGTGGCCCTGAGACCATGATAGGCGCAAC 1190
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DB 261 S|e|r|g|l|u|c|y|s|e|g|n|h|s|e|u|l|e|a|r|g|t|r|p|c|y|s|e|u|a|l|e|u|a|r|g|r|o|s|e|r|a|s|p|h|a|r|g|r|o|t|h|r 280
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QY 1191 TTGGAAGAAATCCGAACCATCCATGAGATGCAAGATGTTCTCTGCCCCAGAAATGCT 1250
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DB 281 P|h|e|g|l|u|l|e|g|l|n|a|s|h|s|p|r|o|t|r|p|m|e|r|g|l|n|a|s|p|h|a|l|e|u|e|u|p|r|o|g|l|n|g|l|u|r|h|a| 300
|||
QY 1251 GAGATCCACCTCCACAGCGCTGTGCGCGGGCGCCGCAAA 1289
|||
DB 301 G|l|u|l|e|h|l|e|u|h|l|s|e|r|l|e|u|s|e|r|p|r|o|g|l|y|p|r|o|s|e|r|l|y|s 313
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RESULT 3
US-10-394-322A-52
; Sequence 52: Application US/10394322A
; Publication No: US20030232391A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-52
Alignment Scores:
Pred. No.: 2,42e-94 Length: 313
Score: 1670.00 Matches: 313
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.87% Indels: 0
DB: 15 Gaps: 0
US-10-705-757-1 (1-2623) x US-10-394-322A-52 (1-313)
QY 351 ATGCTCTGTCCAAATCACTGCTTGGCCACCTGCGCGCGCGCTTCGACAGACGCTG 410
|||
DB 1 M|e|t|l|e|u|s|e|r|l|y|s|l|e|a|s|e|r|l|e|u|a|h|l|e|u|a|r|g|l|a|l|a|p|r|o|c|y|s|a|s|p|h|e|u 20
|||
QY 411 CAGGCCAACAGCTGGCGCGCGCGGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 470
|||
DB 21 H|l|e|a|h|t|r|l|y|l|e|u|h|a|p|r|o|g|l|y|l|e|g|l|u|l|y|l|e|g|l|u|l|y|l|e|u|h|s|e|r|l|y|r|g|l|n|a|l 40
|||
QY 471 GGGCCGCTACTGGGACAGCGCGGCTTGGCTCGGTCTACTCAGGACATCCGCTGTCCGAC 530
|||
DB 41 G|l|y|r|o|l|e|u|e|u|g|l|s|e|r|g|l|y|l|p|h|e|g|l|s|e|r|v|a|l|y|r|s|e|r|g|l|l|e|a|r|g|v|a|l|s|e|r|a|s|p 60
|||
QY 531 AACCTGGCGGTGGCATCAACAGCTGAGAGAGACCGGATTTCCGACTGGGAGAGCTG 590
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DB 61 A|s|h|e|u|r|o|l|a|h|a|l|e|u|s|h|s|v|a|l|g|l|u|l|y|s|a|s|p|h|a|r|g|l|l|e|s|e|r|a|p|r|g|l|y|g|l|u|e|u 80
|||
QY 591 CCTAATGGCACTCGAGTGGCCCATGAGAGTGTCTCTGCTGAGAGAGAGTACGAGCTTTC 650
|||
DB 81 P|r|o|a|s|p|g|l|y|h|r|a|g|v|a|l|p|r|o|m|e|r|g|l|u|a|l|v|a|l|l|e|u|e|u|y|s|v|a|l|s|e|r|s|e|r|g|l|y|p|h|e 100
|||
QY 651 TCGGCGCTCATTTAGCTCCCTCGAGCTGTTTGAAGAGCGCGCAAGTTTCCCTGATCTCTG 710
|||
DB 101 S|e|r|g|l|y|a|l|l|e|a|r|g|l|e|u|e|u|a|s|p|r|p|h|e|g|l|u|a|r|g|r|o|a|s|p|h|e|r|v|a|l|l|e|u 120
|||
QY 711 GAGAGCCCGAGCGGTCGAGAGATCTTCTGACTTCATCAGGAAAGGAGGAGCGCTGCA 770
|||
DB 121 G|l|u|a|r|p|r|o|l|u|r|o|l|a|g|l|n|a|s|p|h|e|r|p|h|e|l|e|h|r|g|l|u|a|r|g|l|a|l|e|u|g|l|n 140
|||
QY 771 GAGAGCTGCGCGCGAGCTTCTTCTGAGCTGTCGAGGCGCGCTGCGCACTCGCACAC 830
|||
DB 141 G|l|u|l|e|u|h|a|a|r|g|s|e|r|p|h|e|r|p|h|e|r|g|l|n|a|l|l|e|u|g|l|u|a|l|a|r|g|h|s|c|y|h|s|a|s|h 160
|||
QY 831 TCGGGGGTGTATACCGCGCATCATAGAGAGAGAAACATCTTATCCACTCATCGCGGC 890
|||
DB 161 C|y|s|g|l|y|a|l|l|e|u|h|s|a|r|g|a|p|h|l|e|l|y|s|a|s|p|h|a|s|h|l|e|u|h|l|e|a|s|p|h|e|u|a|s|h|l|y|g|l|y 180
|||
QY 891 GAGCTCAAGCTCATGCACTTCGGGTCGGGGCGCGCTGCTCAAGAGACACCGTCTACAGCGAC 950
|||
DB 181 G|l|u|e|u|y|s|e|u|l|e|a|s|p|h|e|g|l|y|s|e|r|g|l|a|l|e|u|e|u|y|s|a|s|p|h|r|v|a|l|y|r|h|n|a|s|p 200
|||
QY 951 TTCGATGGGACCCGAGTGTATAGCCCTTCAGAGTGTATCCGCTACATCGCTACCATAGGC 1010
|||
DB 201 P|h|e|a|s|p|g|l|y|h|r|a|g|v|a|l|y|r|s|e|r|p|r|o|b|o|l|u|t|r|p|l|e|a|r|g|y|r|h|s|a|r|g|y|r|h|s|g|l|y 220
|||
QY 1011 AGGTGGCGGCGAGTCTGGTCCCTGGGAGATCCTGCTGTATGTGTGTGTGTGAAGATATT 1070
|||
DB 221 A|r|g|s|e|r|l|a|l|a|v|a|l|t|r|p|s|e|r|l|e|u|g|l|y|l|e|u|e|u|y|r|a|s|p|h|e|v|a|l|c|y|s|g|l|y|a|s|p|h|e 240
|||
QY 1071 CCTTCGAGCATGACGAGAGATCATGAGGCGCGAGGCTTTCTTCAGGCGAGAGGTCTCT 1130
|||
DB 241 P|r|o|p|h|e|l|u|n|h|s|a|s|p|h|e|g|l|u|l|e|l|e|a|r|g|y|g|l|n|a|l|p|h|e|r|a|r|g|l|n|a|g|v|a|l|s|e|r 260
|||
QY 1131 TCAGATGTGACGATCTCATTTAGATGGTGTGGCCCTGAGACCATGATAGGCGCAAC 1190
|||
DB 261 S|e|r|g|l|u|c|y|s|e|g|n|h|s|e|u|l|e|a|r|g|t|r|p|c|y|s|e|u|a|l|e|u|a|r|g|r|o|s|e|r|a|s|p|h|a|r|g|r|o|t|h|r 280
|||
QY 1191 TTGGAAGAAATCCGAACCATCCATGAGATGCAAGATGTTCTCTGCCCCAGAAATGCT 1250
|||
DB 281 P|h|e|g|l|u|l|e|g|l|n|a|s|h|s|p|r|o|t|r|p|m|e|r|g|l|n|a|s|p|h|a|l|e|u|e|u|p|r|o|g|l|n|g|l|u|r|h|a| 300
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QY 1251 GAGATCCACCTCCACAGCGCTGTGCGCGGGCGCCGCAAA 1289
|||
DB 301 G|l|u|l|e|h|l|e|u|h|l|s|e|r|l|e|u|s|e|r|p|r|o|g|l|y|p|r|o|s|e|r|l|y|s 313
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RESULT 4
US-10-348-081-13
; Sequence 13: Application US/10348081
; Publication No: US20040038246A1
; GENERAL INFORMATION:
; APPLICANT: KORN, Marcus
; APPLICANT: MOELLER, Guenter
; APPLICANT: SCHNEIDER, Rudolf
; TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
; FILE REFERENCE: DE42002/0004 US NP
; CURRENT APPLICATION NUMBER: US/10/348,081
; CURRENT FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-348-081-13
Alignment Scores:
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Pred. No. : 2,42e-94 Length: 313
Score: 1670.00 Matches: 313
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.87% Indels: 0
DB: 15 Gaps: 0

US-10-705-757-1 (1-2623) x US-10-348-081-13 (1-313)

QY ATGCTCTGTGCAAAATCAACTGCTTGCCCACTGGCGCGCGCCCTGCAAGACTTG 410
DB 1 MetLeuLeuSerLyIleAenSerLeuAlaHleuAArgLaIaProCySaenAerLeu 20
QY 411 CAGGCCACCAAGCTGGCGCGCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 470
DB 21 HisAlaThrLyLeuAlaProGlyLySGLuLyGluProLeuInuSerGlnTyrgInuAl 40
QY 471 GCGCCGCTACTGGGAGCGCGCGCTTCGCGCTCGGTACTCAGGCAATCCGCTCCGAC 530
DB 41 GlyProLeuLeuInuSerGlyLySGLuLySerValTySerGlyIleAArgValSerAer 60
QY 531 AACTTGCCGCTGGCCATCAAAACAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGCTG 590
DB 61 AenLeuProValAlaIleLySGLuLySGLuLyAerAArgIleSerAerProGlyGluLeu 80
QY 591 CCTAATGGCACTGAGTGGCCATGGAAGTGTCTGCTGAGAGAGAGAGAGAGAGCTTC 650
DB 81 ProAenGlyThrArgValProMetGluValIleuLeuLySGLuLySerSerGlyPhe 100
QY 651 TCCGCGCTATTAAGCTCTGAGACTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGCTG 710
DB 101 SerGlyValIleAArgLeuLeuAerProGlyLySGLuLyAerProAerPheValIleuLeu 120
QY 711 GAGAGGCCGAGCGCGCTGCAAGATCTCTGACTTCATCAACGAGAGAGAGAGAGCTGCA 770
DB 121 GluAerProGlyProValGlnAerPheAerPheIleThrGluAArgGlyIleuGln 140
QY 771 GAGAGAGCTGGCGCGAGCTCTTCTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCTG 830
DB 141 GluGluLeuAlaAerSerPhePheThrGlnValIleuGlnAlaValAArgHleCySGLuAen 160
QY 831 TGGCGGAGTGTACACCGGCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGCTGCG 890
DB 161 CySGLyValIleuHleAerAerPheIleLySGLuLyAenIleuLeuAerPheAenAArgGly 180
QY 891 GAGCTCAAGCTCATCGACTTCGCGGTGGGGGCGCTGTCAGAGACACCGCTTCACAGGAC 950
DB 181 GluLeuLyLeuLeuAerPheGlySerGlyAlaIleuLeuLySGLuLyAerPheAerValTyThrAer 200
QY 951 TTGAGATGGGACCGGAGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCTG 1010
DB 201 PheAerProLyThrArgValTySerProGlyInuTrpIleAArgTyHleAArgTyHleAArg 220
QY 1011 AGGTGGCGGAGCTGTGCTCTGCGGAGAGCTGTGATGATGATGATGATGATGATGATGAT 1070
DB 221 ArgSerAlaIleValIleTrpSerLeuGlyIleLeuLeuTyHleAerMetValCySGLyAerPhe 240
QY 1071 CCTTTCGAGAGATGACGAGAGAGATCATAGGGGCGAGGTTTCTTTCAGGACGAGGCTCT 1130
DB 241 ProPheGlyHleAerAerPheGlyGlyIleIleAArgGlyGlnValPheAerAerGlnAerValSer 260
QY 1131 TCAGAGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1190
DB 261 SerGlyLySGLuLySGLuLySGLuLySGLuLySGLuLySGLuLySGLuLySGLuLySGLu 280
QY 1191 TTGAGAGAGATGACGAGAGAGATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCTG 1250
DB 281 PheGlyGlyIleIleGlnAerHleAerProTrpMetGlnAerValIleuLeuProGlyInuTrpAla 300
QY 1251 GAGATTCACCTTCAGAGAGCTGTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1289
DB 301 GluIleHleAerHleAerSerLeuSerProGlyProSerLyS 313
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RESULT 5
US-10-664-421-1
/ Sequence 1, Application US/10664421
/ Publication No. US20040142864A1
/ GENERAL INFORMATION:
/ APPLICANT: BREMER, RYAN
/ APPLICANT: IBRAHIM, PRABHA
/ APPLICANT: KUMAR, ABHINAV
/ APPLICANT: MANDIVAN, VALSAN
/ APPLICANT: MIBURN, MICHAEL V.
/ TITLE OF INVENTION: CRYSTAL STRUCTURE OF PTM-1 KINASE
/ FILE REFERENCE: 039363/0703
/ CURRENT APPLICATION NUMBER: US/10/664,421
/ PRIOR FILING DATE: 2003-09-16
/ PRIOR FILING DATE: 2002-09-20
/ PRIOR APPLICATION NUMBER: 60/412,341
/ PRIOR FILING DATE: 2002-09-16
/ NUMBER OF SEQ ID NOS: 169
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 1
/ LENGTH: 313
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-664-421-1

Alignment Scores:
Pred. No. : 2,42e-94 Length: 313
Score: 1670.00 Matches: 313
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.87% Indels: 0
DB: 16 Gaps: 0

US-10-705-757-1 (1-2623) x US-10-664-421-1 (1-313)

QY 351 ATGCTCTGTGCAAAATCAACTGCTTGCCCACTGGCGCGCGCCCTGCAAGACTTG 410
DB 1 MetLeuLeuSerLyIleAenSerLeuAlaHleuAArgLaIaProCySaenAerLeu 20
QY 411 CAGGCCACCAAGCTGGCGCGCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGCTG 470
DB 21 HisAlaThrLyLeuAlaProGlyLySGLuLyGluProLeuInuSerGlnTyrgInuAl 40
QY 471 GCGCCGCTACTGGGAGCGCGCGCTTCGCGCTCGGTACTCAGGCAATCCGCTCCGAC 530
DB 41 GlyProLeuLeuInuSerGlyLySGLuLySerValTySerGlyIleAArgValSerAer 60
QY 531 AACTTGCCGCTGGCCATCAAAACAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGCTG 590
DB 61 AenLeuProValAlaIleLySGLuLySGLuLyAerAArgIleSerAerProGlyGluLeu 80
QY 591 CCTAATGGCACTGAGTGGCCATGGAAGTGTCTGCTGAGAGAGAGAGAGAGAGCTTC 650
DB 81 ProAenGlyThrArgValProMetGluValIleuLeuLySGLuLySerSerGlyPhe 100
QY 651 TCCGCGCTATTAAGCTCTGAGACTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGCTG 710
DB 101 SerGlyValIleAArgLeuLeuAerProGlyLySGLuLyAerProAerPheValIleuLeu 120
QY 711 GAGAGGCCGAGCGCGCTGCAAGATCTTCTGACTTCATCAACGAGAGAGAGAGAGCTGCA 770
DB 121 GluAerProGlyProValGlnAerPheAerPheIleThrGluAArgGlyIleuGln 140
QY 771 GAGAGAGCTGGCGCGAGCTTCTTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCTG 830
DB 141 GluGluLeuAlaAerSerPhePheThrGlnValIleuGlnAlaValAArgHleCySGLuAen 160
QY 831 TGGCGGAGTGTACACCGGCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGCTGCG 890
DB 161 CySGLyValIleuHleAerAerPheIleLySGLuLyAenIleuLeuAerPheAenAArgGly 180
QY 891 GAGCTCAAGCTCATCGACTTCGCGGTGGGGGCGCTGTCAGAGACACCGCTTCACAGGAC 950
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Db	181	GlutenuylbLeuileleAspPheGlySerGlyAlaLeuLeuylAspThrValIlyThrAsp	200
QY	951	TTTCGATGGACCCCGAGTGTATAGCCCTTCAGAGTGAATCCGTCACATCGCTACCATGAC	1010
Db	201	PheAspGlyIlyThrArgValIlySerProGlnIlyIleArgIyHlaArgIyHlaIleIy	220
QY	1011	AGATCGGCGGCGAGTGTGGACCCCGGGAGATCCGTCGTATGATATATGGTGTGGAGATATT	1070
Db	221	ArgSerAlaAlaValIlyPheSerLeuGlyIleLeuLeuIyIyAspMetValCysGlyAspIle	240
QY	1071	CCTTTCGAGCATGACGAAGAATCATCAGGAGCGATTTTCTTCAGGACAGAGGTCTCT	1130
Db	241	ProPheGlnIlyAspGlyGlnIlyIleIleArgIyGlnValIlePheAspGlyAlaGlyAlaSer	260
QY	1131	TCAGAAATCGACATCTCATTAAGATGAGTGTGGCCCTGAGACCATCATGATAGGCGAAC	1190
Db	261	SerGlnCysGlnHlaSerLeuIleArgIlyIyPheValAlaAspProSerHlaArgProThr	280
QY	1191	TTTCGAAGAATTCAGAACCATTCATCGATGCGAAGATGTCTCTGCGCCAGAAACTGCT	1250
Db	281	PheGlnGlnIlyIleGlnAsnHlaProThrPheGlnAspValIleLeuLeuProGlnIlyThrAla	300
QY	1251	GAGATCCACCTTCACAGGCTGTCCGCGGGGCGCCAGCAAA	1289
Db	301	GlnIleHlaIleAsnHlaSerLeuSerProGlyProSerIlyS	313

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RESULT 6
US-10-664-421-150
/ Sequence 150, Application US/10664421
/ Publication No. US20040142864A1
/ GENERAL INFORMATION:
/ APPLICANT: BREMER, RYAN
/ APPLICANT: IBRAHIM, PRABHA
/ APPLICANT: KUMAR, ABHINAV
/ APPLICANT: MANDISAN, MADISAN
/ APPLICANT: MILBURN, MICHAEL V.
/ TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
/ FILE REFERENCE: 039363/0703
/ CURRENT APPLICATION NUMBER: US/10/664,421
/ CURRENT FILING DATE: 2003-09-16
/ PRIOR APPLICATION NUMBER: 60/412,341
/ PRIOR FILING DATE: 2002-09-20
/ PRIOR APPLICATION NUMBER: 60/411,398
/ PRIOR FILING DATE: 2002-09-16
/ NUMBER OF SEQ ID NOS: 169
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 150
/ LENGTH: 313
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-664-421-150

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Pred. No.:	2.42e-94	Length:	333
Score:	1670.00	Matches:	333
Percent Similarity:	100.00%	Conservative:	0
Best local Similarity:	100.00%	Mismatches:	0
Query Match:	34.87%	Indels:	0
DB:	16	Gaps:	0

US-10-705-757-1 (1-2623) x US-10-664-421-150 (1-313)

Oy ATGCTCTTGGCAAAATCAACTGGCTTGGCAACTGGCGGGCCCTGGCAAGACTG 410
 351
 Db MetLeuLeuSerIleIleLeuSerLeuAlaIleLeuArgAlaAlaIleProCysAsnAspLeu 20
 1
 Oy CAGCCCAACAAGCTGGCGCGCCGCAAGAGAAAGAGGCCCTTGAGTGGCACTACCAAGTG 470
 411
 Db HisIleIleThrIleLeuAlaProGlyIleGluIleGluProLeuGluIleSerGlnTyrGlnVal 40
 21
 Oy GGCCCGGTAACTGGGCAAGCGCGGCTTGGGCTGGTCTACTCAAGGATCCGGCTTCCGAC 530
 471

Db	41	GIYProleuLeuGIYSerGIYpHcdIYSerValTYSerGIYIleArgValSerAsp	60
QY	531	AACTGGCCGGTGGCCATCAACAACGTGAGAAAGGACCGGATTTCCGATCGGAGGAGCTG	590
Db	61	AsnLeuProValAlaIleuYHsIleValGIuIuYAspArgIleSerAspTrpGIuIuLeu	80
QY	591	CCTAAATGGCACTCGAGTGGCCCATGGAAGTGTCTCTGCTGAAGAAGGTGAGTCCGGTTTC	650
Db	81	ProAsnGIYThrArgValProMetGIuValIValLeuLeuYbYValSerSerGIYPhe	100
QY	651	TCGGAGCGCATTAAGCTCTCGAGTGGTGTGAGAGGCGGACAGTTTCGTGCTGATCTGT	710
Db	101	SerGIYValIleArgLeuLeuAspTrpPheGIuArgProAspSerPheValIleu	120
QY	711	GAGAGGCGCGGAGCGGTGCAAGAACTCTTGCACTTCAACGGAAGAAGGAGCCCTCAAA	770
Db	121	GIuArgProGIuProValGIuAspLeuPheAspPheIleThrGIuArgGIYAlaIleGIu	140
QY	771	GAGAGGCTGGCCCGCCAGCTTCTTTGTGGACAGTGTGTGAGGCGCTGCGGCACTGCSAAC	830
Db	141	GIuIuIleuAlaAspSerPheAspTrpGIuValLeuGIuAlaValAdgHsCysHsAsn	160
QY	831	TGGCGGGGTGTACACGCGCAATCAAGACGAAACAACCTTATGACTTCAATCGGGG	890
Db	161	CysGIYAlaIleuHsArgAspIleuYAspGIuAsnIleuIleAspLeuAsnArgGIY	180
QY	891	GAGCTCAAGCTCATGCACTTCGGGTCCGGGGCGCTGCTCAAGACACCGTCTACCGGAC	950
Db	181	GIuLeuYbYLeuIleAspPheGIYSerGIYAlaIleuLeuYbYAspThrValTYThrAsp	200
QY	951	TTGCAATGGAACCGGAGTGTATAGCCCTCCAGAGTGAATCCGCTACCATTCGCTACATGGC	1010
Db	201	PheAspGIYThrArgValTYSerProProGIuTrpIleArgTYHsAspTYHsGIY	220
QY	1011	AGTCCGGCGGAGCTGTGTCCTCGGGAGATCCTGCTGATATATATGTGTGAGATATT	1070
Db	221	ArgSerIleAlaValITrpSerIleGIYIleuLeuTYAspMetValCYsGIYAspIle	240
QY	1071	CCTTTGAGCATGACGAAGAGATCATCAGGAGGCGGAGTTTCTTCAGGACAGGGTCTCT	1130
Db	241	ProPheGIuHsAspArgIuGIuIleIleArgGIYAlaIlePheAspArgGIuArgValSer	260
QY	1131	TCAGATATGCAGCATCTCATTAATGATGTCCTTGCCCTGAGACCATCATATAGGCCAAC	1190
Db	261	SerGIuCYsGIuHsIleuIleArgTrpCYuLeuAlaLeuArgProSerAspArgProThr	280
QY	1191	TTGCAAGAATCCGAAGACCATCCATGAGATGCAAGATGTTCTCTGCGCCCAAGAACTGCT	1250
Db	281	PheGIuGIuIleGIuAsnHsAspTrpMetGIuAspValLeuLeuProGIuIuThrAla	300
QY	1251	GAGATTCACCTCCACAGCTGTGGCGGGGCGCACAGCAA	1289
Db	301	GIuIleHsIleuHsSerIleSerProGIYProSerTYs	313

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RESULT 7
US-10-377-268--9
; Sequence 9, Application US/10377268
; Publication No. US20040171062A1
; GENERAL INFORMATION:
; APPLICANT: HIRTH, KLAUS-PETER
; APPLICANT: MILBURN, MICHAEL VANCE
; TITLE OF INVENTION: METHOD FOR THE DESIGN OF MOLECULAR SCAFFOLDS AND LIGANDS
; FILE REFERENCE: 039363/0303
; CURRENT APPLICATION NUMBER: US/10/377,268
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: 60/437,929
; PRIOR FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: 60/360,651
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
;

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Db 141 GUGUGUUAUAARSerPhePheTrpGlnValLeuGluValAlaArgHisCysHisValAsn 160

Qy 831 TCGGGGGGTGTACACCGCGACATCAAGGACGAAAAATCTTATGCACTTAATGCGCGC 890

Db 161 CysGluValLeuHisAlaArgAspIleuYanArgIleuHisLeuHisLeuAspLeuHisArgGly 180

Qy 891 GAGCTCAAGCTCATGACTTCGGGTGGGGGGCGCTGTCAAGAGACACCGTTACACGGAC 950

Db 161 GlnLeuLysLeuHisAlaAspPheGlySerGlyAlaLeuLeuLysAspThrValTyrThrAsp 200

Qy 951 TTCATGTGGAGCCAGATGATATGAGCCCTCAGAGTGAATCCGGTACATCCGTCACCATGAC 1010

Db 201 PheAspGlyHisArgValTyrSerProGluTrpIleAspGlyHisArgTyrHisIleGly 220

Qy 1011 AGGTGGCGGCGAGTGTGGTCCCTGGGGAATCTGTGTAATGATATGTTGTGTGAGATATT 1070

Db 221 ArgSerAlaAlaValIleTrpSerLeuGlyIleLeuLeuLeuTyrAspMetValCysGlyAspIle 240

Qy 1071 CCTTCCGAGCATGACAGAGAAGATCATCAAGGGGCGAGTTTCTTCAAGACAGAGGTCTCT 1130

Db 241 ProPheGlnHisAspGluGlnIleIleArgGlyGlnValPhePheArgGlnArgValSer 260

Qy 1131 TCAGATGTACAGCATCTATTAGATGTGTGGTGGCCCTGAAGACCATCAGATAGGCGAAC 1190

Db 261 SerGlnCysGlnHisLeuLeuIleArgTrpPyrGlyMetAlaLeuAlaGlyProSerAspArgProThr 280

Qy 1191 TTCCAGAAATCCAGAACCATTCATGATGATGCAGATGATTTCTTCCTGCCCCAGAAATCTGT 1250

Db 281 PheGluGlnIleGlnHisAsnIleProTrpMetGlnAspValLeuLeuProGlnGluThrAla 300

Qy 1251 GAGATCCACCTCCACAGCGCTGGCGGGGGCGCCAGCAAA 1289

Db 301 GlnIleHisLeuHisSerLeuSerProGlyProSerLys 313

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RESULT 9
US-10-951-406-18
/ Sequence 18, Application US/10951406
/ Publication NO. US20050059630A1
/ GENERAL INFORMATION:
/ APPLICANT: Reinhard, Christoph
/ APPLICANT: Jefferson, Anne B.
/ APPLICANT: Chan, Vivien W.
/ TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
/ TITLE OF INVENTION: Target in Cancer
/ FILE REFERENCE: 16932_002
/ CURRENT APPLICATION NUMBER: US/10/951,406
/ CURRENT FILING DATE: 2004-09-27
/ PRIOR APPLICATION NUMBER: US/10/081,119
/ PRIOR FILING DATE: 2002-02-21
/ PRIOR APPLICATION NUMBER: 60/289,813
/ PRIOR FILING DATE: 2001-02-21
/ NUMBER OF SEQ ID NOS: 38
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 18
/ LENGTH: 313
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-951-406-18

Alignment Scores:
Pred. No.:      2,42e-94      Length:      313
Score:          1670.00      Matches:     313
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    34.87%      Indels:      0
DB:             17          Gaps:         0

US-10-705-757-1 (1-2623) x US-10-951-406-18 (1-313)

QY      351 ATGCTCTTGTCCAAATCACTGCGCTTGCCGACCTGCGGCGCGCTTGCAACGACTTG 410
DB      1 MettLeuLeuSerLyseIleAsnSerLeuAlaHisLeuArgAlaIaIaProCysAsnAspLeu 20

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QY	411	CAGCGACCAAGCTGAGCCCGCGCAAGAAAGACCCCTGGAGTGGCACTACCAAGTG	470
Db	21	HiSa1aTtrLrVleuA1aProG1VlybG1uLrVg1uPProLeuG1uSerG1uTyrG1nV1	40
QY	471	GAGCCGCACTAGGGGAGGAGGCGGCTGGGCTGGGCTACTAGGAGATCCGCGCTCCGAC	530
Db	41	G1PProLeuLrVleuG1uSerG1uG1PheG1uSerV1a1LyrSerG1u11LeuV1a1SerV	60
QY	531	AACTTGCSCGTGGCCATCAAAACAAGTGGAGAAGACCCGATTTCCGACTGGGAGAGCTG	590
Db	61	AsnLeuPProV1a1a11e1uYh1eV1aG1uLrVh1aPb1rG11eS1aPb1rPbG1uG1Leu	80
QY	591	CCTAATGCACTCGAGTSCCATGAGATGGTCTCTGTAAGAAAGTGAAGCTCGGATTTG	650
Db	81	ProAenG1uTTrV1aPProMeG1uV1a11e1uLrVleuLrVlyV1a1SerSerG1uPhe	100
QY	651	TCCGCGCGCATTAAGCTCTTGAGCTGGTGGAGAGCCGCAAGTTCCTGCTGATCTGT	710
Db	101	SerG1uV1a11e1aTg1uLrVleuA1bP1rPheG1uTg1uTgProA1bSerPheV1a11e1u	120
QY	711	GAGAGCCCGAGCCGCTGCAAGATCTTCCACTTCTTCAACGAAAGGAGCCCTGCA	770
Db	121	G1uTgTgProG1uPProV1aG1nA1bPLeuPheA1bPhe11eTtG1uV1a1bG1u1a1LeuG1n	140
QY	771	GAGAGCTGAGCCCGACAGCTTCTTGAGCAAGTGTGAGAGCCGTGCGACATGCGACAC	830
Db	141	G1uG1uLeuA1a1aTgSerPhePheTtG1nV1a1LeuG1u1a1aV1a1A1gH1a1bCyH1a1bVn	160
QY	831	TGCGGGGCTGTACACCCGAGATCAAGAGCAAAACATCCTTAATGACCTCAATCGCGGC	890
Db	161	CyS1uV1a11e1uH1aV1aTgA1bP1r1e1uV1aPb1uA1bVn11e1u11eA1bPLeuA1bA1bTg1u	180
QY	891	GAGCTCAAGCTCATCGACTTGAGGTCGGGGGCGCTGCTCAAGAGCAACCGTGTACAGGAC	950
Db	181	G1uLeuLrVleuL1eA1bPheG1uSerG1uV1a1a1e1uLrVleuV1aPb1rV1a1LyrTTrA1bP	200
QY	951	TTCGATGGGACCCGAGTGTATAGCCCTCCAGAGTGATCCGCTACATCCGTATACATGGC	1010
Db	201	PheA1bPb1uTTrV1aV1a1LyrSerPProPbG1uTTr11eA1bTg1uH1aV1aTg1uH1a1bG1u	220
QY	1011	AGGTGGGCGGAGTGTGGTCCCTGGGAGATCTGTGTAATGATATGTTGTGTGAGATATT	1070
Db	221	ArgSer1a1a1aV1a1TTrP1e1uLrVleuG1u11e1uLrVleuTg1uA1bPMe1a1CyG1uA1bP1e	240
QY	1071	CCTTTCGAGCATGAGCAAGAGATATATCAAGGCGCAAGTTCCTTCAGAGCAAGGCTCT	1130
Db	241	ProPheG1uH1aA1bPb1uG1uL1e1e1aTgG1uG1nV1a1PhePheA1bTgG1nV1aV1a1Ser	260
QY	1131	TCAAGATGTCAAGATCTCATAGATGGTGTCTGGCCCTGAGACCATAGATAGGSCAAC	1190
Db	261	SerG1uCyS1uG1nH1aV1e1uL1eH1uTTrCyV1e1uA1a1e1uA1bTgProSerA1bPb1uTTrH	280
QY	1191	TTGCAAGAAATCGAAGAACCATCGATGATGCAAGATGTCTCTGCGCCAGAAATCTGT	1250
Db	281	PheG1uG1uL1eG1nA1bH1aPProTTrPMeG1uA1bP1aV1a1LeuLrVleuPProG1nG1uTTrA1a	300
QY	1251	GAGATCAACCTCCACAGCTGTCCGCGGCGGCCCAAGCAA	1289
Db	301	G1u11eH1aV1eH1a1Ser1e1uSerPbG1u1PProSer1uV	313

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RESULT 10
US-10-951-477-18
; Sequence 18, Application US/10951477
; Publication NO. US2005063974A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,477

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CURRENT FILING DATE: 2004-09-27
PRIOR APPLICATION NUMBER: US/10/081,119
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/289,813
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
US-10-951-477-18

Alignment Scores:
Pred. No: 2.42e-94 Length: 313
Score: 1670.00 Matches: 313
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.87% Indels: 0
DB: 17 Gaps: 0

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Db 1 MetleuLeuSerlyslLeaSerLeuAlaHisLeuArgAlaIaProCyAsnAspLeu 20
Qy 411 CAGGCCCAACAGCTGGGCGCGGCAAGAAAGAGCCCTGGAGTGGCACTACAGAGT 470
Db 21 HisAlaThrlyLeuAlaProGlyLysGlnLysGlnProLeuGlnSerGlnTyGlnVal 40
Qy 471 GGCCCGCTACTGGGCAAGCGGCGCTTGGCTGGCTACTACAGGACCTCCGGTCCGAC 530
Db 41 GlyProLeuLeuGlnSerGlyGlyPheGlySerValTySerGlyLeuArgValSerAsp 60
Qy 531 AACTGGCGGTGGCCATCAACACGTGAGAGAGACCGGATTTCCGACTGGAGAGCTG 590
Db 61 AsnLeuProValAlaIleLysHisValGlnLysAspArgIleSerAspTrpGlyGlnLeu 80
Qy 591 CCAATATGGCACTGAGAGTGGCCCAATGGAATGCTCTGTGAAAGAAAGTACGAGTTC 650
Db 81 ProAsnGlyThrArgValProMetGlnValValLeuLysLysValSerSerGlyPhe 100
Qy 651 TCCGGCGTCAATTAAGCTCTGAGTGGTTCGAGAGCGCGACAGTTTCGTCTGATCTGT 710
Db 101 SerGlyValIleArgLeuLeuAspTrpPheGlnArgProAspSerPheValLeuLeu 120
Qy 711 GAGAGCGCCGAGCGCGGTGCAAGATCTTCTGACTTCAACGAAAGGAGCGCTGCA 770
Db 121 GluArgProGlnProValGlnAspLeuPheAspPheIleThrGlnArgGlyAlaLeuGln 140
Qy 771 GAGAGCTGGCGCGGAGCTTCTTCTGGCAGGTGTGTGAGGCGGTGGCGCACTGCCAC 830
Db 141 GlnGlnLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgHisCyHisAsn 160
Qy 831 TGGCGGGTGTCTACACCGCGCATCAAGAGAGAAACCTCTTATCGACCTCATTCGCG 890
Db 161 CyGlyValLeuHisArgAspIleLysAspGlnAsnIleLeuIleAspHisAsnArgGly 180
Qy 891 GAGCTCAAGCTCATCGACTTCGGGTTCGGGCGCGCTGTCAGAGACACCGTCTACACG 950
Db 181 GlnLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyTrpHisAsp 200
Qy 951 TTCGATGGGACCCGAGTGTATAGCCCTTCAGAGTGCATCCGCTACCATCGCTACG 1010
Db 201 PheAspGlyThrArgValTySerProGlnTrpIleArgTyHisAsnGly 220
Qy 1011 AGGTGGCGGCGAGTCTGGTCTCTGGGAGTCTGTGTATGATATAGTGTGAGATATT 1070
Db 221 ArgSerAlaAlaValTrpSerLeuGlyIleLeuLeuTyAspMetValCyGlyAspIle 240
Qy 1071 CCTTTCGAGCATGACGAAGATCATCAAGGCGCGAGTTTCTTTCAGGCAAGGCTCT 1130
Db 241 ProPheGlnHisAspGlnGlnIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
Qy 1131 TCGAATGTGACATCTCATTAATGTGCTTGGCCCTGAGACCATCATGATAGCCCAAC 1190
Db 261 SerGlnCyGlnHisLeuIleArgTrpCyLeuAlaLeuArgProSerAspArgProThr 280
Qy 1191 TTCGAAGAATTCGAACATCATGAGTGAATGATGTTCTCTGCGCCCGAGAACTGCT 1250
Db 281 PheGlnGlnIleGlnHisAsnHisProTrpMetGlnAspValLeuLeuProGlnGlnTrpAla 300
Qy 1251 GAGATCCACTTCACAGCTGTGTGGCGGCGCGCCAGCAAA 1289
Db 301 GlnIleHisLeuHisSerLeuSerProGlyProSerLys 313
RESULT 12
US-10-705-757-2
; Sequence 2, Application US/10705757
; Publication No. US20040146942A1
; GENERAL INFORMATION:
; APPLICANT: GRUNENTHAL, GMBH
; TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE OR PIM3-KINASE
; FILE REFERENCES: 029310, 528180S
; CURRENT APPLICATION NUMBER: US/10/705,757
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/EP02/05234

; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: DE 101 23 055.9
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 313
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-705-757-2
Alignment Scores:
Pred. No.: 2,42e-94 Length: 313
Score: 1670.00 Matches: 313
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34,87% Indels: 0
DB: 18 Gaps: 0
US-10-705-757-1 (1-2623) x US-10-705-757-2 (1-313)
Qy 351 ATGCTCTTGTCAAAATCAATCTGCTTGGCCACCTGGCGCGCGCTGCAACGACTG 410
Db 1 MetleuLeuSerlyslLeaSerLeuAlaHisLeuArgAlaIaProCyAsnAspLeu 20
Qy 411 CAGGCCCAACAGCTGGGCGCGGCAAGAAAGAGCCCTGGAGTGGCACTACAGAGT 470
Db 21 HisAlaThrlyLeuAlaProGlyLysGlnLysGlnProLeuGlnSerGlnTyGlnVal 40
Qy 471 GGCCCGCTACTGGGCAAGCGGCGCTTGGCTGGCTACTACAGGACCTCCGGTCCGAC 530
Db 41 GlyProLeuLeuGlnSerGlyGlyPheGlySerValTySerGlyLeuArgValSerAsp 60
Qy 531 AACTGGCGGTGGCCATCAACACGTGAGAGAGACCGGATTTCCGACTGGAGAGCTG 590
Db 61 AsnLeuProValAlaIleLysHisValGlnLysAspArgIleSerAspTrpGlyGlnLeu 80
Qy 591 CCAATATGGCACTGAGAGTGGCCCAATGGAATGCTCTGTGAAAGAAAGTACGAGTTC 650
Db 81 ProAsnGlyThrArgValProMetGlnValValLeuLysLysValSerSerGlyPhe 100
Qy 651 TCCGGCGTCAATTAAGCTCTGAGTGGTTCGAGAGCGCGACAGTTTCGTCTGATCTGT 710
Db 101 SerGlyValIleArgLeuLeuAspTrpPheGlnArgProAspSerPheValLeuLeu 120
Qy 711 GAGAGCGCCGAGCGCGGTGCAAGATCTTCTGACTTCAACGAAAGGAGCGCTGCA 770
Db 121 GluArgProGlnProValGlnAspLeuPheAspPheIleThrGlnArgGlyAlaLeuGln 140
Qy 771 GAGAGCTGGCGCGGAGCTTCTTCTGGCAGGTGTGTGAGGCGGTGGCGCACTGCCAC 830
Db 141 GlnGlnLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgHisCyHisAsn 160
Qy 831 TGGCGGGTGTCTACACCGCGCATCAAGAGAGAAACCTCTTATCGACCTCATTCGCG 890
Db 161 CyGlyValLeuHisArgAspIleLysAspGlnAsnIleLeuIleAspHisAsnArgGly 180
Qy 891 GAGCTCAAGCTCATCGACTTCGGGTTCGGGCGCGCTGTCAGAGACACCGTCTACACG 950
Db 181 GlnLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyTrpHisAsp 200
Qy 951 TTCGATGGGACCCGAGTGTATAGCCCTTCAGAGTGCATCCGCTACCATCGCTACG 1010
Db 201 PheAspGlyThrArgValTySerProGlnTrpIleArgTyHisAsnGly 220
Qy 1011 AGGTGGCGGCGAGTCTGGTCTCTGGGAGTCTGTGTATGATATAGTGTGAGATATT 1070
Db 221 ArgSerAlaAlaValTrpSerLeuGlyIleLeuLeuTyAspMetValCyGlyAspIle 240
Qy 1071 CCTTTCGAGCATGACGAAGATCATCAAGGCGCGAGTTTCTTTCAGGCAAGGCTCTCT 1130
Db 241 ProPheGlnHisAspGlnGlnIleIleArgGlyGlnValPhePheArgGlnArgValSer 260

xy / 119A060CCLGAA0C0013CA00A1C1C11C0A011CA1CA000A0000000A000CCL10CA0 /

QY 711 GAGAGCCGAGCCGGTGCAGATCTCTTGACTTCATCAGGAAGGGAGCCCTGCA 770

```

DEBC LOCAL CHARACTERISTICS: 100.00%
Indels: 0
Query Match: 34.87%

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DEBC LOCAL CHARACTERISTICS: 100.00%
Indels: 0
Query Match: 34.87%

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US-10-705-757-1 (1-2623) x US-10-941-635-152 (1-313)

QY ATGCTCTTTCGCAAAATCACTCGCTTGCSCACCTGCGCGCGCCCTGCAAGCACTG 410
 DB 1 MetLeuLeuSerLysIleAenSerLeuLAlHleuLArgLAlaLProCybAaAaPLeu 20
 QY 411 CAGGCCCAAGCTGGGGCGCGGCAAGAGAAGAGCCCTGAGTGCAGTACAGAGTG 470
 DB 21 HlaLAlaThrLysLeuLAlaProGlyLysGluLysGluProLeuGusSerGlnYGLVal 40
 QY 471 GGGCCGCTACTGGGCAAGCGCGCTTGCCTGCTGCTACTCAGGCACTCGGCTCCGAC 530
 DB 41 GlyProLeuLeuGlySerGlyLysPheGlySerValYLeaGlyValSerAsp 60
 QY 531 AACTTGCCTGCGCATCAAAACAGTGAAGAAGACCCGATTCGACTGGAGAGAGTG 590
 DB 61 AaLeuProValAlaLLeuYbHLeuValGluLysAaPArgLLeSerAaPTrpGlyGluLeu 80
 QY 591 CCTAATGCACTGAGTGCCTGCAAGAGTGGCTCTGCTGAAGAAAGTGAAGCTGGGTTTC 650
 DB 81 ProAaAaGlyThrArgValLProMeGluValValLeuLeuYbYbValSerSerGlyPhe 100
 QY 651 TCCGGGCTCATTTAGGCTCTGCAAGTGGTGAAGAGCGGACAGTTTCGCTGATCTG 710
 DB 101 SerGlyValLLeaGlyLeuLeuAaPTrpPheGluArgProAaPserPheValLeuLLeu 120
 QY 711 GAGAGCCCGAGCGCGTGAAGATCTTCTGACTTCACTCAAGAAAGGAGGCGCTGCA 770
 DB 121 GluArgProGluProValGlnAaPLeuPheAaPheLLeThrGluArgGlyAlaLeuGln 140
 QY 771 GAGAGCTGGCGCGCAGCTTCTTGGCAAGTGTGAGAGCGCTGCGGCACTGCGACAC 830
 DB 141 GluGluLeuLAlaArgSerPhePheTrpGlnValLeuGluValAlaLArgHLeCybHLeAa 160
 QY 831 TGGGGGGTGTACACCGCGCATCAAGAGCAAAACATCTTATCCGACTCATTCGCGG 890
 DB 161 CybGlyValLLeuHLeuLbAaPArgLLeYbAaPArgLLeuLLeuLLeuLLeuLLeuLLeu 180
 QY 891 GAGCTCAAGCTCATGACTTCGAGTCCGAGGCGCTGCTCAAGAGCACTGCTCAACGAG 950
 DB 181 GluLeuLysLeuLLeaPheGlySerGlyAlaLeuLeuLysAaPArgLLeuLLeuLLeu 200
 QY 951 TTGAGTGGACCCGAGTGTATAGCTTCCAGAGTGAATCCGCTACATCCGCTACATG 1010
 DB 201 PheAaPArgLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeu 220
 QY 1011 AGGTGGCGGCGAGTGTCTGCTGCGGAGTCTGCTGATGATATGCTGTGAGATAT 1070
 DB 221 ArgSerLAlaLAlaLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeu 240
 QY 1071 CCTTTCAGAGTGAAGAGATCATCAAGGAGCGGAGTTTCTTCAAGAGAGGAGTCT 1130
 DB 241 ProPheGluLAlaAaPArgLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeu 260
 QY 1131 TCAGAAATGTCAGATCTCATTAAGATGCTTGGCCCTGAGACCATCAATAGAGCCAAC 1190
 DB 261 SerGluCybGlnHLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeu 280
 QY 1191 TTGGAAGAATCCAGAACCATCCATGATGCAAGATGTTCTTCCGCGCCAGAACTGCT 1250
 DB 281 PheGluLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeu 300
 QY 1251 GAGATTCACCTCCACAGCTGTGCGCGGCGCCAGCAAA 1289
 DB 301 GluLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeu 313

RESULT 15

US-10-620-052A-22
 ; Sequence 22, Application US/10620052A
 ; Publication No. US20040126784A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hitoshi, Yasumichi

APPLICANT: Jenkins, Yonchu
 APPLICANT: Markovtsov, Vadim
 APPLICANT: Rigel Pharmaceuticals, Inc.
 TITLE OF INVENTION: Modulators of Cellular Proliferation
 FILE REFERENCE: 021044-004010US
 CURRENT APPLICATION NUMBER: US/10/620,052A
 CURRENT FILING DATE: 2003-07-14
 PRIOR APPLICATION NUMBER: US 60/395,443
 PRIOR FILING DATE: 2002-07-12
 NUMBER OF SEQ ID NOS: 78
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO 22
 LENGTH: 313
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: PIM1 oncogene serine threonine kinase
 US-10-620-052A-22

Alignment Scores:

Pred. No.: 1,53e-93 Length: 313
 Score: 1657.00 Matches: 311
 Percent Similarity: 99.36% Conservative: 0
 Best Local Similarity: 99.36% Mismatches: 2
 Query Match: 34,608 Indels: 0
 DB: 16 Gaps: 0

US-10-705-757-1 (1-2623) x US-10-620-052A-22 (1-313)

QY 351 ATGCTCTTTCGCAAAATCACTCGCTTGCSCACCTGCGCGCGCCCTGCAAGCACTG 410
 DB 1 MetLeuLeuSerLysIleAenSerLeuLAlHleuLArgLAlaLProCybAaAaPLeu 20
 QY 411 CAGGCCCAAGCTGGGGCGCGGCAAGAGAAGAGCCCTGAGTGCAGTACAGAGTG 470
 DB 21 HlaLAlaThrLysLeuLAlaProGlyLysGluLysGluProLeuGusSerGlnYGLVal 40
 QY 471 GGGCCGCTACTGGGCAAGCGCGCTTGCCTGCTGCTACTCAGGCACTCGGCTCCGAC 530
 DB 41 GlyProLeuLeuGlySerGlyLysPheGlySerValYLeaGlyValSerAsp 60
 QY 531 AACTTGCCTGCGCATCAAAACAGTGAAGAAGACCCGATTCGACTGGAGAGAGTG 590
 DB 61 AaLeuProValAlaLLeuYbHLeuValGluLysAaPArgLLeSerAaPTrpGlyGluLeu 80
 QY 591 CCTAATGCACTGAGTGCCTGCAAGAGTGGCTCTGCTGAAGAAAGTGAAGCTGGGTTTC 650
 DB 81 ProAaAaGlyThrArgValLProMeGluValValLeuLeuLysYbValSerSerGlyPhe 100
 QY 651 TCCGGGCTCATTTAGGCTCTGCAAGTGGTGAAGAGCGGACAGTTTCGCTGATCTG 710
 DB 101 SerGlyValLLeaGlyLeuLeuAaPTrpPheGluArgProAaPserPheValLeuLLeu 120
 QY 711 GAGAGCCCGAGCGCGTGAAGATCTTCTGACTTCACTCAAGAAAGGAGGCGCTGCA 770
 DB 121 GluArgProGluProValGlnAaPLeuPheAaPheLLeThrGluArgGlyAlaLeuGln 140
 QY 771 GAGAGCTGGCGCGCAGCTTCTTGGCAAGTGTGAGAGCGCTGCGGCACTGCGACAC 830
 DB 141 GluGluLeuLAlaArgSerPhePheTrpGlnValLeuGluValAlaLArgHLeCybHLeAa 160
 QY 831 TGGGGGGTGTACACCGCGCATCAAGAGCAAAACATCTTATCCGACTCATTCGCGG 890
 DB 161 CybGlyValLLeuHLeuLbAaPArgLLeYbAaPArgLLeuLLeuLLeuLLeuLLeuLLeu 180
 QY 891 GAGCTCAAGCTCATGACTTCCGAGTCCGAGGCGCTGCTCAAGAGCACTGCTCAACGAG 950
 DB 181 GluLeuLysLeuLLeaPheGlySerGlyAlaLeuLeuLysAaPArgLLeuLLeuLLeu 200
 QY 951 TTGAGTGGACCCGAGTGTATAGCTTCCAGAGTGAATCCGCTACATCCGCTACATG 1010
 DB 201 PheAaPArgLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeu 220


```
QY 1011 AGGTCGGCGGCAAGTCTGGTCCCTGGGGATCTGCTGTATGATATGTTGTGTGAGATATT 1070
    |||||
Db 221 ArgSerAlaIleValIlePheSerLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
    |||||
QY 1071 CTTTGCAGCATGACGAGAGATCATACAGGGGCCAGGTTTCTTCAAGGCAGAGGTTCTCT 1130
    |||||
Db 241 ProPheGlnHisAspGlnGlnIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
    |||||
QY 1131 TCAGAAATGTCAGCATCTCATTAAGATGGTGGCTGGCCCTGAGACCATCAGATAGGCCAAC 1190
    |||||
Db 261 SerGlnCysGlnHisLeuIleArgTyrCysLeuAlaLeuArgProSerAspArgProThr 280
    |||||
QY 1191 TTGGAAGAAATCCAGAAACCATCCATGAGATCAAGATGTTCTCTGCCCCAGAAACTGCT 1250
    |||||
Db 281 PheGlnGlnIleGlnHisProTyrMetGlnAspValLeuLeuProGlnGlnIleThrAla 300
    |||||
QY 1251 GAGATCCACCTCCACAGCCTGTGGCCGGGGCCAGCMAA 1289
    |||||
Db 301 GlnIleHisLeuHisSerLeuSerProGlyProSerLys 313
    |||||
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Search completed: September 22, 2005, 17:46:35
Job time : 374.236 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 22, 2005, 15:57:45 ; Search time 342.494 Seconds

(without alignments)
5924.037 Million cell updates/sec

Title: US-10-705-757-1

Perfect score: 4789
Sequence: 1 gggagagccgcgagagagc.....aataaaaccttgcttc 2623

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+np.model -DEV=xlp
-Q/cg2.1/USPTO.spool_p/US10705757/runat_22092005_115014_22122/app_query.fasta_1.5333
-DB=A.Geneseq -QMT=fastran -SUFF=n2p.xsg -MINMATCH=0.1 -LOOPL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=pro -NOR=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10705757_QCGN_1.1_753_@runat_22092005_115014_22122 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

A.Geneseq_16Dec04:.*
1: geneseqp19808:.*
2: geneseqp19908:.*
3: geneseqp20008:.*
4: geneseqp20018:.*
5: geneseqp20028:.*
6: geneseqp20038:.*
7: geneseqp20038:.*
8: geneseqp20048:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1670	34.9	313	5	ABP54943 Human P1m
2	1670	34.9	313	5	ABG33017 Human PRO
3	1670	34.9	313	6	AAO19788 Human P1M
4	1670	34.9	313	7	ABU61613 Human P1M
5	1670	34.9	313	7	ABR62938 Human ser
6	1670	34.9	313	7	ADBS5368 Human PRO
7	1670	34.9	313	7	ADP45083 Human kin
8	1670	34.9	313	8	ADO19690 Human PRO
9	1670	34.9	313	8	ADR88370 Human P1M
10	1670	34.9	313	8	ADP24227 PRO polyp

11	1657	34.6	313	2	AAW08139 Human cyt
12	1657	34.6	313	3	AAV87959 Human CR7
13	1657	34.6	313	8	ADI57202 Human P1M
14	1657	34.6	313	8	ADN03170 Human P1M
15	1636	34.2	313	5	ABG33016 Rat prote
16	1636	34.2	313	6	AAO19789 Rat P1M
17	1636	34.2	313	7	ABR62938 Rat berin
18	1582	33.0	313	5	ABG33015 Mouse pro
19	1582	33.0	313	6	AAO19790 Murine PI
20	1582	33.0	313	7	ABR62940 Mouse ser
21	1582	33.0	313	8	ADN97347 Murine PI
22	1582	33.0	313	8	ADR88371 Mus muscu
23	1362	28.4	253	8	ADI57241 P1M1 dom1
24	1296.5	27.1	254	8	AAV33942 Rat prote
25	1294.5	27.0	254	8	ADK71853 Human kin
26	1149.5	24.0	455	5	AAE23836 Rat K1D-1
27	1149.5	24.0	455	5	ABG33013 Rat prote
28	1149.5	24.0	455	7	ADE55366 Rat Prote
29	1145	23.9	382	8	ADO20314 Human PRO
30	1145	23.9	382	8	ADP55593 Human PRO
31	1140	23.8	323	8	ADR88376 Colunlix
32	1135	23.7	326	2	AAV06886 HWHJ20 p
33	1133	23.7	326	4	AAAB29788 Human ser
34	1133	23.7	326	5	AAE23834 Human HKI
35	1133	23.7	326	5	ABG33011 Human ser
36	1133	23.7	326	7	ABR62932 Human pro
37	1133	23.7	326	8	ADJ96625 Human cal
38	1133	23.7	326	8	ADL97960 Human P1M
39	1129.5	23.6	326	6	AAO19792 Murine PI
40	1129.5	23.6	326	7	ABR62933 Mouse pro
41	1129.5	23.6	326	8	ADO60032 CRH b1gna
42	1129.5	23.6	326	8	ADR88375 Mus muscu
43	1128.5	23.6	326	5	AAO20524 Protein B
44	1128.5	23.6	326	6	AAO19791 Rat P1M3
45	1128.5	23.6	326	7	ABR62936 Rat prote

ALIGNMENTS

RESULT 1
ABP54943
ID ABP54943 standard; protein; 313 AA.
XX
AC ABP54943;
XX
DT 13-JAN-2003 (first entry)
XX
DE Human P1m1.
XX
KW P1m1, tyrosine threonine kinase; TTK; protein kinase; enzyme;
KW mitotic checkpoint; colon cancer; breast cancer; tumour; cytostatic;
KW human; gene therapy.
XX
OS Homo sapiens.
XX
PN WO20026444-A1.
XX
PD 06-SEP-2002.
XX
PF 21-FEB-2002; 2002WO-US005278.
XX
PR 21-FEB-2001; 2001US-0271254P.
XX
PA (CHIR) CHIRON CORP.
XX
PI Reinhard C, Jefferson AB, Chan VW;
XX
DR WPI, 2002-698650/75.
XX
DR N-PSDB; ABV73989.
XX
PT Reducing growth of cancer cells comprises reducing Tyrosine Threonine
PT Kinase (TTK) activity, useful in diagnosing and treating disorders with
PT abnormal expression levels and activity of TTK, such as lung, colon,

PT prostate and ovarian cancer.
 XX
 XX Disclosure: Page 80-81; 113pp; English.
 CC The present sequence is the protein sequence of human Pim1, a protein
 CC related to tyrosine threonine kinase (TTK, see ABP54938). TTK
 CC polynucleotides and polypeptides of the invention encompass
 CC polynucleotides and polypeptides having sequence similarity or sequence
 CC identity to human TTK and other genes and gene products related to TTK,
 CC such as Pim1. The invention is based on the finding that TTK is
 CC differentially expressed in various forms of cancer. It provides methods
 CC for the identification of cancerous cells, especially breast cancer and
 CC colon cancer cells, by detection of expression levels of TTK, as well as
 CC diagnostic, prognostic and therapeutic methods. These methods can be used
 CC as the basis of rational therapy. Assays for identifying molecules that
 CC modulate the activity of these genes in cancers, as well as methods of
 CC inhibiting tumour growth by inhibiting the activity of TTK are also
 CC provided
 CC
 XX
 XX Sequence 313 AA:
 SQ
 Alignment Scores:
 Pred. No.: 7.05e-113 Length: 313
 Score: 1670.00 Matches: 313
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 34.87% Indels: 0
 DB: 5 Gaps: 0
 US-10-705-757-1 (1-2623) x ABP54943 (1-313)
 QY 351 ATGCTCTTGTCGCAAAATCAACTGCTTGCCACCTGGCGCGCCGCTTCAGACGACTG 410
 DB 1 MetLeuLeuSerIleAsnSerLeuAlaHisLeuAlaHisProCysAsnAspLeu 20
 QY 411 CACGCCACCAAGCTGGCGCGCCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 470
 DB 21 HisAlaThrIleLeuAlaProGlyLySGluLyGluProLeuHisSerGlnTyrglnVal 40
 QY 471 GGGCCGCTACTGGCGAGCGCGCGCTTGCGCTCGCTACTACAGGACTCCGCTCCGAC 530
 DB 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTySerIlyIleArgValSerAsp 60
 QY 531 AACTTCGCGGTGGCCATCAACAACGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 590
 DB 61 AsnLeuProValAlaIleIleYshIleValGluLyAspArgIleSerAspTrpGlyGluLeu 80
 QY 591 CCTAATGGCACTGAGTGGCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 650
 DB 81 ProAsnGlyThrArgValPrometGluValIleLeuLeuValSerSerGlyPhe 100
 QY 651 TCCGGGCTCATTTAGGCTCCCTGGACTGGTTGAGAGAGCGCCGACGTTCCGCTGATCC 710
 DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleuIleLeu 120
 QY 711 GAGAGCGCCGAGCGCGGTGCAAGATCTTCTGACTTCATCAGGAAAGGGAGCGCTGCA 770
 DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
 QY 771 GAGAGCTGGCCCGGAGCTTCTTCTGGCAGGTGCTGAGAGCGCGTGGCGCATGCCAC 830
 DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValIleGlnIleValAlaArgHisCysHisAsn 160
 QY 831 TGGGGGGTGTACACCCGCGCATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 890
 DB 161 CysGlyValAlaLeuHisArgAspIleIleYAspGlyAsnIleLeuIleAspLeuAsnArgGly 180
 QY 891 GAGCTCAAGCTCATCGACTTCGGGTTGGGGGCGCTGCTCAAGAGACCGCTACAGCGAG 950
 DB 181 GluLeuLeuLeuLeuLeuAspPheGlySerGlyAlaIleLeuLeuLeuYAspHisValTyrHisAsp 200
 QY 951 TTGATGGGAGCCGAGGTATAGCCCTCCAGAGTGAATCCGCTACCAATCCATGGC 1010

DB 201 PheAspGlyThrArgValTySerProProGluTrpIleArgTyHisArgTyHisGly 220
 QY 1011 AGTGGGCGGAGCTGTGGTCCCTGGGAGATCCGTGTTGATATAGTGTGTGAGATATT 1070
 DB 221 ArgSerAlaAlaValArgSerLeuGlyIleLeuLeuTyTrAspMetValCysGlyAspIle 240
 QY 1071 CCTTTCGAGCATGAGAGAGATCATCAGGGCGCAGGTTTCTTCAGGAGAGGCTCT 1130
 DB 241 ProPheGluHisAspGluGluIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
 QY 1131 TCAGATGTCAGCATCTCATTTGATGTCCTTGGCCCTGACACCATCAGATAGCGCAACC 1190
 DB 261 SerGluCysGlnHisIleLeuIleArgTrpCysLeuAlaLeuArgProSerAspArgProThr 280
 QY 1191 TTGGAAGAAATCAGAACCATCATGAGATGCAAGATGTTCTCTGCCCCAGGAACTGCT 1250
 DB 281 PheGluGluIleGlnHisAsnIleProTrpMetGlnAspValLeuLeuProGlnGluTrpAla 300
 QY 1251 GAGATCCACTTCACAGCCTGTGCGCGGCGCCAGACAA 1289
 DB 301 GluIleHisLeuHisSerLeuSerProGlyProSerIle 313
 RESULT 2
 ABG33017
 ID ABG33017 standard; protein, 313 AA.
 XX
 XX ABG33017;
 AC
 XX 20-DEC-2002 (first entry)
 DT
 XX
 DE Human protein kinase phosphorylation site.
 KW HK1D-1; serine/threonine kinase; cellular proliferative disorder;
 KW differentiative disorder; cancer; haematopoietic neoplastic disorder;
 KW acute promyeloid leukaemia; APLM; Chronic myelogenous leukaemia; CML;
 KW Waldenstrom's macroglobulinaemia; WM; human.
 XX
 OS Homo sapiens.
 XX
 PN US2002115120-A1.
 XX
 PD 22-AUG-2002.
 XX
 PF 04-OCT-2001; 2001US-00971791.
 XX
 PR 26-JAN-1999; 99US-00237543.
 PR 23-AUG-2000; 2000US-00644450.
 XX
 XX (MILL-) MILLENNIDM PHARM INC.
 XX
 PI Kapeller-Libermann R, Rudolph-Owen LA, Macbeth K;
 DR WPI, 2002-712471/77.
 XX
 PT Modulating levels or activity of HK1D-1 polypeptides, a member of
 PT serine/threonine kinase superfamily, for treating cancer, by contacting
 PT cell expressing the polypeptide with a modulator of the polypeptide.
 XX
 PS Example 3; Page 40-41; 48pp; English.
 XX
 CC The invention describes a method of modulating the level or activity of
 CC human HK1D-1 polypeptide, a member of serine/threonine kinase
 CC superfamily. The method involves contacting a cell expressing the
 CC polypeptide or nucleic acid with an agent to modulate the level or
 CC activity of polypeptide, or level of nucleic acid molecule. The method is
 CC useful for modulating the level or activity of HK1D-1 polypeptide or
 CC polynucleotide in a subject having or predisposed to having a disorder
 CC involving cancer. Modulating HK1D-1 expression or activity is useful for
 CC therapeutic purposes, for treating cellular proliferative and/or
 CC differentiative disorders including cancer or haematopoietic neoplastic
 CC disorders e.g. Acute promyeloid leukaemia (APML), Chronic myelogenous
 CC leukaemia (CML) and Waldenstrom's macroglobulinaemia (WM). This is the
 CC amino acid sequence of a human protein kinase phosphorylation site

XX Sequence 313 AA:
 SQ
 Alignment Scores:
 Pred. No.: 7.05e-113 Length: 313
 Score: 1670.00 Matches: 313
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 34.87% Indels: 0
 DB: 5 Gaps: 0
 US-10-705-757-1 (1-2623) x ABG3017 (1-313)
 QY 351 ATGCTCTTTCACAAATCAACTGCTGCGCCACCTGGCGCGCGCCCTGCAAGCACTG 410
 DB 1 MetLeuLeuSerLyseIleAsnSerLeuAlaHisLeuArgAlaAlaProCyAsnAspLeu 20
 QY 411 CACGCCACCAAGCTGGCGCGCGCGCAAGAGAGAGCCCTGAGTGCAGTACAGTG 470
 DB 21 HisAlaThrIleLeuAlaProGlyLyseGluLeuGluProLeuGluSerGlnTyrglnVal 40
 QY 471 GGGCCGCTACTGGGCGCGCGCGCTTGGCTCGGTCTACTCAGGCATCCGGTCTCCGAC 530
 DB 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTySerGlyIleArgValIserAsp 60
 QY 531 AACTGCGCGTGGCGCATCAACAACGTGAGAGAGAGCCGATTCCCGATCGGGAGAGCTG 590
 DB 61 AsnLeuProValAlaIleIleValHisValGluLeuAspArgIleSerAspTrpGlyGluLeu 80
 QY 591 CCTAATGGCACTGAGTGCCTCATGAAAGTGTCTGCTGCAAGAGTGAAGCTCGGTTTC 650
 DB 81 ProAsnGlyThrArgValProMetGluValValLeuLeuIleValIserSerGlyPhe 100
 QY 651 TCCGGCGTCAATTAGCTCTGCAAGCTGTTGCAAGGCCCAAGTTTCGTTGATCTTG 710
 DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleLeu 120
 QY 711 GAGAGCCCGGAGCGCGGCAAGATCTCTGACTTCACTCAAGAAAGGAGCGCCCTGGCA 770
 DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
 QY 771 GAGGAGCTGGCGCGAGCTTCTTCTGGCAGGTGCTGAGAGCGCGTGGCGCACTCCCAAC 830
 DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGluAlaValArgHisCyHisAsn 160
 QY 831 TGGGGGTGTCAACCGCGCATCAAGAGAGCAAAACCTCTTAATCCAGCTCAATCCGGCG 890
 DB 161 CyseGlyValLeuHisArgAspIleIleAspGluAsnIleLeuIleAspLeuAsnArgGly 180
 QY 891 GAGCTCAAGCTCATGCACTTGGGGTGGGGCGCTGCTCAAGAGACCCGTTACAGGAC 950
 DB 181 GluLeuLeuLeuLeuIleAspPheGlySerGlyAlaLeuLeuIleAspThrValTyrrTrpAsp 200
 QY 951 TTCGATGGGACCCGAGTGTATAGCCCTCAGAGTGGATCCGCTACCATCGCTACATGGC 1010
 DB 201 PheAspGlyThrArgValTyrrSerProProGluTrpIleArgTyrrHisArgTyrrHisGly 220
 QY 1011 AGGTGGCGGCACTGTGGTCCCTGGGAGATCTGCTGTATGATATAGTGTGTGAGATATT 1070
 DB 221 ArgSerAlaIleValIleTrpSerLeuGlyIleLeuLeuTyrrAspMetValCyseGlyAspIle 240
 QY 1071 CCTTGGAGATGACGAAGAGATCATCAGGGGCGAGTTTCTTTCAGGACGAGAGGTCTCT 1130
 DB 241 ProPheGluHisAspGluGluIleIleArgGlyGlnValPhePheArgGlnArgValIser 260
 QY 1131 TCAGAAATGTCAGCATCTCATTAATGATGTTGCTGGCCCTGAGACCATCAGATAGCCAAC 1190
 DB 261 SerGluCyseGlnHisIleuIleArgTrpCyseLeuAlaLeuArgProSerAspArgProThr 280
 QY 1191 TTGGAAGAAATCCAGAACCATCATGATGATCAAGATGTTCTCTGCGCCCAAGAACTGCT 1250
 DB 281 PheGluGluIleGlnAsnHisProTrpMetGlnAspValLeuLeuProGluGlnGluThrAla 300

QY 1251 GAGATCCACTCCACAGACCTGTGCGCGGCGCGCCAGCAAA 1289
 DB 301 GluIleHisLeuHisSerLeuSerProGlyProSerIle 313
 RESULT 3
 ID AA019788 standard; protein; 313 AA.
 AC AA019788;
 XX 11-AUG-2003 (first entry)
 XX Human PIM1 kinase.
 DE Human PIM1 kinase.
 KW Human; PIM1 kinase; PIM3 kinase; pain; analgesic.
 OS Homo sapiens.
 XX WO200293173-A2;
 PN 21-NOV-2002.
 PD 13-MAY-2002; 2002WO-EP005234.
 PF 11-MAY-2001; 2001DE-01023055.
 PR (CHEP) GRUENENTHAL GMBH.
 XX Weihe E, Schaefer MK;
 PI WPI; 2003-120715/11.
 DR N-PSDB; ABZ69186.
 DR Method for identifying analgesics, useful particularly for treating
 PT chronic pain, by screening compounds for interaction with PIM-1 or -3
 PT kinase, or related compounds.
 XX
 PS Claim 1; Fig 1B; 97p; German.
 CC The present invention relates to a method of identifying pain-regulating
 CC compounds, involving screening candidate compounds for interaction with
 CC PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are
 CC useful for treating chronic pain, particularly of neuropathic or
 CC inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or
 CC neurodegenerative diseases). The present sequence is human PIM1 kinase
 XX
 SQ Sequence 313 AA:
 SQ
 Alignment Scores:
 Pred. No.: 7.05e-113 Length: 313
 Score: 1670.00 Matches: 313
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 34.87% Indels: 0
 DB: 6 Gaps: 0
 US-10-705-757-1 (1-2623) x AA019788 (1-313)
 QY 351 ATGCTCTTTCACAAATCAACTGCTGCGCCACCTGGCGCGCGCCCTGCAAGCACTG 410
 DB 1 MetLeuLeuSerLyseIleAsnSerLeuAlaHisLeuArgAlaAlaProCyAsnAspLeu 20
 QY 411 CACGCCACCAAGCTGGCGCGCGCGCAAGAGAGAGCCCTGAGTGCAGTACAGTG 470
 DB 21 HisAlaThrIleLeuAlaProGlyLyseGluLeuGluProLeuGluSerGlnTyrglnVal 40
 QY 471 GGGCCGCTACTGGGCGCGCGCGCTTGGCTCGGTCTACTCAGGCATCCGGTCTCCGAC 530
 DB 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTySerGlyIleArgValIserAsp 60
 QY 531 AACTGCGCGTGGCGCATCAACAACGTGAGAGAGAGCCGATTCCCGATCGGGAGAGCTG 590
 DB 61 AsnLeuProValAlaIleIleValHisValGluLeuAspArgIleSerAspTrpGlyGluLeu 80

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QY 591 CCTATGCACTGAGTGGCCATGGAAGTGTCTGTGAAGAAAGGCTCGGGTTTC
DB 81 ProAenglyThrArgValProMetGluValValLeuLeuLeuValSerSerGlyPhe
QY 651 TCCGGGCTATTAGGCTCTGTGACTGTTCGAGAGGCCGACAGTTCGTCTGATCTCTG
DB 101 SerGlyValIleArgLeuLeuLeuAspIlePheGluArgProAspSerPheValLeuIleLeu
QY 711 GAGAGGCCGAGCCGGTGCAGAACTCTTTCGACTTCACGGAAGGGAGCCCTTCGCA
DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln
QY 771 GAGAGCTGGCCGCGAGCTTCTTTCGACAGGTCTGACGAGCCGTGGCCGCTGCACAC
DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValValLeuGluAlaValArgIleCysHisAsn
QY 831 TCCGGGGTGTACACCCGACATCAAGAGGAAAGATCCTTATCGACCTCAATCGCGC
DB 161 CysGlyValLeuLeuIleArgAspIleLeuAspGluAsnIleLeuIleAspLeuAsnArgGly
QY 891 GAGCTCAAGCTCATTCGACTTCGGGTGGGGGCGCTGTCAAGACACCGTCTACAGGAC
DB 181 GluLeuLeuLeuIleAspPheGlySerGlyAlaLeuLeuLeuAspThrValTyrrHisAsp
QY 951 TTGAGTGGAGCCGAGGTATAGCCCTCCAGAGTGGATCCGCTACCATGCTACATGGC
DB 201 PheAspGlyThrArgValTyrrSerProGluTrpIleArgTyrrHisArgTyrrHisGly
QY 1011 AGGTGGCGGCACTGTGTCTCTGGGAGATCTCTGTATGATATGATGTGTGGAGATTT
DB 221 ArgSerAlaIleValTrpSerLeuGlyIleLeuLeuTyrrAspMetValCysGlyAspIle
QY 1071 CCTTTGAGAGTATGACGAAGATCATACAGGGCCAGGTTTCTTCAGGCGAGGGTCTCT
DB 241 ProPheGluHisAspGluGluIleIleArgGlyGlnValPhePheArgGlnArgValSer
QY 1131 TCAGAAATGATGATCTCATTAGATGGTCTGACCCCTGAGACATCAGATAGCCAAAC
DB 261 SerGluCysGlnHisLeuIleArgTrpCysLeuAlaLeuArgProSerAspArgProTrp
QY 1191 TTGGAAGAAATCCAGAACCATTCATGGATGCAAGATGTTCTCTGCCCCAGAAATGCT
DB 281 PheGluGluIleGlnIleAsnHisProTrpMetGlnAspValLeuLeuProGlnGluThrAla
QY 1251 GAGATTCACCTCCACAGCCTGTGTGGCGGGCCGACGAAA 1289
DB 301 GluIleHisLeuHisSerLeuSerProGlyProSerIys 313

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PA (JEFF/) JEFFERSON A. B.
 PA (CHAN/) CHAN V. W.
 PI Reinhard C, Jefferson AB, Chan VW;
 DR WPI; 2003-456566/43.
 DR N-PSDB; ACA62265.
 XX
 PT Detecting cancer in a subject, by comparing expression levels of tyrosine
 PT threonine kinase polypeptide or polynucleotide in a subject cell and a
 PT normal cell, where an increase in the expression level in the test cell
 PT is indicative of cancer.
 XX
 PS Disclosure; Page 34-35; 79pp; English.

CC The invention relates to detecting cancer (other than ovarian cancer) in
 CC a subject, comprising comparing the expression levels of tyrosine
 CC threonine kinase (TTK, a mitotic checkpoint gene) polypeptide or
 CC polynucleotide in a test cell obtained from the subject and in a normal
 CC non-cancer cell, where an increase in the expression level of TTK protein
 CC or nucleic acid in the test cell compared to that in the normal cell,
 CC indicates the presence of cancer other than ovarian cancer. Also included
 CC are reducing growth of a cancerous cell (by contacting a cancerous cell
 CC with an amount of an agent effective to reduce TTK polypeptide activity
 CC in the cell), an assay for identifying a candidate agent that reduces
 CC growth of a cancerous cell (comprising: (i) detecting the activity of a
 CC TTK polypeptide in the presence of a candidate agent; and (ii) comparing
 CC the activity of TTK polypeptide in the presence of a candidate agent
 CC relative to TTK polypeptide activity in the absence of the candidate
 CC agent), identifying an agent that reduces TTK activity (comprising: (i)
 CC contacting a cancerous cell displaying elevated expression of a TTK-
 CC encoding polynucleotide with a candidate agent; and (ii) determining the
 CC effect of the candidate agent on TTK polypeptide activity) and assessing
 CC the prognosis of a cancerous disease other than ovarian cancer in a
 CC subject (comprising: (i) detecting expression of TTK encoding
 CC polynucleotide in a test cancer cell of a subject; and (ii) comparing a
 CC level of expression of TTK-encoding polynucleotide in the test cancer
 CC cell with a level of expression of the polynucleotide in a control non-
 CC cancer cell, where the level of expression of TTK in the test cancer cell
 CC is relative to the level of expression in the control non-cancer cell is
 CC indicative of the prognosis of the cancerous disease). The methods are
 CC useful for detecting cancer (other than ovarian cancer) in a subject,
 CC reducing growth of cancerous cells, identifying a candidate agent that
 CC reduces growth of a cancerous cell, identifying an agent that reduces TTK
 CC activity and assessing the prognosis of a cancerous disease other than
 CC ovarian cancer. The methods are also useful for determining the ability
 CC of a subject to respond to a particular therapy e.g. as a basis of
 CC rational therapy. The present sequence represents a closely related
 CC protein to human TTK, in this case human PIM1 (not defined)

XX
 SQ Sequence 313 AA;

Alignment Scores:

Pred. No.:	7.05e-113	Length:	313
Score:	1670.00	Matches:	313
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	34.87%	Indels:	0
DB:	7	Gaps:	0

US-10-705-757-1 (1-2623) x ABU61613 (1-313)

```

QY 351 ATGCTCTGTCCAAATCAACTGCTTGGCCACTGCGCGCGCTTCAGACACTG 410
DB 1 MetLeuLeuSerIysIleLeuSerLeuAlaHisLeuArgAlaIleProCysAsnAspLeu 20
QY 411 CACGCCACCAAGCTGGCGCCGCGCAAGAGAGAGCCCTGAGTGCAGTACAGGTG 470
DB 21 HisAlaThrIleLeuAlaProGlyIysGluValPheProLeuGlnSerGlnTyrrGlnVal 40
QY 471 GCGCGCTACTGTGGGCGCGCGCTTGGCTGTCTACTTCAGGCACTCCGCTCTCCGAC 530
DB 41 GlyProLeuLeuGlySerGlyIysPheGlySerValTyrrSerGlyIleArgValSerAsp 60

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QY 531 AACTGGCGGTGGCCATCAAAACAGTGGAGAAGACCCGGAATTCCGACTGGGAGACTG 590
DB 61 AsnLeuProValAlaIleValSHLeValGluLysAspArgIleSerAspTrpGlyGluLeu 80
QY 591 CCTAATGGCACTGAGTGGCCATGGAAGTGGTCTCTGTAAGAAAGTGAAGTCCGGTTC 650
DB 81 ProAsnGlyThrArgValProMetGluValValLeuLeuLysValSerSerGlyPhe 100
QY 651 TCCGGCGCTCATTAAGCTCTTGGAGCTGGTTCGAGAAGCCGACAGTTTCCTGATCTG 710
DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleLeu 120
QY 711 GAGAGGCCGACCGCGGTGCAAGATCTTTCGACTTCATCAGAAAGGAGCCCTGCA 770
DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
QY 771 GAGAGCTGGCCGCGAGCTTCTTGGCAGAGTGTGAGGCGCGGCACTGGCAAC 830
DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGluAlaValArgHisCySHAsn 160
QY 831 TGGCGGGTGTACACCGGCAATCAAGAGACGAAACATCTTATCGACTTCGCGGC 890
DB 161 CyseGlyValIleuHisArgAspIleLysAspGluAsnIleLeuIleAspLeuAsnArgGly 180
QY 891 GAGCTCAAGCTCACTCGACTTCGGGTTCGGGGCGCTGCTCAAGACACCGCTTACCGAC 950
DB 181 GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValIlyrThrAsp 200
QY 951 TTGATGGAGACCGGAGTGTATAGCCCTCGAGAGTGAATCCGCTACCATGCG 1010
DB 201 PheAspGlyThrArgValIlyrSerProProGluTrpIleArgIlyrHisArgIlyrHisGly 220
QY 1011 AGGTCCGCGGCACTGTGGTCTCTGGGAGATCTGCTGATGATATGCTGTGAGATATT 1070
DB 221 ArgSerIleAlaValIleTrpSerLeuGlyIleLeuLeuLysAspMetValCyseGlyAspIle 240
QY 1071 CCTTTCGAGCATGACGAAAGATCATACAGGGGCGAGTTTCTTCAGGCAAGAGGTTCT 1130
DB 241 ProPheGluHisAspGluGluIleIleArgGlyAlaLeuLeuLysAspThrValIlyrThrAsp 260
QY 1131 TCAGAAATGTCAGCATCTCATTAAGTGGTGTGGCCCTGAGACCATCAGATAGGCCAAC 1190
DB 261 SerGluCyseGlnHisLeuIleArgTrpCyseLeuAlaLeuArgProSerAspArgProthr 280
QY 1191 TTGGAAGAAATCCAGAACATCCATGAGATGCAAGATGTTCTCTGCCCCAGAAACTGCT 1250
DB 281 PheGluGluIleGlnHisAspTrpMetGlnAspValLeuLeuProGluGlnIleThrAla 300
QY 1251 GAGATCCACTCCACAGCTGTGGCGGGGCCGACGAAA 1289
DB 301 GluIleHisLeuHisSerLeuSerProGlyProSerIlys 313

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RESULT 5
ID ABR62939 standard, protein, 313 AA.

AC ABR62939,
DT 04-DEC-2003 (first entry)
DE Human serine/threonine protein kinase PIM-1.
KW Human, PIM-1, protein kinase, enzyme.
OS Homo sapiens.
XX
XX MO2003060130-A2.
XX
XX 24-JUL-2003.
XX
XX 20-JAN-2003; 2003MO-BP000492.
XX

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PR 19-JAN-2002; 2002EP-00001401.
XX
XX (AVET ) AVENTIS PHARMA DEUT GMBH.
PA
XX
XX Korn M, Mueller G, Schneider R, Techank G;
PI
XX WPI; 2003-598536/56.
DR
XX
XX New human or murine PIM-3 DNAs or polypeptides, useful for as a screening
PT agent for identifying anti-type 2 diabetes mellitus drugs, or for
PT treating insulin resistance or type 2 diabetes mellitus.
XX
PS Example 2; Page 40; 40pp; English.
XX
XX The present sequence is the protein sequence of the human
CC serine/threonine protein kinase and proto-oncogene, PIM-1. PIM-1 proteins
CC are the paralogues of novel human and murine PIM-3 proteins (see ABR62932
CC and ABR62933) of the invention, which are therefore expected to be
CC involved in cancer and cell growth regulation. PIM-3 is also involved in
CC the development of insulin resistance and type 2 diabetes mellitus. The
CC invention relates to the use of PIM-3 nucleic acids and proteins in:
CC screening assays for compounds that modulate insulin resistance or type 2
CC diabetes mellitus; detection assays for detecting insulin resistance or
CC type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing,
CC forensic biology); predictive medicine (e.g. diagnostic or prognostic
CC assays, monitoring clinical trials, pharmacogenomics); and for the
CC preparing a medication for the treatment of insulin resistance or type 2
CC diabetes mellitus.
XX
SQ Sequence 313 AA;
Alignment Scores:
Pred. No.: 7.05e-113 Length: 313
Score: 1670.00 Matches: 313
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.87% Indels: 0
DB: 7 Gaps: 0
US-10-705-757-1 (1-2623) x ABR62939 (1-313)
QY 351 ATGCTCTTGTCGCAAAATCAACTGCTTGGCCACCTGGGCGGCGCTTCGACAGCACTG 410
DB 1 MetLeuLeuSerIysIleAsnSerLeuAlaHisLeuArgAlaIleProCyAsnAspLeu 20
QY 411 CACGCCACCAAGCTGGCGCGCGCGGCAAGAGAGACCCCTGAGTTCGACATCAGAGTGT 470
DB 21 HisAlaThrIleValLeuAlaProGlyLysGluLysGluProLeuGluSerGlnIlyrGlnVal 40
QY 471 GGGCGGCTACTGGGCAAGCGCGGCTTGGCTCGGTCTACTCAGGATCCGCGTCTCCGAC 530
DB 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValIlyrSerGlyIleArgValSerAsp 60
QY 531 AACTGGCGGTGGCCATCAAAACAGTGGAGAAGACCCGGAATTCCGACTGGGAGACTG 590
DB 61 AsnLeuProValAlaIleValSHLeValGluLysAspArgIleSerAspTrpGlyGluLeu 80
QY 591 CCTAATGGCACTGAGTGGCCATGGAAGTGGTCTCTGTAAGAAAGTGAAGTCCGGTTC 650
DB 81 ProAsnGlyThrArgValProMetGluValValLeuLeuLysValSerSerGlyPhe 100
QY 651 TCCGGCGCTCATTAAGCTCTTGGAGCTGGTTCGAGAAGCCGACAGTTTCCTGATCTG 710
DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleLeu 120
QY 711 GAGAGGCCGACCGCGGTGCAAGATCTTTCGACTTCATCAGAAAGGAGCCCTGCA 770
DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
QY 771 GAGAGCTGGCCGCGAGCTTCTTGGCAGAGTGTGAGGCGCGGCACTGGCAAC 830
DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGluAlaValArgHisCySHAsn 160

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Oy	891	GAGCTCAAGCTTCATGACTTGGAGTCGGGGGCGCTGCTCAAGACAACCTGTACACCGAC	950
Db	181	GlutLeuYsVLeuIleAspPheGlySerGlyAlaLeuLeuYsAspTrpValTyThrAsp	200
Oy	951	TTCCATGGGACCCGAGTGTATGAGCCCTCCAGAGTGGATCCGGTCACATCGGTACATGGC	1010
Db	201	PheAspGlyTrpArgValTySerProGluTrpIleArgTyHisArgTyHisGly	220
Oy	1011	AGGTCGGCGGAGTCTGGTCCCTGGGGATCCCTGTTATGATATAGTGTGTGGAGATATT	1070
Db	221	ArgSerAlaAlaValTrpSerLeuGlyIleLeuLeuTyHisAspMetValCysGlyAspIle	240
Oy	1071	CCTTTCCAGCATGACGAAGAATCATCAAGGGCCAGGTTTCTTCAGGCAGAGGCTCT	1130
Db	241	ProPheGlyHisAspArgLeuGlyIleIleArgGlyGlnValPhePheArgGlnArgValSer	260
Oy	1131	TCAGATGTGAGCATCTCATATGATGGTGGCTGGCGCTGAACATCATGATGAGGCCAAC	1190
Db	261	SerGlnCysGlnHisLeuIleArgTrpCysLeuAlaLeuArgProSerAspArgProThr	280
Oy	1191	TTCCAGAAATCCAGAACCATTCATGATGCAAGATGTTCTCTCGCCCAAGAAATGCT	1250
Db	281	PheGlnGlyIleGlnAsnHisProIlePheGlnAspValLeuLeuLeuProGlnGluThrAla	300
Oy	1251	GAGATCCACCTTCACAGCTGTTCGCCGGGGGCCCAAGCAAA	1289
Db	301	GluIleHisLeuHisSerLeuSerProGlyProSerIys	313

RESULT 7
 ADR45083
 ID ADR45083 standard; protein, 313 AA.
 XX
 AC ADR45083;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human kinase PIM1.
 XX
 KM Human; protein kinase; enzyme; inhibitor; PIM1.
 XX
 OS Homo sapiens.
 XX
 PN W02003081210-A2.
 XX
 PD 02-OCT-2003.
 XX
 XX 20-MAR-2003; 2003WO-US0008725.
 XX
 PR 21-MAR-2002; 2002US-0366892P.
 XX
 PA (SUNE-) SUNESIS PHARM INC.
 XX
 PI Prescott JC, Braisted A;
 XX
 DR WPI; 2003-865136/80.
 XX
 PT Identifying ligand binding to inactive conformation of target protein
 PT kinase (T) comprises contacting the conformation modified (T) which
 PT contains reactive group at binding site, with ligands and detecting
 PT kinase-ligand conjugate formation.
 XX
 XX Disclosure; SEQ ID NO 52; 260pp; English.
 XX
 XX The present invention relates to a method for identifying a ligand (L),
 CC which binds to an inactive conformation of target protein kinase (T). The
 CC method involves contacting inactive conformation of (T), which contains
 CC or is modified to contain a reactive group at or near a binding site of
 CC interest, with one or more ligand candidates capable of covalently
 CC bonding to the reactive group thus forming a kinase-(L) conjugate (C).
 CC The method is useful for identifying protein kinase inhibitors that
 CC preferentially bind to inactive conformation of a target protein kinase.
 CC The present sequence is a protein kinase which may be modified via an

CC amino acid substitution, for use in the method of the invention.
XX
SQ Sequence 313 AA;

Alignment Scores:

Pred. No.:
Score:

7.05e-113
1670 00

Length: 313
Marches: 313

Percent Similarity:

100.00%

Conservative: 0

Query Match:

34.87%

```
Indels: 0
```

DB: / GdP

[illegible]

QY 1251 GAGATCCACCTGCAGACGCTGTGCGCGGAGCCAGCAAA 1289
 |||||
 DB 301 GUILIEHISLEUHSISERLEUSERPROGLYPROSERLYS 313

RESULT 8

ID ADO19690 standard; protein; 313 AA.
 XX ADO19690;

AC ADO19690;
 XX 12-AUG-2004 (first entry)
 XX Human PRO polypeptide #308.

DE Human PRO, immune related disorder; systemic lupus erythematosus;
 XX Human PRO, immune related disorder; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
 KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
 KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
 KW diabetes mellitus; renal disease; demyelinating disease;
 KW central nervous system; peripheral nervous system;
 KW demyelinating polyneuropathy; Guillain-Barre syndrome;
 KW chronic inflammatory demyelinating polyneuropathy.

XX Homo sapiens.

XX MO2004043361-A2.

XX 27-MAY-2004.

XX 06-NOV-2003; 2003WO-US035268.

XX 08-NOV-2002; 2002US-0425235P.

XX (GETH) GENENTECH INC.

PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PW,
 PI Wood WI, Wu TD;

XX MPI, 2004-420067/39.

DR N-PSDB; ADO19689.

PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
 PT treating an immune related disorder such as systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
 PT spondyloarthritis.

PS Claim 7; SEQ ID NO 616; 1731pp; English.

XX The invention relates to human PRO polypeptides and the polynucleotides
 CC encoding them. The polypeptides and polynucleotides are useful for
 CC treating and diagnosing immune related disorders in mammals. The immune
 CC related disorders include systemic lupus erythematosus, rheumatoid
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
 CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the
 CC central or peripheral nervous system, demyelinating polyneuropathy,
 CC Guillain-Barre syndrome and chronic inflammatory demyelinating
 CC polyneuropathy. This sequence represents a human PRO polypeptide of the
 CC invention.

XX Sequence 313 AA;

Alignment Scores:

Pred. No.: 7.05e-113 Length: 313
 Score: 1670.00 Matches: 313
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 34.87% Indels: 0
 DB: 8 Gaps: 0

US-10-705-757-1 (1-2623) x ADO19690 (1-313)

QY 351 ATGCTCTTGTCCAAAATCAACTCGCTTGCCCACTGCGCGCGCCCTGCAACGACCTG 410
 |||||
 DB 1 MetLeuLeuSerLyIleahSerLeuAlahSleuAlahIahIahProCyahamhPheU 20
 QY 411 CAGGCCACCAAGCTGGCGCCCGGCAAGAGAAAGAGCCCTTGAGTCCGACATACAGGTG 470
 |||||
 DB 21 HisAlahTrhLyLeuAlahProGlyLybGlybGlybProLeuGlySerGlyTrhGlybAl 40
 QY 471 GGGCCGCTACTGGGCAAGGGCGGCTTCCGCTCCGCTTACTCAGGACATCCGCTCCGAC 530
 |||||
 DB 41 GlyProLeuLeuGlySerGlyGlybPheGlySerValTySerGlyLyIleArgValSerhP 60
 QY 531 AACTGGCCGCTGGCCATCAACACGTGGAGAAAGACCCGATTTCCGACTGGGAGAGCTG 590
 |||||
 DB 61 AmhLeuProValAlahIleLyahhIstValGlybAbahPahGlyIleSerhPTrpGlybLeu 80
 QY 591 CCTAATGGCACTCGAGTGGCCCATGGAAAGTGTCTCTGTGAAAGAGTGAAGTCCGGTTC 650
 |||||
 DB 81 ProahngLyThArgValProhGlybValValLeuLeuLybValSerSerGlyPhe 100
 QY 651 TCCGCGCTCATTAAGCTCTCGACTGCTTCCGAGAGAGCCCGACAGTTTCTCTGATCTG 710
 |||||
 DB 101 SerGlyValIleArgLeuLeuAhPTrpPheGlybArgProhPbSerPheValLeuIleU 120
 QY 711 GAGAGGCCCGAGCCGGTGCAAGATCTCTTCGACTTCATCAACGAAAGGGAGCCCTGCA 770
 |||||
 DB 121 GlnhArgProGlybProValGlnhPbPhehPhehPhehIethGlybArgLybAlahUgln 140
 QY 771 GAGAGCTGGCCCGGAGCTTCTTGGCAGGTGTGTGAAGCCGTCGACCTCCACAAAC 830
 |||||
 DB 141 GlnGlybLeuAlahArgSerPhehPhehPhehPhehGlnValLeuGlybAlahValArgIstCyahhAah 160
 QY 831 TGGCGGGTCTTACACCGGACATCAAGACGAAACATCTTATGACCTCAATGGCGGC 890
 |||||
 DB 161 CybGlybValLeuNhIstArgbPheLybAhPbGlybAhbIleUahIstAhPbLeuAhbArgLy 180
 QY 891 GAGCTCAAGCTCATGCACTTCGAGGTCCGAGGCGCGCTGTCAAGAGACCGTCTTACAGGAC 950
 |||||
 DB 181 GlnLeuLybLeuIleAhPbPheGlybSerGlybAlahLeuLeuLybAhPTrhValTyThrhP 200
 QY 951 TTGATGGAGCCCGAGTGTATGACCTTCGAGAGTGGATCCGCTACCATCGTCAATGGC 1010
 |||||
 DB 201 PheAhPbGlyThArgValTybSerProhProGlybTrpIleArgTyhIstArgTyhIstGly 220
 QY 1011 AGGTGGCGGCAAGTGTGCTTCCGCGGATCCGCTGATGATAGTGTGAGATAT 1070
 |||||
 DB 221 ArgSerAlahAlahValTrpSerLeuGlyIleUleUeTybAhPbMetValCybGlybAhPhe 240
 QY 1071 CCTTCGAGCATGAGAAAGATCATCAGGGGCGCAGGTTTCTTCAGGCAAGGCTTCT 1130
 |||||
 DB 241 ProhPheGlybNhIstArgGlybGlybIleIleArgGlybGlnValPhehPhehArgGlnhArgValSer 260
 QY 1131 TCAGAAATGCAGCATCTCATTAAGATGTGTGCTTGGCCCTGAGACCATCAGATAGCCCAAC 1190
 |||||
 DB 261 SerGlybCybGlnhIleUahIleUahIleArgTybLeuAlahLeuArgProSerhPbArgProTrh 280
 QY 1191 TTGCAAGAAATCCAAACCATTCATGATGCAAGATGTTCTCTCCGCCAGGAACCTGT 1250
 |||||
 DB 281 PheGlybGlybIleGlnhAhbPbProTrpMetGlnhPbValLeuLeuProGlnGlybTrhAla 300
 QY 1251 GAGATCCACCTGCAGACGCTGTGCGCGGAGCCAGCAAA 1289
 |||||
 DB 301 GUILIEHISLEUHSISERLEUSERPROGLYPROSERLYS 313

RESULT 9

ADR88370
 ID ADR88370 standard; protein; 313 AA.
 XX ADR88370;

AC ADR88370;
 XX 18-NOV-2004 (first entry)
 XX

DE Human PIM 1 protein.
 XX Molecular scaffold; nuclear hormone receptor; TNF receptor;
 KM G-protein coupled receptor; methyl transferase; ligase; PIM; human.
 XX Homo sapiens.
 PN US2004171062-A1.
 XX 02-SEP-2004.
 PD 02-SEP-2004.
 PF 28-FEB-2003; 2003US-00377268.
 XX 28-FEB-2002; 2002US-0360651P.
 PR 16-SEP-2002; 2002US-0411398P.
 PR 20-SEP-2002; 2002US-0412341P.
 PR 02-JAN-2003; 2003US-0437929P.
 XX (PLEX-) PLEXIXON INC.
 XX
 PI Hirth K, Milburn MV;
 DR WPI, 2004-642017/62.
 XX
 PT Designing a ligand binding to a target molecule, comprises identifying as
 PT molecular scaffold compounds binding to members of a molecular family,
 PT detecting orientation of scaffolds at a binding site of target, and
 PT synthesizing ligand.
 XX
 XX Disclosure; SEQ ID NO 9; 186bp; English.
 XX
 CC The present invention relates to a method of designing a ligand binding
 CC to a target molecule. The method involves identifying a molecular
 CC scaffold compounds binding to members of a molecular family, detecting
 CC orientation of scaffolds at a binding site of target, and synthesizing
 CC ligand. The invention is useful for designing drug products and for
 CC designing ligand binding to target molecules such as nuclear hormone
 CC receptors, TNF receptors, G-protein coupled receptors, methyl
 CC transferases, ligases, etc. The present sequence is the human PIM 1
 CC protein. This sequence is used to illustrate the method of invention.
 CC
 XX Sequence 313 AA;
 XX
 Alignment Scores:
 Pred. No.: 7.05e-113 Length: 313
 Score: 1670.00 Matches: 313
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 34.87% Indels: 0
 DB: 8 Gaps: 0
 US-10-705-757-1 (1-2623) x ADR88370 (1-313)
 QY 351 ATGCTCTTGTCAAAATCAACTGCTTGCACCTGCGCGCGCCCTGCAAGACTG 410
 DB 1 MetLeuLeuSerIySileAenSerIeuaIHieLeuAryIaIaIaProCySaBaNaBpLeu 20
 QY 411 CAGCCCAACAGCTGCGCGCGCGCAAGAGAGAGAGCCCTGAGTGCAGTACCAAGTG 470
 DB 21 HieAlaThryIeLeuAIPaProGIyLyGIuLyGIuProlenGIuSerGIuTyrgIuVal 40
 QY 471 GGGCCCGTACTGGCGCGCGCGCGCTTGGCTCGGTCTACTCAGGACTCCGCTCTCGAC 530
 DB 41 GlyProlenLeuGIySerGIyGlyPneGIySerValTySerGIyIleAryValSerAaP 60
 QY 531 AACTTGGCGGTGACCATCAACAGTGAAGAGAGACCGGATTCGCACTGGGAGAGACTG 590
 DB 61 AsnLeuProValaIaIeIyShIeValGIuLyAaPaRgIleSerAaPTrpGIyGIuLeu 80
 QY 591 CCTAAATGCACTGAGTGGCCCATGAGAAAGTGTCTCTGTAAGAGAGTGAAGCTGGGTTTC 650
 DB 81 ProAenGIyThraRyValIPrometGIuValIleuLeuLybValSerSerGIyPhe 100

QY 651 TCCGGGCTATTAGGCTCCGAGCTGGTTGAGAGCGCGAGACTTTGCTGATCTG 710
 DB 101 SerGIyValIleAryLeuLeuAaPTrpPheGIuAryProAaPserPheValIleLeu 120
 QY 711 GAGAGGCCCGAGCGGTGCAAGATCTTTCAGCTTCATCAGCAAGAGGAGCCCTGCA 770
 DB 121 GIuAryProGIuProValGIuAryLeuPheAaPserPheIleThrgIuAryGIyAlaGIu 140
 QY 771 GAGAGAGTGGCCCGAGCTTCTTCTGAGCTGTGAGGCGGTGGGCACTGCCCAAC 830
 DB 141 GIuGIuLeuAIAaRySerPhePheTrpGIuValIleuGIuAlaValAryHISCySHISaSn 160
 QY 831 TGGCGGCTGCTACCGCGCATCAAGAGAGAGAAACCTCTTACGCTCAATCGCGG 890
 DB 161 CyGIyValIleuHISaRyAaPTrpIleuYAspGIuAaSnIleuHISaPheAaAaRyGIy 180
 QY 891 GAGCTCAAGCTCATGCACTTCGAGTGGGGGCGCTGTCAGAGACACCTGTACAGGAC 950
 DB 181 GIuLeuLyLeuHISaPheAaPserGIyAlaLeuLeuLyAaPTrpValTyTrpAaP 200
 QY 951 TTGCAATGGACCCGAGTGTATACCTCCAGAGTGAATCGCTACATGCTACATGCG 1010
 DB 201 PheAaPGIyThraRyValTySerProProGIuTrpIleAryTyHISaRyGIy 220
 QY 1011 AGGTCCGCGGAGCTGCTGCTCCGAGATCCCTGCTATGATATGAGTGTGAGATATT 1070
 DB 221 ArgSerAlaIaIaValTrpSerLeuGIyIleuLeuTyAaPTrpValCybGIyAaPTrp 240
 QY 1071 CCTTTCAGCATGACCAAGAGATCATCAGGGGCGAGTTTCTTCAAGCGAGGCTCT 1130
 DB 241 ProPheGIuHISaPserGIuGIuIleIleAryGIyGIuValPheAaPTrpGIuAryValSer 260
 QY 1131 TCGAATGTCAAGATCTCATTAATGATGCTTGGCTGAGACCATCAATAGCCCAAC 1190
 DB 261 SerGIuGIuGIuHISaPserIleAryTrpCybLeuAlaLeuAryProSerAaPTrp 280
 QY 1191 TTGCAAGAAATCCAGAACCATCAATGAGAGCAAGATGTTCTTGGCCCAAGAACTGT 1250
 DB 281 PheGIuGIuIleIleAaSnHISaPTrpMetGIuAaPValLeuLeuProGIuGIuTrpAla 300
 QY 1251 GAGATCCACCTCCAGAGCTGTGCGGGGCGCCAGCAAA 1289
 DB 301 GIuIleHISaPserIleuSerProGIyProSerLyS 313
 RESULT 10
 ADP24227
 ID ADP24227 standard; protein; 313 AA.
 XX
 AC ADP24227;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE PRO polypeptide SEQ ID NO:1405.
 XX
 KM PRO: antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
 KM osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
 KM antistaphyloc; hepatotropic; respiratory; gene therapy; immune system.
 XX
 OS Unidentified.
 XX
 PN WO2004041170-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 30-OCT-2003; 2003WO-US034312.
 XX
 PR 01-NOV-2002; 2002US-0423394P.
 XX
 PA (GENT) GENTECH INC.
 XX
 XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
 PI Wu TD;
 XX

DR WPI; 2004-419628/39.
 DR N-PSDB; ADP24226.
 XX
 PT New PRO polypeptides and polynucleotides, useful for treating e.g.
 PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
 PT renal disease, or demyelinating diseases of the central or peripheral
 PT nervous system.
 XX
 PS Claim 7; SEQ ID NO 1405; 2940bp; English.
 CC
 CC The invention relates to a novel isolated nucleic acid and the PRO
 CC polypeptide encoded by it. A protein of the invention has
 CC antiinflammatory, antirheumatic, antirheumatic, immunosuppressive,
 CC osteoprotective, antidiabetic, dermatological, antipruritic, antiallergic,
 CC antineoplastic, hepatotropic, and respiratory activity. A polynucleotide
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its
 CC agonist, antagonist, or antibody that specifically binds to the
 CC polypeptide is useful for treating an immune related disorder such as
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.
 CC
 XX
 SO Sequence 313 AA:
 Alignment Scores:
 Pred. No.: 7.05e-113 Length: 313
 Score: 1670.00 Matches: 313
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 34.87% Indels: 0
 DB: 8 Gaps: 0
 US-10-705-757-1 (1-2623) x ADP24227 (1-313)
 QY 351 ATGCTCTGTCCAAATCAACTGCTGCTGCCACCTGGCGCGCGCCCTCAAGACGCTG 410
 DB 1 MetLeuLeuSerLysIleAsnSerLeuAlaHisLeuArgAlaIleProCysAsnAspLeu 20
 QY 411 CACGCCCAAGAGTGGCGCGCGCGCAAGAGAGAGAGCCCTGAGTGCAGTACCAAGTGC 470
 DB 21 HisAlaThrLysLeuAlaProGlyLysGluLysGluProLeuGlnSerGlnVal 40
 QY 471 GGCCTGCTATGGCGAGCGCGCGCTTGGCTCGGTCTACTCAGGACCTCGCTCCGAC 530
 DB 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValLysSerGlyIleArgValSerAsp 60
 QY 531 AACCTGGCGGTGGCGCATCAACACGTGAGAGAGACCGGATTTCCGACTGGGAGAGCTG 590
 DB 61 AsnLeuProValAlaIleLysHisValGluLysAspArgLysSerAspTrpGlyGluLeu 80
 QY 591 CCTAATGCACTCGAGTCCCATGAGAGTGTCTCTGGAAGAAGTGAAGCTCGGGTTTC 650
 DB 81 ProAsnGlyThrArgValProMetGluValValLeuLeuLysValSerSerGlyPhe 100
 QY 651 TCGGGCGCTATTAGGCTCTGGAAGTGTGAGAGGCGCGCAAGTTTCGTCGATCTCTG 710
 DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleLeu 120

QY 711 GAGAGCCCGAGCCGGTGCAGATCTTTCATTCATCAGGAAAGGGAGCCCTGCAA 770
 DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
 QY 771 GAGAGCTGGCCCGAGCTTCTTTCGAGAGTGTGAGAGCCGTGCGCACTGCCAAGC 830
 DB 141 GluGluLeuAlaArgSerPheThrGlnValLeuGluAlaValAlaArgHisCysHisAsn 160
 QY 831 TGGCGGGTGGCTACCGGAGCATCAAGAGGAAACATCTTATGAGCTCAATGCGCGC 890
 DB 161 CysGlyValLeuHisArgAspIleLysAspGlnAsnIleLeuIleAspLeuAsnArgGly 180
 QY 891 GAGCTCAAGCTCATGCACTTCGGGTGGGGGCGCTGCTCAAGAGACCGTCTTACGAGAC 950
 DB 181 GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValLysThrAsp 200
 QY 951 TTGATGGAGACCCGAGTGTATAGCCCTCCAGAGTGATCCGTACCATCTGCAATGGC 1010
 DB 201 PheAspGlyThrArgValLysSerProProGluTrpIleArgTyrHisArgTyrHisGly 220
 QY 1011 AGTGGCGGCGAGCTGTGCTGCTGGGAGTCCGCTGATATGATAGTGTGTGAGATATT 1070
 DB 221 ArgSerAlaAlaValTrpSerLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
 QY 1071 CCTTTCGAGCATGAGAGAGATCATCAGGGGCGCAGTTTCTTCAAGCAGAGGCTCTCT 1130
 DB 241 ProPheGluHisAspGluGluIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
 QY 1131 TCAGAAATGCACATCTCATTAAGATGTGCTTGGCCCTGAGACCATCAGATAGGCCAAC 1190
 DB 261 SerGluCysGlnHisLeuLeuIleArgTrpCysLeuAlaLeuArgProSerAspArgProThr 280
 QY 1191 TTCGAAGAAATCCAGAACCATCCATGAGATGGAAGTGTCTGCTGCCAGAGAACTGCT 1250
 DB 281 PheGluGluIleGlnHisAsnIleProTrpMetGlnAspValLeuLeuProGlnIleTrpAla 300
 QY 1251 GAGATCCACCTCCAGAGCTGTGCGCGGCGCCAGCAAA 1289
 DB 301 GluIleHisLeuHisSerLeuSerProGlyProSerLys 313
 RESULT 11
 ID AAM08139
 XX AAM08139 standard; protein; 313 AA.
 XX
 AC AAM08139;
 XX
 DT 11-MAR-1997 (first entry)
 XX
 DE Human cytokine response protein CR7.
 XX
 KW Cytokine response protein; CR7; interleukin-2; IL-2;
 KW ligand-stimulated gene expression; diagnosis; therapy; proto-oncogene;
 KW p1m1; protein kinase; lymphoma.
 XX
 OS Homo sapiens.
 XX
 PN MO9639427-Al.
 XX
 PD 12-DEC-1996.
 XX
 PF 05-JUN-1996; 96WO-US009194.
 XX
 PR 05-JUN-1995; 95US-00461379.
 PR 05-JUN-1995; 95US-00462337.
 PR 05-JUN-1995; 95US-00462390.
 PR 05-JUN-1995; 95US-00463074.
 PR 05-JUN-1995; 95US-00463081.
 PR 05-JUN-1995; 95US-00465585.
 XX
 PA (DART-) DARTMOUTH COLLEGE.
 XX
 PI Smith KA, Beadling C;

Alignment Scores:

Pred. No.:	6,24e-112	Length:	313
Score:	1657.00	Matches:	311
Percent Similarity:	99.36%	Conservative:	0
Best Local Similarity:	99.36%	Mismatches:	2
Query Match:	34.60%	Indels:	0
DB:	3	Gaps:	0

US-10-705-757-1 (1-2623) x AAY87959 (1-313)

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QY 351 ATGCTTGTCCAAATCACTGCTTGCCCACTGCGCGCGCGCTTCCAGACGACGCTG 410
DB 1 MetLeuLeuSerIySrlleuSenSerleuAlaHleuHArgAlaArgAlaCysaSenApleu 20
QY 411 CACGCCAACAGCTGGCGCGCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 470
DB 21 HleAlArthLySleuAlaProGlyLySgluLySgluProleuIuSerGlnVal 40
QY 471 GGGCGGCTACTGGGCGCGCGCGCTTCCGCTGCTACTCAGGACGCTCGCTCGAC 530
DB 41 GlyProleuLeuSerIySrlleuSenSerleuAlaHleuHArgAlaArgAlaCysaSenApleu 60
QY 531 AACTGCGCGTGGCCATCAACACGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 590
DB 61 AenLeuProValAlaIleuYshIeValGluLyAaPArgIleSerAerItrpGlyIuLeu 80
QY 591 CCTAATGGCACTGAGTGGCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 650
DB 81 ProAaNgLyThArzArgValProMetGluValIleuLeuLySgluValSerSerGlyPhe 100
QY 651 TCGGGGGTCAATTGGGCTCGGAGCTGGTTCGAGAGGCGCGAGTTCGCTCGATCCG 710
DB 101 SerGlyValIleArzGleuLeuAaPArgIleSerAerItrpGlyIuLeuLeuLeu 120
QY 711 GAGAGGCGCGAGCGCGTGAAGATCTCTTGACTTCATACGAGAAAGGAGAGCGCTGCA 770
DB 121 GluArgProIuProValGlnAaPleuPheAaPArgIleThrGluArgGlyAlaLeuGln 140
QY 771 GAGAGAGTGGCGCGAGCTTCTTCTGGCAGGTCCTGAGAGCGCGTGGCGCACTCCCAAC 830
DB 141 GluGlnLeuAlaArzGleuPheArzGlnValIleuGlnAlaValAlaArgIshCysHlaAa 160
QY 831 TGGGGGGTGTACACGCGGACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 890
DB 161 CysGlyValLeuHlaArzAaPArgIleLyAaPArgIleuLeuLeuAaPArgIle 180
QY 891 GAGCTCAAGCTCATGCACTTCGGGTCGGGCGCGCTGCAAGAGACACCGTCTACAGCGAC 950
DB 181 GluLeuLySleuLeuAaPArgIleSerGlyAlaIleuLeuLySleuAaPArgIle 200
QY 951 TTGAGATGGAGCCGAGTGTATACCTCTCCAGAGTGCATCCGCTACCATCCATCCG 1010
DB 201 PheAaPArgIyThArzArgValTySerProGlnItrpIleArgTyHlaArgTyHla 220
QY 1011 AGATCGCGCGAGCTGGTTCCTCGGAGATCTCTGTAATGAGTGTGAGATATT 1070
DB 221 ArzSerAlaAlaValItrpSerLeuGlyLySleuLeuLySleuAaPArgIle 240
QY 1071 CCTTTCGAGCATGACGAGAGATCATCAGGAGCGAGGCTTCTTCAGCGAGAGGCTTCT 1130
DB 241 ProPheGlnIuHlaAaPArgIuGlnIleIleArgGlyGlnAlaPheAaPArgIle 260
QY 1131 TCGAATGTCAAGCTCATTTAAGTGTGCTTGGCGCTGAGACCATCAAGTACGAGCC 1190
DB 261 SerGlyCysGlnIshleuLeuIleArgItrpCysleuAlaLeuAaPArgIle 280
QY 1191 TTGAGAGAAATCGAGAGACATCATGAGTGTGATGTTCTCTCGCGCGAGAACTGCT 1250
DB 281 PheGlnIuIleGlnAaPArgIleAaPArgIleAaPArgIleAaPArgIleAaPArgIle 300
QY 1251 GAGATCCAGCTTCACAGCTGTGCGCGCGCGCGCGAGCAAA 1289

```

DB 301 GluLeuHleuHleuSerleuSerProGlyProSerLyS 313

RESULT 13

ID ADI57202 standard; protein; 313 AA.

AC ADI57202;

XX 22-APR-2004 (first entry)

DT

XX

DE Human PIM1 protein SEQ ID NO:22.

XX

XX cell cycle arrest; CK2-specific siRNA molecule; short interfering RNA;

KW CK2 inhibition; PIM1-specific siRNA molecule; PIM1 inhibition;

KW Hbo1-specific siRNA molecule; Hbo1 inhibition; cytoskeletal gene therapy;

KW cancer; proliferative disorder; human; PIM1.

OS

XX Homo sapiens.

XX

PN MO2004007754-A2.

XX

PD 22-JAN-2004.

XX

XX

PF 14-JUL-2003; 2003WO-US022164.

XX

PR 12-JUL-2002; 2002US-0395443P.

XX

PA (RIGB-) RIGEL PHARM INC.

XX

PI Hitoshi Y, Jenkins Y, Markovtsov Y,

XX

DR MPI; 2004-122975/12.

DR N-PDB; ADI57201.

XX

PT Identifying a compound that modulates cell cycle arrest, useful for

PT developing therapeutic reagents for treating cancer comprising contacting

PT a cell comprising a target polypeptide with the compound.

XX

PS Claim 1, SEQ ID NO 22; 180bp; English.

XX

XX The present invention describes a method for identifying a compound (C)

CC that modulates cell cycle arrest. The method comprises contacting a cell

CC comprising a target polypeptide with the compound (C), where the target

CC polypeptide encoded by the complement of a nucleic acid that hybridizes

CC under stringent conditions to a nucleic acid encoding a polypeptide

CC having an amino acid sequence selected from 18 148-1408 amino acid

CC sequences (SEQ ID NO: 2-36, even numbers only). Also described: (1)

CC modulating cell cycle arrest in a subject; (2) a CK2-specific short

CC interfering RNA (siRNA) molecule comprising the sequence: (i)

CC AACATGATATGATCCAGT, where the siRNA molecule is from 21-30 nucleotide

CC base pairs in length; (3) inhibiting expression of a CK2 gene in a cell;

CC (4) a PIM1-specific siRNA molecule comprising the sequence: (ii)

CC AAATCTCGAGTGAATGCTG, where the siRNA molecule is from 21-30 nucleotide

CC base pairs in length; (5) inhibiting expression of a PIM1 gene in a cell;

CC (6) an Hbo1-specific siRNA molecule comprising the sequence: (iii)

CC AACAGCAGAGAGGATGATTT, where the siRNA molecule is from 21-30 nucleotide

CC base pairs in length; and (7) inhibiting expression of an Hbo1 gene in a

CC cell. (C) has cytostatic activity, and can be used in gene therapy. The

CC method is useful for identifying a compound (C) that modulates cell cycle

CC arrest. Compounds that modulate cell cycle arrest are useful for

CC developing therapeutic reagents for treating cancer and other

CC proliferative disorders. The present sequence represents human PIM1,

CC which is used in the exemplification of the present invention.

XX

XX Sequence 313 AA;

XX

Alignment Scores:

Pred. No.:	6,24e-112	Length:	313
Score:	1657.00	Matches:	311
Percent Similarity:	99.36%	Conservative:	0
Best Local Similarity:	99.36%	Mismatches:	2
Query Match:	34.60%	Indels:	0
DB:	8	Gaps:	0

US-10-705-757-1 (1-2623) x AD157202 (1-313)

QY 351 ATGCTTTGTCCAAATCAACTGGCTTGGCCCACTGCGCGCGCCCTTGCACGACCTG 410
 DB 1 MetLeuLeuSerIysIleAsnSerLeuAlaH1leuAlaArgAlaCysAsnAspLeu 20
 QY 411 CAGGCCCAAGAGCTGGCGCGCGCAAGAGAGAGCCCTTGAGTGGCACTCCAGCTG 470
 DB 21 HisAlaThrIysLeuAlaProGlyLysGlyIleuLeuProLeuGlnSerGlnIyrGlnVal 40
 QY 471 GGCCTGCTACTGGGCAAGCGCGCGCTTGGCTCGGCTACTCAGGCACTCCGCTCCGAC 530
 DB 41 GlyProLeuLeuGlySerGlyIleuPheGlySerValIyrSerGlyIleArgValSerAsp 60
 QY 531 AACTTGGCGGTGGCCATCAACACGTGGAGAGAGACCGGATTTCCGACTGGGAGAGCTG 590
 DB 61 AsnLeuProValAlaIleIysH1sValGlyIysAspArgIleSerAspTrpGlyGlnLeu 80
 QY 591 CCTAATGGCACTGAGTGGCCATGGAAGTGTCTCTGTAAGAGAGTGGAGCTGGGTTTC 650
 DB 81 ProAsnGlyThrArgValProMetGlnValValLeuLeuIysValSerSerGlyPhe 100
 QY 651 TCCGCGCTCATTAAGCTCTGCACTGGTTCGAGAGCGCCGACAGTTTCGTCTGATCTTG 710
 DB 101 SerGlyValIleArgLeuLeuAspTrpPheGlyIArgProAspSerPheValIleuLeu 120
 QY 711 GAGAGCGCCGAGCGCGGTGCAAGATCTTCTGACTTCATCGAAGAGGAGCGCTTGCA 770
 DB 121 GluArgProGlyIupProValGlnAspLeuPheAspPheIleThrGlyIArgIleuGln 140
 QY 771 GAGAGCTGGCGCGCGCTTCTTGTGCAAGTCTGAGAGCGCGCTGGCGCACTGCGCAAC 830
 DB 141 GlnGlyIleuAlaArgSerPheMetTrpGlnValLeuGlnIleValArgH1sCysH1sAsp 160
 QY 831 TGGCGGGTGTCTACACGCGCATCAAGAGAGAGAAACATCTTTCGACTTCGACTTCGCGG 890
 DB 161 CysGlyValIleuH1sArgAspIleIysAspGlnAsnIleuLeuIleAspLeuAsnArgGly 180
 QY 891 GAGCTCAAGCTCATCGACTTCGCGGTGGGCGCGCTGTCAGAGACACCGTCTACACGAGC 950
 DB 181 GluLeuIleuLeuIleAspPheGlySerGlyAlaIleuLeuIysAspTrpValIyrThrAsp 200
 QY 951 TTTCGATGGGACCCGAGTGTATAGCTTCCGAGTGGATCCGCTACCATCGCTTACATGGC 1010
 DB 201 PheAspGlyThrArgValIyrSerProGlyIupTrpIleArgIyrH1sArgIyrH1sGly 220
 QY 1011 AGGTGGCGGCACTGCTGCTCGTGGGATCTGCTGATGATATGAGTGTGAGATATT 1070
 DB 221 ArgSerH1aH1aValItrpSerIleuGlyIleuLeuIyrAspMetValCysGlyAspIle 240
 QY 1071 CCTTTCGAGCATGACGAAGATCATCGGAGCGCAGGTTTCTTCAGCGCAGAGGCTCTCT 1130
 DB 241 ProPheGlyH1sAspGlnGlyIleIleArgGlyGlnValaPhePheArgGlnValSer 260
 QY 1131 TCGAATGTTCAGCATCTCATTAATAGTGTGCTTGGCTTGGAGACATCAAGTAGCCCAAC 1190
 DB 261 SerGlnCysGlnH1sIleuIleAspTrpCysLeuAlaLeuArgProSerAspArgProThr 280
 QY 1191 TTTCGAAGAATTCAGAACATCATCGATGATGATGATTTCTGCGCCCGAGAACTGCT 1250
 DB 281 PheGlnGlnIleGlnIleAsnH1sProTrpMetGlnAspValIleuLeuProGlnGlnItrH1a 300
 QY 1251 GAGATCCACCTTCACAGCCTGTGCGCGGCGCCGACGAA 1289
 DB 301 GluIleH1sIleuH1sSerIleuSerProGlyProSerIys 313
 RESULT 14
 ADN03170
 ID ADN03170 standard; protein; 313 AA.
 XX
 AC ADN03170;
 XX

DT 29-JUL-2004 (first entry)
 XX
 DE Human P1M-1 polypeptide.
 XX
 KM Human; P1M-1; antisense oligonucleotide; phosphorothioate linkage;
 KM 2'-O-methoxyethyl sugar moiety; 5-methylcytosine;
 KM hyperproliferative disorder; cancer; cytostatic.
 OS Homo sapiens.
 XX
 PN US2004092463-A1.
 XX
 PD 13-MAY-2004.
 XX
 PF 11-NOV-2002; 2002US-00292849.
 XX
 PR 11-NOV-2002; 2002US-00292849.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Wact AT;
 XX
 DR MPI; 2004-374981/35.
 DR N-PSDB; ADN03035.
 XX
 PT New compound that modulates P1M-1 expression, useful in treating an
 PT animal having a disease or condition, i.e. hyperproliferative disorder.
 XX
 PS Claim 1; SEQ ID NO 4; 51bp; English.
 XX
 CC The invention relates to a compound targeted to a nucleic acid molecule
 CC encoding the human P1M-1 polypeptide. The compound is an antisense
 CC oligonucleotide that specifically hybridizes with the nucleic acid and
 CC inhibits expression of the polypeptide. The antisense oligonucleotide
 CC comprises at least one modified internucleoside linkage i.e. a
 CC phosphorothioate linkage, at least one modified sugar moiety, preferably
 CC a 2'-O-methoxyethyl sugar moiety, or at least one modified nucleobase
 CC comprising a 5-methylcytosine. The antisense compounds are useful for
 CC modulating the expression of the human P1M-1 polypeptide and in
 CC preparation of a composition for treating hyperproliferative disorders,
 CC e.g. cancer. This sequence represents the human P1M-1 polypeptide of the
 CC invention.
 XX
 SQ Sequence 313 AA:
 Alignment Scores:
 Pred. No.: 6,24e-112 Length: 313
 Score: 1657.00 Matches: 311
 Percent Similarity: 99.36% Conservative: 0
 Best Local Similarity: 99.36% Mismatches: 2
 Query Match: 34,60% Indels: 0
 DB: 8 Gaps: 0
 US-10-705-757-1 (1-2623) x ADN03170 (1-313)
 QY 351 ATGCTTTGTCCAAATCAACTGGCTTGGCCCACTGCGCGCGCCCTTGCACGACCTG 410
 DB 1 MetLeuLeuSerIysIleAsnSerLeuAlaH1leuAlaArgAlaCysAsnAspLeu 20
 QY 411 CAGGCCCAAGAGCTGGCGCGCGCAAGAGAGAGCCCTTGAGTGGCACTCCAGCTG 470
 DB 21 HisAlaThrIysLeuAlaProGlyLysGlyIleuLeuProLeuGlnSerGlnIyrGlnVal 40
 QY 471 GGCCTGCTACTGGGCAAGCGCGCGCTTGGCTCGGCTACTCAGGCACTCCGCTCCGAC 530
 DB 41 GlyProLeuLeuGlySerGlyIleuPheGlySerValIyrSerGlyIleArgValSerAsp 60
 QY 531 AACTTGGCGGTGGCCATCAACACGTGGAGAGAGACCGGATTTCCGACTGGGAGAGCTG 590
 DB 61 AsnLeuProValAlaIleIysH1sValGlyIysAspArgIleSerAspTrpGlyGlnLeu 80
 QY 591 CCTAATGGCACTGAGTGGCCATGGAAGTGTCTCTGTAAGAGAGTGGAGCTGGGTTTC 650


```

Db      81 ProAsnGlyThrArgValProMetGluValLeuLeuLeuValSerSerGlyPhe 100
QY      651 TCCGGGCGTATTGGCTCCCTGAGCTGTTGAGAGGCCGCGGCTTCGCTCGTGAACCG 710
Db      101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleu 120
QY      711 GAGAGCCCCGAGCCGCTGCAAGATCTCTTCGACTTCATACGAGAAAGGAGGAGCCCTGCAA 770
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QY      831 TGGGGGTGCTACACCGCGCATCAAGACGAAACCTCTTTCGACCTCAATCGCGGC 890
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Db      301 GluIleHisIleuHisSerLeuSerProGlyProSerIle 313

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XX      XX Kapeller-Iibermann R, Rudolph-Owen LA, Machbeth K;
PI      PI
XX      DR WPI; 2002-712471/77.
XX      PT Modulating levels or activity of HKID-1 polypeptides, a member of
XX      PT serine/threonine kinase superfamily, for treating cancer, by contacting
XX      PT cell expressing the polypeptide with a modulator of the polypeptide.
XX      PS
XX      PS Example 3; Page 39-40; 48pp; English.
XX      CC The invention describes a method of modulating the level or activity of
XX      CC human HKID-1 polypeptide, a member of serine/threonine kinase
XX      CC superfamily. The method involves contacting a cell expressing the
XX      CC polypeptide or nucleic acid with an agent to modulate the level or
XX      CC activity of polypeptide, or level of nucleic acid molecule. The method is
XX      CC useful for modulating the level or activity of HKID-1 polypeptide or
XX      CC polynucleotide in a subject having or predisposed to having a disorder
XX      CC involving cancer. Modulating HKID-1 expression or activity is useful for
XX      CC therapeutic purposes, for treating cellular proliferative and/or
XX      CC differentiative disorders including cancer or haematopoietic neoplastic
XX      CC disorders e.g. acute promyeloid leukaemia (APML), chronic myelogenous
XX      CC leukaemia (CML) and Waldenstrom's macroglobulinaemia (WM). This is the
XX      CC amino acid sequence of a rat protein kinase phosphorylation site
XX      CC
SQ      Sequence 313 AA;
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Score: 1636.00 Matches: 304
Percent Similarity: 99.04% Conservative: 6
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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus.n2p model

Run on: September 22, 2005, 16:26:26 ; Search time 176.628 Seconds

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Perfect score: 2443

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Searched: 1826521 seqs, 407012169 residues

Total number of hits satisfying chosen parameters: 3653042

Minimum DB seq length: 0

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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1668	68.3	313	15 US-10-348-081-12	Sequence 12, Appl1
3	1668	68.3	313	18 US-10-705-757-4	Sequence 4, Appl1
4	1636	67.0	313	9 US-09-971-791-9	Sequence 9, Appl1
5	1636	67.0	313	14 US-10-081-119-18	Sequence 18, Appl1
6	1636	67.0	313	15 US-10-394-322A-52	Sequence 52, Appl1
7	1636	67.0	313	15 US-10-348-081-13	Sequence 13, Appl1
8	1636	67.0	313	16 US-10-664-421-1	Sequence 1, Appl1
9	1636	67.0	313	16 US-10-664-421-150	Sequence 150, App
10	1636	67.0	313	16 US-10-377-268-9	Sequence 9, Appl1
11	1636	67.0	313	17 US-10-951-389-18	Sequence 18, Appl1
12	1636	67.0	313	17 US-10-951-406-18	Sequence 18, Appl1
13	1636	67.0	313	17 US-10-951-477-18	Sequence 18, Appl1
14	1636	67.0	313	18 US-10-977-087-18	Sequence 18, Appl1
15	1636	67.0	313	18 US-10-705-757-2	Sequence 2, Appl1
16	1636	67.0	313	18 US-10-941-635-1	Sequence 1, Appl1
17	1636	67.0	313	18 US-10-941-635-152	Sequence 152, App
18	1623	66.4	313	16 US-10-620-052A-22	Sequence 22, Appl1
19	1584	64.8	313	9 US-09-971-791-7	Sequence 7, Appl1
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22	1584	64.8	313	16 US-10-377-268-10	Sequence 10, Appl1
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44	1104	45.2	323	15 US-10-348-081-11	Sequence 11, Appl1
45	1104	45.2	323	16 US-10-664-421-8	Sequence 8, Appl1

ALIGNMENTS

RESULT 1
US-09-971-791-8
; Sequence 8, Application US/09971791
; Patent No. US20020115120A1
; GENERAL INFORMATION:
; APPLICANT: Roseanna Kapeller-Libermann
; APPLICANT: Laura A. Rudolph-Owen
; APPLICANT: Kyle MacBeth
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES TH
; FILE REFERENCE: 35800/238856
; CURRENT APPLICATION NUMBER: US/09/971, 791
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/644, 450
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/237, 543
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 313

TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-971-791-8

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US-10-705-757-3 (1-1302) x US-09-971-791-8 (1-313)

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RESULT 2

US-10-348-081-12
Sequence 12, Application US/10348081
Publication No. US20040038246A1
GENERAL INFORMATION:
APPLICANT: KORN, Marcus
APPLICANT: MUELLER, Guenter
APPLICANT: SCHNEIDER, Rudolf
APPLICANT: TSCHAN, Georg
TITLE OF INVENTION: PIV-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
FILE REFERENCE: DE42002/0004 US NP
CURRENT APPLICATION NUMBER: US/10/348,081
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.2
SEQ ID NO 12
LENGTH: 313
TYPE: PRT
ORGANISM: Rattus norvegicus
US-10-348-081-12

Alignment Scores:

Pred. No.:	2,12e-111	Length:	313
Score:	1668.00	Matches:	313
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
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US-10-705-757-3 (1-1302) x US-10-348-081-12 (1-313)

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RESULT 3

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/ Sequence 4, Application US/10705757
/ Publication No. US20040146942A1
/ GENERAL INFORMATION:
/ APPLICANT: GRUENTHAL GMBH
/ TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE OR PIM3-KINASE
/ FILE REFERENCE: 029310.52818US
/ CURRENT APPLICATION NUMBER: US/10/705,757
/ PRIOR FILING DATE: 2003-11-12
/ PRIOR APPLICATION NUMBER: PCT/EP02/05234
/ PRIOR FILING DATE: 2002-05-13
/ PRIOR APPLICATION NUMBER: DE 101 23 055.9
/ PRIOR FILING DATE: 2001-05-11
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 313
/ TYPE: PRT
/ ORGANISM: Rattus norvegicus
US-10-705-757-4

Alignment Scores:

Pred. No.: 2,12e-111 Length: 313
Score: 1668.00 Matches: 313
Percent Similarity: 100.00% Conservative: 0
Beet Local Similarity: 100.00% Mismatches: 0
Query Match: 68.28% Indels: 0
Gaps: 0

US-10-705-757-3 (1-1302) x US-10-705-757-4 (1-313)

QY 4 ATGCTCTTGTCAAGATCAACTCCCTGGGCCACCTGGGAGAGCCCTTGCACAGACCTG 63
Db 1 MetLeuLeuSerYalIleAspSerLeuAlaHisLeuArgAlaIleProCysAspAspLeu 20
QY 64 CAGCGCAACAAGCTGGCGCGGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
Db 21 HisAlaAsnIleAspIleProGlyLysGluValGluProLeuHisSerGlnTyrGlnVal 40
QY 124 GGGCCGCTGTGGGAGCGGCTTCCGCTCTAATCGGGCATCCGCGTCCGAGC 183
Db 41 GlyProLeuLeuIleSerGlyGlyPheGlySerValTyrSerGlyIleArgValAlaAsp 60
QY 184 AACTTCGCGGTGCGCATCAAGCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243

Db 61 AsnLeuProValAlaIleIleYbHisValGluYbAspArgIleSerAspTyrGlyGluLeu 80
QY 244 CCCAAGCGCACCCGAGTGTCCCATGAGAGTGTCTCTCTGAAGAGAGTGAAGTCTGGGCTTC 303
Db 81 ProAsnGlyThrArgValIleProMetGluValIleLeuLeuYbValSerSerGlyPhe 100
QY 304 TCGGGGCTCAATTGACTTTCGAGCTGTGCGAGAGGCGCGATGTTTCCGCTGATCCG 363
Db 101 SerGlyValIleIleArgLeuLeuAspTyrPheGluArgProAspSerPheValIleLeu 120
QY 364 GAGAGCGCGCAACCCGTCGAAGACTCTTCACTTATCAACGAGGAGAGAGCGCTTCAG 423
Db 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGlnArgGlyAlaLeuGln 140
QY 424 GAGAGCTGGCCCGAGACTTCTTCTGAGAGTGTGAGAGCGCTGGCGCATTCGCAAC 483
Db 141 GluGluLeuAlaArgSerPheThrProGlnValIleGluAlaValArgHisCysHisAsn 160
QY 484 TGGGGGGTCTCCACCGCGCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 543
Db 161 CysGlyValLeuHisAspAspIleYbAspGluAsnIleLeuIleAspLeuAsnArgGly 180
QY 544 GAACTCAAACTCATCGACTTGGGGTGGGGGCGCTGTCAAGGACAGTCTACAGGAC 603
Db 181 GluLeuYbLeuIleAspPheGlySerGlyAlaLeuLeuYbAspThrValTyrThrAsp 200
QY 604 TTTGACGGAACCCGAGTGTACAGTCTCTCAAGTGAATTCGTAACCATCGCTACCAAGGC 663
Db 201 PheAspGlyThrArgValTyrSerProGluTyrIleArgTyrHisArgTyrHisGly 220
QY 664 AGTGGCGCTGCTTTGGTCCCTGGGAGATCTGTCTATGACATAGTCTGCGAGATAT 723
Db 221 ArgSerIleAlaValTyrSerLeuGlyIleLeuLeuYbAspMetValCysGlyAspIle 240
QY 724 CCATTGAGCAGCAGAGAGATCGTCAAGGCGCAAGTACTTATGACAAAGGATCTT 763
Db 241 ProPheGluHisAspGluGluIleValGlyGlnValTyrPheArgGlnArgValSer 260
QY 784 TCAGATGTCAACATCTTATTAATGATGTCCTGTCCCTGAGACATCGAAGCGCCCTCC 843
Db 261 SerGluCysGlnHisLeuIleAspThrCysLeuSerLeuArgProSerAspArgProSer 280
QY 844 TTTGAAGAATCCAGAACCATCCGTGATGATGATGATTTCTCTGCGCCGAGGCAAGCC 903
Db 281 PheGluGluIleGlnHisAspProTyrMetGlnAspValLeuLeuProGlnIleAla 300
QY 904 GAGATTCATCTGCACAGCTGTCAACCATCAGCCAGCAAA 942
Db 301 GluIleHisLeuHisSerLeuSerProSerProSerLys 313

RESULT 4

US-09-971-791-9
/ Sequence 9, Application US/09971791
/ Patent No. US20020115120A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosanna Kapeller-Libermann
/ APPLICANT: Kyle Macbeth
/ TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES TH
/ FILE REFERENCE: 35800/238856
/ CURRENT APPLICATION NUMBER: US/09/971,791
/ PRIOR FILING DATE: 2001-10-04
/ PRIOR APPLICATION NUMBER: 09/644,450
/ PRIOR FILING DATE: 2000-08-23
/ PRIOR APPLICATION NUMBER: 09/237,543
/ PRIOR FILING DATE: 1999-01-26
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9
/ LENGTH: 313
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-971-791-9

Alignment Scores:

Pred. No.:	4,256-109	Length:	313
Score:	1636.00	Matches:	304
Percent Similarity:	99.04%	Conservative:	6
Best Local Similarity:	97.12%	Mismatches:	3
Query Match:	66.97%	Indels:	0
DB:	9	Gaps:	0

US-10-705-757-3 (1-1302) x US-09-971-791-9 (1-313)

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QY 4 ATGCTTTGTCCAAAGATCAACTCCCTGGCCACCTGGCGGACGCCCTTTCACAGACTG 63
DB 1 MetLeuLeuSerlyllleAensSerleuAlahleuAghAlalArProCySaenAhpLeu 20
QY 64 CACGCCAACAAGCTGGCGCGCGGCAAGAAGAGAGCCCTGGAGTGCAGTACAGGTTG 123
DB 21 HleAlAthrlYseuAlaProGlyLybGluLybGluProLeuGluSerGlnTyrglnVal 40
QY 124 GGGCCGCTGTGGGCGCGGTGGCTTCGGCTCGCTACCTCGGGCATTCGGCGTCCGAC 183
DB 41 GlyProLeuLeuLySerGlyLybneGlySerValTySerGlylleArgValSerAap 60
QY 184 AACTTCGCGGTGGCCATCAAGACAGTGAAGAGACCGGATTTCCGACTGGGGGAACTG 243
DB 61 AenLeuProValAlaIleYshIeValGluLybAhpArgIleSerAapTrpGlyGluLeu 80
QY 244 CCCAAGCGGACCCGAGTCCCATGAGAGTGTCTCTGCTGAAGAAGTGAAGCTCGGCTTC 303
DB 81 ProAenGlyThzArzValProMetGluValValLeuLeuLybValSerSerGlyPhe 100
QY 304 TCGGGGGTCAATTGACTTTCGACTGCTGGTTCGAGAGGCGGATGTTTCGTCGATCCG 363
DB 101 SerGlyValIleArgLeuLeuAapTrpPheGluArgProAapSerPheValLeuIleLeu 120
QY 364 GAGAGCGCCGAAACCCGTGCAAGACTCTTTCGACTTCATCACGAGCGAGAGCCCTTCAG 423
DB 121 GluArgProGluProValGlnAhpLeuPheAapPheIleThrcGluArgGlyAlaLeuGln 140
QY 424 GAGGAGCTGGCCCGGAGCTTCTTCTGGCAGGTGCTGAGGCGGTGGCGCATTCGCCAAC 483
DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgHisCybHisAan 160
QY 484 TGGGGGGTTCACACCGGACATCAAGAGAGAGAACTTATTCGACTGGAACCGCGGCG 543
DB 161 CybGlyValLeuHisArgAapIleYbAhpGluAenIleLeuIleAhpLeuAenArgGly 180
QY 544 GAACTCAAACTCATCGACTTCGGGTCGGGGCGCTGCTCAAGACACAGTTTACAGCGAC 603
DB 181 GluLeuLybLeuIleAhpPheGlySerGlyAlaLeuLeuLybAhpTrValTyTrhAap 200
QY 604 TTTGAGAGGAACCCGAGTGTACAGTCCCTCCAGAGTGTGCTACCATCGCTCCACGCGC 663
DB 201 PheAapGlyThzArzValTySerProGluTrpIleArgTyHisAagTyHisAgl 220
QY 664 AGGTCCGCTGCTGTTTGGTCCCTGGGGATCTGCTCATGACATGAGTTCGGAGATATT 723
DB 221 ArgSerAlaIaValIleTrpSerLeuGlyIleLeuLeuTyAhpPheValCybGlyAapIle 240
QY 724 CCAATTGAGCAGCAGAAAGATCGTCAAGGCGCAAGTGTACTTTAGCAGAAAGGCTCTCT 783
DB 241 ProPheGluHisAhpGluGluIleIleArgGlyGlnValAhpPheAapTrpGlnValSer 260
QY 784 TCGAAGTGTCAACATCTTATTAATGATGTGCTCTCCCTGAGACCATCGGACCGGCTCC 843
DB 261 SerGlyCybGlnHisLeuIleArgTrpCybAenAlaLeuAapTrpSerAapAapProTrh 280
QY 844 TTTGAAGAATAATCAAGAACATCGGTGAGATGACAGATGTTCTCGGCGCCGAGCGCGC 943
DB 281 PheGluGluIleGlnHisAhpTrpTrpMetGlnAhpAlaLeuLeuProGlnGluTrhAla 300
QY 904 GAGATTCATCTGACAGCTGTGACCATCAACCCAGCAAA 942

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DB 301 GluIleHisLeuHisSerLeuSerProGlyProSerLyS 313

RESULT 5

US-10-081-119-18

Sequence 18, Application US/10081119

Publication No. US20030045491A1

GENERAL INFORMATION:

APPLICANT: Reinhard, Christoph

APPLICANT: Jefferson, Anne B.

APPLICANT: Chan, Vivien W. Diagnosis and as a Therapeutic

TITLE OF INVENTION: Target in Cancer

FILE REFERENCE: 16932.002

CURRENT APPLICATION NUMBER: US/10/081,119

PRIOR FILING DATE: 2002-02-21

PRIOR APPLICATION NUMBER: 60/289,813

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 18

LENGTH: 313

TYPE: PRT

ORGANISM: Homo sapiens

US-10-081-119-18

Alignment Scores:

Pred. No.:	4,256-109	Length:	313
Score:	1636.00	Matches:	304
Percent Similarity:	99.04%	Conservative:	6
Best Local Similarity:	97.12%	Mismatches:	3
Query Match:	66.97%	Indels:	0
DB:	14	Gaps:	0

US-10-705-757-3 (1-1302) x US-10-081-119-18 (1-313)

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QY 4 ATGCTTTGTCCAAAGATCAACTCCCTGGCCACCTGGCGGACGCCCTTTCACAGACTG 63
DB 1 MetLeuLeuSerlyllleAensSerleuAlahleuAghAlalArProCySaenAhpLeu 20
QY 64 CACGCCAACAAGCTGGCGCGCGGCAAGAAGAGAGCCCTGGAGTGCAGTACAGGTTG 123
DB 21 HleAlAthrlYseuAlaProGlyLybGluLybGluProLeuGluSerGlnTyrglnVal 40
QY 124 GGGCCGCTGTGGGCGCGGTGGCTTCGGCTCGCTACCTCGGGCATTCGGCGTCCGAC 183
DB 41 GlyProLeuLeuGlySerGlyLybneGlySerValTySerGlylleArgValSerAap 60
QY 184 AACTTCGCGGTGGCCATCAAGACAGTGAAGAGACCGGATTTCCGACTGGGGGAACTG 243
DB 61 AenLeuProValAlaIleYshIeValGluLybAhpArgIleSerAapTrpGlyGluLeu 80
QY 244 CCCAAGCGGACCCGAGTCCCATGAGAGTGTCTCTGCTGAAGAAGTGAAGCTCGGCTTC 303
DB 81 ProAenGlyThzArzValProMetGluValValLeuLeuLybValSerSerGlyPhe 100
QY 304 TCGGGGGTCAATTGACTTTCGACTGCTGGTTCGAGAGGCGGATGTTTCGTCGATCCG 363
DB 101 SerGlyValIleArgLeuLeuAapTrpPheGluArgProAapSerPheValLeuIleLeu 120
QY 364 GAGAGCGCCGAAACCCGTGCAAGACTCTTTCGACTTCATCACGAGCGAGAGCCCTTCAG 423
DB 121 GluArgProGluProValGlnAhpLeuPheAapPheIleThrcGluArgGlyAlaLeuGln 140
QY 424 GAGGAGCTGGCCCGGAGCTTCTTCTGGCAGGTGCTGAGGCGGTGGCGCATTCGCCAAC 483
DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgHisCybHisAan 160
QY 484 TGGGGGGTTCACACCGGACATCAAGAGAGAGAACTTATTCGACTGGAACCGCGGCG 543
DB 161 CybGlyValLeuHisArgAapIleYbAhpGluAenIleLeuIleAhpLeuAenArgGly 180
QY 544 GAACTCAAACTCATCGACTTCGGGTCGGGGCGCTGCTCAAGACACAGTTTACAGCGAC 603

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Db 181 GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyrThrAsp 200
 QY 604 TTGACCGGAACCCGAGGTGTACAGTCTTCAGAGTGGATTGGTACCATCGCTACACGCG 663
 Db 201 PheAspGlyThrArgValTyrSerProGlyIleArgTyrHisArgTyrHisGly 220
 QY 664 AGGTCGCTGCTGTTGGTCCGTGGAGATCCTGCTCATGACATGAGTCTGCGGAGATATT 723
 Db 221 ArgSerIleAlaValIlePheSerLeuGlyIleLeuLeuLysAspMetValCysGlyAspIle 240
 QY 724 CCATTGAGCAGCAGAAAGATGTGACAGGCGCAAGTGTACTTTAGCAAGGCTTCT 783
 Db 241 ProPheGlyIleHisAspGlyGlyIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
 QY 784 TCGAAGTCAACATCTTATTAGTGGTCTGCTCCCTGAGACCATGTGACCGGCTCC 843
 Db 261 SerGlyCysGlnHisLeuIleAspGlyTyrCysLeuAlaLeuArgProSerAspArgProThr 280
 QY 844 TTGAAGAAATCCAGAACCATCCGTGGATGACAGATGTTCTCCGCGCCAGGCGACCGCC 903
 Db 281 PheGlyGlyIleGlnHisAspIleProTyrMetGlnAspValLeuLeuProGlnGlyThrAla 300
 QY 904 GAGATTCATCTGCACAGCTGTGCACATCAACCCAGCAA 942
 Db 301 GluIleHisLeuHisSerLeuSerProGlyProSerLys 313

RESULT 6

US-10-394-322A-52
 / Sequence 52, Application US/10394322A
 / Publication No. US20030232391A1
 / GENERAL INFORMATION:
 / APPLICANT: SUNEIS PHARMACEUTICALS, INC.
 / APPLICANT: Prescott, John C.
 / TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
 / FILE REFERENCE: 39750-0006 US
 / CURRENT APPLICATION NUMBER: US/10/394,322A
 / PRIOR FILING DATE: 2003-03-20
 / PRIOR APPLICATION NUMBER: US 60/366,892
 / NUMBER OF SEQ ID NOS: 70
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 52
 / LENGTH: 313
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-10-394-322A-52

Alignment Scores:

Pred. No.: 4,25e-109 Length: 313
 Score: 1636.00 Matches: 304
 Percent Similarity: 99.04% Conservative: 6
 Best Local Similarity: 97.12% Mismatches: 3
 Query Match: 66.97% Indels: 0
 DB: 15 Gaps: 0

US-10-705-757-3 (1-1302) x US-10-394-322A-52 (1-313)

QY 4 ATGCTCTTGTCAGAGATCAATCCCTGGCCACCTGGCGACGCCCTTGCAAGACTG 63
 Db 1 MetLeuLeuSerLysIleAsnSerLeuAlaHisLeuArgIleAlaIleProCysAsnAspLeu 20
 QY 64 CAGGCCAAACAGCTGGCGCGCGGCAAGAGAGAGAGCCCTGAGTGCAGTACCAAGT 123
 Db 21 HisAlaIleThrLysLeuAlaProGlyLysGlyLeuGlyLeuLeuGlySerGlyIleVal 40
 QY 124 GGCCTGCTGTTGGCAGAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 183
 Db 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValSerAsp 60
 QY 184 AACTTGGCGGTGGCCATCAAGCAGTGAAGAGAGACCGGATTTCCGATGGGGGAACTG 243
 Db 61 AsnLeuProValAlaIleLysHisValGlnLysAspArgIleSerAspTyrGlyGlyLeu 80

QY 244 CCGAACGGACCCGAGTGGCCCATGAGTGGTCTGCTGTAAGAAAGGAGCTGGGCTTC 303
 Db 81 ProAsnGlyThrArgValProMetGlyValValLeuLeuLysValSerSerGlyPhe 100
 QY 304 TCGGGGCTCATTTAGACTTTCGACTGTTTCGAGAGGCCGCGATAGTTCGTGATCTTG 363
 Db 101 SerGlyValIleArgLeuLeuAspTyrPheGlyIleArgProAspSerPheValLeuLeu 120
 QY 364 GAGAGGCCGACACCCGTGCAGACCTCTTCGACTTCATCAACGAGGAGAGCCCTTCAG 423
 Db 121 GluArgProGlyProValGlnAspLeuPheAspPheIleThrGlnArgGlyAlaLeuGln 140
 QY 424 GAGAGCTGGCCGAGGCTTCTTCTGAGCGTCTGAGGCGGTGGGCGCATTCGCAAC 483
 Db 141 GluGlnLeuAlaArgSerPhePheThrPheGlnValLeuGlnAlaValIleArgHisCysHisAsn 160
 QY 484 TCGGGGATTCCTCCACCGCAGCATCAAGAGAGAAATCTTAAATGACCTGAAACCGGCG 543
 Db 161 CysGlyValLeuHisAspArgPheLysAspGlyAsnIleLeuIleAspLeuAsnArgGly 180
 QY 544 GAACCTCAACTCATCGACTTCGGGTGGGGGCGCTCTCAGAGACACAGTCTTCACGGAC 603
 Db 181 GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyrThrAsp 200
 QY 604 TTGACGGAACCCGAGGTGTACAGTCTTCAGAGTGGATTGGTACCATCGCTACACGCG 663
 Db 201 PheAspGlyThrArgValTyrSerProGlyIleArgTyrHisArgTyrHisGly 220
 QY 664 AGGTCGCTGCTGTTGGTCCGTGGAGATCCTGCTCATGACATGAGTCTGCGGAGATATT 723
 Db 221 ArgSerIleAlaValIlePheSerLeuGlyIleLeuLeuLysAspMetValCysGlyAspIle 240
 QY 724 CCATTGAGCAGCAGAAAGATGTGACAGGCGCAAGTGTACTTTAGCAAGGCTTCT 783
 Db 241 ProPheGlyIleHisAspGlyGlyIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
 QY 784 TCGAAGTCAACATCTTATTAGTGGTCTGCTCCCTGAGACCATGTGACCGGCTCC 843
 Db 261 SerGlyCysGlnHisLeuIleAspGlyTyrCysLeuAlaLeuArgProSerAspArgProThr 280
 QY 844 TTGAAGAAATCCAGAACCATCCGTGGATGACAGATGTTCTCCGCGCCAGGCGACCGCC 903
 Db 281 PheGlyGlyIleGlnHisAspIleProTyrMetGlnAspValLeuLeuProGlnGlyThrAla 300
 QY 904 GAGATTCATCTGCACAGCTGTGCACATCAACCCAGCAA 942
 Db 301 GluIleHisLeuHisSerLeuSerProGlyProSerLys 313

RESULT 7

US-10-348-081-13
 / Sequence 13, Application US/10348081
 / Publication No. US20040038246A1
 / GENERAL INFORMATION:
 / APPLICANT: KOEN, Marcus
 / APPLICANT: MOELLER, Guenter
 / APPLICANT: SCHNEIDER, Rudolf
 / APPLICANT: TSCHANZ, Georg
 / TITLE OF INVENTION: P1M-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
 / FILE REFERENCE: DE4V2002/0004 US NP
 / CURRENT APPLICATION NUMBER: US/10/348,081
 / PRIOR FILING DATE: 2003-01-21
 / NUMBER OF SEQ ID NOS: 14
 / SOFTWARE: PatentIn version 3.2
 / SEQ ID NO 13
 / LENGTH: 313
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-10-348-081-13

Alignment Scores:
 Pred. No.: 4,25e-109 Length: 313
 Score: 1636.00 Matches: 304
 Percent Similarity: 99.04% Conservative: 6

Best Local Similarity: 97.12% Mismatches: 3
 Query Match: 66.97% Indels: 0
 DB: 15 Gaps: 0

US-10-705-757-3 (1-1302) x US-10-348-081-13 (1-313)

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QY 4 ATGCTCTTTCAGATCAACTCCCTGGCCCACTGCGCGCAGCCCTTTCAGACGACTG 63
DB 1 MetLeuLeuSerIylLeuAsnSerLeuAlaHisLeuArgHisAlaProCysAsnAspLeu 20
QY 64 CACGCCAACAAGCTGCGCGCGGCAAGAGAGAGACCCCTGAGTTCGACATTCAGGTG 123
DB 21 HisAlaThrIleLeuAlaProGlyIleGluLeuGluProLeuIndSerGlnIleVal 40
QY 124 GGGCCGCTGTGGGCGCGGTGCTTCCGCTCGCTTACTCCGGGACATCCGCGCGCGAC 183
DB 41 GlyProLeuLeuIndSerGlyIlePheGlySerValIleSerGlyIleArgValSerAsp 60
QY 184 AACTTCCGGTGGCCATCAAGACGTCGAGAGAGACCGGATTTCCGACTGGGGAGACTG 243
DB 61 AsnLeuProValAlaIleIleYshIleValGluLeuAspArgIleSerAspTrpGlyIleLeu 80
QY 244 CCCAAGCGGACCCGAGTGCCTATGAAAGTGTCTCTGTAAGAGGTGAGCTCGGCTTC 303
DB 81 ProAsnGlyThrArgValIleProMetGluValIleLeuLeuIleYshValSerSerGlyPhe 100
QY 304 TCGGGCGCTATTAAGTCTTTCGAGCTGTTCCAGAGCCCGATAGTTTGGTCTGATTCG 363
DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleLeuIleu 120
QY 364 GAGAGCCCGAAGCCGTCGAGACCTCTTCACTTCAATCAACGAGCGAGAGCCCTCGAC 423
DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgIleAlaLeuGln 140
QY 424 GAGAGCTGCGCGGAGCTTCTTCTGCGAGTGTCTGAGGCGCTGCGGACATTCGCAAC 483
DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValIleGluAlaValAlaArgHisCysHisAsn 160
QY 484 TGGGGGGTCTCCACCGCGCATCAAGAGAGAGACATCTTATCGACCTGAACCGCGGCG 543
DB 161 CysGlyValLeuHisArgAspIleIleYshAspGluAsnIleLeuIleAspLeuAsnArgGly 180
QY 544 GAACCTAACTCATCGACTTCGAGGTCGAGGCGCTGTCGAGAGACAGTCTTACAGCGAC 603
DB 181 GluLeuLeuLeuIleAspPheGlyIleArgGlyAlaLeuLeuIleYshAspThrValIleThrAsp 200
QY 604 TTTGAGCGAAGCCGAGTGTACAGTCTCCAGAGTGTGCTTACATCGCTACCAACGCG 663
DB 201 PheAspGlyThrArgValIleArgProProGluTrpIleArgIleArgIleArgIleArgIle 220
QY 664 AGGTGGGCTGTGTTGGTCCCTGGGGATCTGCTCATGACATGGTTCGCGGAGATTT 723
DB 221 ArgSerAlaIleValIleTrpSerLeuGlyIleLeuLeuIleYshAspValIleCysGlyAspIle 240
QY 724 CCATTTGAGCAGCAGAGAGATCTGTCAGAGGCGCAAGTGTACTTTAGCGAAGGCTCTG 783
DB 241 ProPheGluHisAspGluGluIleIleArgGlyGlnValIlePheAspArgGlnValSer 260
QY 784 TCGAATGTCAACATCTTATTAAGTGTGCTGCTCCCTGAGACCATCGACCGGCTTC 843
DB 261 SerGluCysGlnHisLeuIleArgIleArgIleArgIleArgIleArgIleArgIleArgIle 280
QY 844 TTTGAGGAATTCAGAGACATCGGTGAGTGCAGAGATTTCTCGTGGCCCGAGCGCACGCG 903
DB 281 PheGluGluIleGlnAsnHisProTrpMetGlnAspAlaIleLeuLeuProGlnGluIleAla 300
QY 904 GAGATTCATTCGACAGCTGTGACATCAACCCAGCAAA 942
DB 301 GluIleHisLeuHisSerLeuSerProGlyProSerIle 313

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Publication No. US2004014286A1
 GENERAL INFORMATION:
 APPLICANT: BREMER, RYAN
 APPLICANT: IBRAHIM, PRABHA
 APPLICANT: KUMAR, ABHINAV
 APPLICANT: MANDIVAN, VALSAN
 APPLICANT: MILEURN, MICHAEL V.
 TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
 FILE REFERENCE: 039363/0703
 CURRENT APPLICATION NUMBER: US/10/664,421
 CURRENT FILING DATE: 2003-09-16
 PRIOR APPLICATION NUMBER: 60/412,341
 PRIOR FILING DATE: 2002-09-20
 PRIOR APPLICATION NUMBER: 60/411,398
 PRIOR FILING DATE: 2002-09-16
 NUMBER OF SEQ ID NOS: 169
 SOFTWARE: Patentin Ver. 3.2
 SEQ ID NO 1
 LENGTH: 313
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-664-421-1

Alignment Scores:
 Pred. No.: 4,256-109 Length: 313
 Score: 1636.00 Matches: 304
 Percent Similarity: 99.04% Conservative: 6
 Best Local Similarity: 97.12% Mismatches: 3
 Query Match: 66.97% Indels: 0
 DB: 16 Gaps: 0

US-10-705-757-3 (1-1302) x US-10-664-421-1 (1-313)

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QY 4 ATGCTCTTTCAGATCAACTCCCTGGCCCACTGCGCGCAGCCCTTTCAGACGACTG 63
DB 1 MetLeuLeuSerIylLeuAsnSerLeuAlaHisLeuArgHisAlaProCysAsnAspLeu 20
QY 64 CACGCCAACAAGCTGCGCGCGGCAAGAGAGAGACCCCTGAGTTCGACATTCAGGTG 123
DB 21 HisAlaThrIleLeuAlaProGlyIleGluLeuGluProLeuIndSerGlnIleVal 40
QY 124 GGGCCGCTGTGGGCGCGGTGCTTCCGCTCGCTTACTCCGGGACATCCGCTCGCGAC 183
DB 41 GlyProLeuLeuIndSerGlyIlePheGlySerValIleSerGlyIleArgValSerAsp 60
QY 184 AACTTCCGGTGGCCATCAAGACGTCGAGAGAGACCGGATTTCCGACTGGGGAGACTG 243
DB 61 AsnLeuProValAlaIleIleYshIleValGluLeuAspArgIleSerAspTrpGlyIleLeu 80
QY 244 CCCAAGCGGACCCGAGTGCCTATGAAAGTGTCTCTGTAAGAGGTGAGCTCGGCTTC 303
DB 81 ProAsnGlyThrArgValIleProMetGluValIleLeuLeuIleYshValSerSerGlyPhe 100
QY 304 TCGGGCGCTATTAAGTCTTTCGAGCTGTTCCAGAGCCCGATAGTTTGGTCTGATTCG 363
DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleLeuIleu 120
QY 364 GAGAGCCCGAAGCCGTCGAGACCTCTTCACTTCAATCAACGAGCGAGAGCCCTCGAC 423
DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgIleAlaLeuGln 140
QY 424 GAGAGCTGCGCGGAGCTTCTTCTGCGAGTGTCTGAGGCGCTGCGGACATTCGCAAC 483
DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValIleGluAlaValAlaArgHisCysHisAsn 160
QY 484 TGGGGGGTCTCCACCGCGCATCAAGAGAGACATCTTATTAAGCCTGAACCGCGGCG 543
DB 161 CysGlyValLeuHisArgAspIleIleYshAspGluAsnIleLeuIleAspLeuAsnArgGly 180
QY 544 GAACCTAACTCATGACTTTCGAGGTCGAGGCGCTGTCGAGAGACAGTCTTACAGCGAC 603
DB 181 GluLeuLeuLeuIleAspPheGlyIleArgGlyAlaLeuLeuIleYshAspThrValIleThrAsp 200

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RESULT 8
 US-10-664-421-1
 ; Sequence 1, Application US/10664421


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; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-377-268-9

Alignment Scores:
Pred. No.: 4,25e-109 Length: 313
Score: 1636.00 Matches: 304
Percent Similarity: 99.04% Conservative: 6
Best Local Similarity: 97.12% Mismatches: 3
Query Match: 66.97% Indels: 0
DB: 16 Gaps: 0

US-10-705-757-3 (1-1302) x US-10-377-268-9 (1-313)

QY 4 ATGCTCTTTCAGATCAATCCCTGCGCCACCTGCGCGACCCCTTGCAACGACTTG 63
DB 1 MetLeuLeuSerLysIleAenSerLeuLAlAIsLeuAArgAlAAlProCySaAnaPLeu 20
QY 64 CACGCCAACAAGCTGGCGCGCGCAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
DB 21 HIsAlAThrLysLeuAlAProGlyLysGluLysGluProLeuGluSerGlnTyrGlnVal 40
QY 124 GGCCCGCTGTGGCGAGCGGTGCTTCCGCTCTTACTCGGCGCATCCGCGTCCGCGAC 183
DB 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValSerAap 60
QY 184 AACTTCGCGGTGGCCATCAAGCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
DB 61 AenLeuProValAlAlIleLysHIsValGluLysAaPArgIleSerAaPTrpGlyGluLeu 80
QY 244 CCCAAGCGGACCGAGTGGCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 303
DB 81 ProAenGlyThrArgValAProMetGluValValLeuLeuLysValSerSerGlyPhe 100
QY 304 TCGGCGCTATTGACTTGTGAGCTGGTGAAGAGCGCGAGATTCGTCGTGATCTTG 363
DB 101 SerGlyValIleArgLeuLeuAaPTrpPheGlyLysArgProAaPSerPheValIleLeu 120
QY 364 GAGAGCGCGGACCCGTCGCAAGACCTTTCGACTTCACTCAACGAGAGAGAGAGAGAG 423
DB 121 GluArgProGluProValGlnAaPLeuPheAaPPhelIeThrGluArgGlyAlaLeuGln 140
QY 424 GAGAGGTGGCGCGAGACTTCTTGTGAGAGTGTGAGAGCGCGCGCGCATTCGCAAC 483
DB 141 GluGluLeuAlAArgSerPhePheTrpGlnValLeuGlnAlaValArgHIsCySHIsAaen 160
QY 484 TGGCGGCTTTCGACCGGCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 543
DB 161 CyGglYValLeuHIsArgAaPTrpIleLysAaPArgIleAaenIleAaPLeuAaenArgGly 180
QY 544 GAATCAAACTCAATCGACTTCGAGTGGCGCGCGCTGTAAGAGAGAGAGAGAGAGAGAG 603
DB 181 GluLeuLysLeuLysIleAaPPhelGlyAlaLeuLeuLysAaPTrpValTyrTrpAaP 200
QY 604 TTGAGACGGAACCGAGTGTACAGTCTCCAGAGTGTGATTCGTAACCATCGCTCCAG 663
DB 201 PheAaPTrpGlyThrArgValTyrSerProProGluTrpIleArgTyrHIsAaGlyTrpHIsGly 220
QY 664 AGGTGGCTGCTGTTGGTCCCTGAGGAGCTTCGCTATGACATGCTTCGAGAGATAT 723
DB 221 ArgSerAlaAlaValTyrPheSerLeuGlyIleLeuLeuLysAaPTrpValCySHIsAaPTrp 240
QY 724 CCATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 783
DB 241 ProPheGluLysHIsArgGluGlnIleLeaArgGlyGlnValAaPheAaPArgGlnArgValSer 260
QY 784 TCAGATGTCAACATCTTATTAGTGTGCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAG 843
DB 261 SerGluCySHIsHIsLeuLysIleArgTyrCySHIsLeuAlAaenArgProSerAaPArgProThr 280
QY 844 TTGAGAGAAATCCAGAACATCCGTGAGTCAAGAGATTTCTCTGCGCCAGGCGACCGGC 903
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DB 281 PheGluGluIleGlnAaHIsAProTrpMetGlnAaPValLeuLeuProGlnGluThrAla 300
QY 904 GAGATTTCATTCGACAGCGCTGTCACCATCACCAGCAAA 942
DB 301 GluIleHIsLeuHIsSerLeuSerProGlyProSerLys 313

RESULT 11
US-10-951-389-18
; Sequence 18, Application US/10951389
; Publication No. US20050058627A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,389
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-951-389-18
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Alignment Scores:

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Pred. No.: 4,25e-109 Length: 313
Score: 1636.00 Matches: 304
Percent Similarity: 99.04% Conservative: 6
Best Local Similarity: 97.12% Mismatches: 3
Query Match: 66.97% Indels: 0
DB: 17 Gaps: 0
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US-10-705-757-3 (1-1302) x US-10-951-389-18 (1-313)

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DB 1 MetLeuLeuSerLysIleAenSerLeuLAlAIsLeuAArgAlAAlProCySaAnaPLeu 20
QY 64 CACGCCAACAAGCTGGCGCGCGCAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
DB 21 HIsAlAThrLysLeuAlAProGlyLysGluLysGluProLeuGluSerGlnTyrGlnVal 40
QY 124 GGCCCGCTGTGGCGAGCGGTGCTTCCGCTCTTACTCGGCGCATCCGCGTCCGCGAC 183
DB 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValSerAap 60
QY 184 AACTTCGCGGTGGCCATCAAGCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
DB 61 AenLeuProValAlAlIleLysHIsValGluLysAaPArgIleSerAaPTrpGlyGluLeu 80
QY 244 CCCAAGCGGACCGAGTGGCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 303
DB 81 ProAenGlyThrArgValAProMetGluValValLeuLeuLysValSerSerGlyPhe 100
QY 304 TCGGCGCTATTGACTTGTGAGCTGGTGAAGAGCGCGAGATTCGTCGTGATCTTG 363
DB 101 SerGlyValIleArgLeuLeuAaPTrpPheGlyLysArgProAaPSerPheValIleLeu 120
QY 364 GAGAGCGCGGACCGGTCGCAAGACCTTTCGACTTCACTCAACGAGAGAGAGAGAGAG 423
DB 121 GluArgProGluProValGlnAaPLeuPheAaPPhelIeThrGluArgGlyAlaLeuGln 140
QY 424 GAGAGCTGGCGCGAGACTTCTTGTGAGAGTGTGAGAGCGCGTGGAGATTCGCAAC 483
DB 141 GluGluLeuAlAArgSerPhePheTrpGlnValLeuGlnAlaValArgHIsCySHIsAaen 160
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Db      21 HislaLthrlyLeuAlaProGlyLyVgIuLeuLeuProLeuGlnSerGlnTyrgInVal 40
Qy      124 GGGCCGCTGTTGGGCAAGCGGTGGCTTCGGCTCTACTTCGGGCAATCCGCGTCCGAC 183
Db      41 GlyProLeuLeuGlnSerGlyGlyPheGlySerValTySerGlyIleArgValSerAsp 60
Qy      184 AACTGGCGGTGGGCAATCAAGACAGTGAAGAGGACGGGATTTCCGATGGGGGAACTG 243
Db      61 AsnLeuProValAlaIleLyShIsvaGlnLyAspArgIleSerAspTrpGlyGlnLeu 80
Qy      244 CCCAAGCGGCAAGCGGAGTGCCTCAAGAGTGGTCTCGCTGCAAGAGTGAAGTGAAGTTC 303
Db      81 ProAsnGlyThrArgValProMetGlnValValLeuLeuLySerValSerSerGlyPhe 100
Qy      304 TCGGGCGCTCAATTAAGCTTCTTGAGCTGGTTCGAGAGCGCCGATAGTTTCGTGATCTTG 363
Db      101 SerGlyValIleArgLeuLeuAspTrpPheGlnArgProAspSerPheValLeuIleLeu 120
Qy      364 GAGAGCGCGGACCCGCGCAAGACCTTCCTGCACTTCATCCAGCGAGGAGGACGCTTCAG 423
Db      121 GlnArgProGlnProValGlnAspLeuPheAspPheIleThrGlnArgGlyAlaLeuGln 140
Qy      424 GAGAGCTGGCGCGGAGCTTCTTCGCAAGTGTGAGGCGCGTCCGCAATTCGCAAC 483
Db      141 GlnGlnLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgIleScyShIAsn 160
Qy      484 TCGGGGCTTCCACCGGCAATCAAGACAGAGAACATCTTAATCGACTGAACCGCGGC 543
Db      161 CyGlyValLeuAlaArgAspIleLyAspGlnAsnIleLeuIleAspLeuAsnArgGly 180
Qy      544 GAATCTCAAACTCATCGACTTCGGGTCCGGGGCGCTGCTCAAGACACAGTCTACAGGAC 603
Db      181 GlnLeuLySerLeuIleAspPheGlySerGlyAlaLeuLeuLyAspThrValTyTrnAsp 200
Qy      604 TTGACGGAACCCGAGTGTACAGTCTCCAGAGTGAATTCGATACCATCGCTACAGCGC 663
Db      201 PheAspGlyThrArgValTyTrSerProProGlnTrpIleArgTyTrnIleArgTyTrnIle 220
Qy      664 AGGTGGCTGCTGTTGGTCCCTGGGGATCTGCTGTATGACATGGTCTGCGGAGATATT 723
Db      221 ArgSerAlaIleValTrpSerLeuGlyIleLeuLeuTyAspMetValCyGlyAspIle 240
Qy      724 CCAATTGAGACAGACGAGAGATCGTCAAGGCGCAAGTGAATCTTAAGGCAAAAGGCTCTC 783
Db      241 ProPheGlnIleAspGlnGlnIleIleArgGlyGlnAlaPhePheArgGlnArgValSer 260
Qy      784 TCAGAAATGTCAAATCTTATTAGATGGTGCCTGCTGAGACCATCGACCGGCGCTCC 843
Db      261 SerGlnCyGlnIleIleuIleArgTrpCyLeuAlaLeuArgProSerAspArgProThr 280
Qy      844 TTGAGAAATTCAGAACATCCGCTGAGATCCAGAGATGTTCTCTGCCCGGCGACCGCC 903
Db      281 PheGlnGlnIleGlnIleAsnIleAspTrpMetGlnAspValLeuLeuProGlnIleTrnAla 300
Qy      904 GAATTCATCTGCACAGCTCTGATCCATCAACCCGCAAGCAA 942
Db      301 GlnIleIleIleuIleSerLeuSerProGlyProSerIle 313

RESULT 15
US-10-705-757-2
/ Sequence 2, Application US/10705757
/ Publication No. US20040146942A1
/ GENERAL INFORMATION:
/ APPLICANT: GRUNENTHAL GMBH
/ TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE OR PIM3-KINASE
/ FILE REFERENCE: 029310.52818US
/ CURRENT APPLICATION NUMBER: US/10/705,757
/ PRIOR FILING DATE: 2003-11-12
/ PRIOR APPLICATION NUMBER: PCT/EP02/05234
/ PRIOR FILING DATE: 2002-05-13
/ PRIOR APPLICATION NUMBER: DE 101 23 055.9
/ PRIOR FILING DATE: 2001-05-11

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/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 313
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-705-757-2

Alignment Scores:
Pred. No.: 4.25e-109 Length: 313
Score: 1636.00 Matches: 304
Percent Similarity: 99.04% Conservative: 6
Best Local Similarity: 97.12% Mismatches: 3
Query Match: 66.97% Indels: 0
DB: 18 Gaps: 0

US-10-705-757-3 (1-1302) x US-10-705-757-2 (1-313)

Qy      4 ATGCTCTGTCGAAGATCAACTCCCTGGCCACCTGGCGGACGCGCTTGGCAAGACCTG 63
Db      1 MetLeuLeuSerTySIIeAsnSerLeuAlaHisLeuArgAlaIleProCyAsnAspLeu 20
Qy      64 CAGCCCAACAGCTGGCGCGCGGCAAGAGAGACCCCTGAGTTCGAGTACCAAGT 123
Db      21 HislaLthrlyLeuAlaProGlyLyVgIuLeuLeuProLeuGlnSerGlnTyrgInVal 40
Qy      124 GGGCCGCTGTTGGGCAAGCGGTGGCTTCGGCTCTACTTCGGGCAATCCGCGTCCGAC 183
Db      41 GlyProLeuLeuGlnSerGlyGlyPheGlySerValTySerGlyIleArgValSerAsp 60
Qy      184 AACTGGCGGTGGGCAATCAAGACAGTGAAGAGGACGGGATTTCCGATGGGGGAACTG 243
Db      61 AsnLeuProValAlaIleLyShIsvaGlnLyAspArgIleSerAspTrpGlyGlnLeu 80
Qy      244 CCCAAGCGGCAAGCGGAGTGCCTCAAGAGTGGTCTCGCTGCAAGAGTGAAGTGAAGTTC 303
Db      81 ProAsnGlyThrArgValProMetGlnValValLeuLeuLySerValSerSerGlyPhe 100
Qy      304 TCGGGCGCTCAATTAAGCTTCTTGAGCTGGTTCGAGAGCGCCGATAGTTTCGTGATCTTG 363
Db      101 SerGlyValIleArgLeuLeuAspTrpPheGlnArgProAspSerPheValLeuIleLeu 120
Qy      364 GAGAGCGCGGACCCGCGCAAGACCTTCCTGCACTTCATCCAGCGAGGAGGACGCTTCAG 423
Db      121 GlnArgProGlnProValGlnAspLeuPheAspPheIleThrGlnArgGlyAlaLeuGln 140
Qy      424 GAGAGCTGGCGCGGAGCTTCTTCGCAAGTGTGAGGCGCGTCCGCAATTCGCAAC 483
Db      141 GlnGlnLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgIleScyShIAsn 160
Qy      484 TCGGGGCTTCCACCGGCAATCAAGACAGAGAACATCTTAATCGACTGAACCGCGGC 543
Db      161 CyGlyValLeuAlaArgAspIleLyAspGlnAsnIleLeuIleAspLeuAsnArgGly 180
Qy      544 GAATCTCAAACTCATCGACTTCGGGTCCGGGGCGCTGCTCAAGACACAGTCTACAGGAC 603
Db      181 GlnLeuLySerLeuIleAspPheGlySerGlyAlaLeuLeuLyAspThrValTyTrnAsp 200
Qy      604 TTGACGGAACCCGAGTGTACAGTCTCCAGAGTGAATTCGATACCATCGCTGAGCGGC 663
Db      201 PheAspGlyThrArgValTyTrSerProProGlnTrpIleArgTyTrnIleArgTyTrnIle 220
Qy      664 AGGTGGCTGCTGTTGGTCCCTGGGGATCTGCTGTATGACATGGTCTGCGGAGATATT 723
Db      221 ArgSerAlaIleValTrpSerLeuGlyIleLeuLeuTyAspMetValCyGlyAspIle 240
Qy      724 CCAATTGAGACAGACGAGATCGTCAAGGCGCAAGTGAATCTTAAGGCAAAAGGCTCTC 783
Db      241 ProPheGlnIleAspGlnGlnIleIleArgGlyGlnAlaPhePheArgGlnArgValSer 260
Qy      784 TCAGAAATGTCAAATCTTATTAGATGGTGCCTGCTGAGACCATCGACCGGCGCTCC 843
Db      261 SerGlnCyGlnIleIleuIleArgTrpCyLeuAlaLeuArgProSerAspArgProThr 280

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Qy	844	TTTGAAGAAATCCAGAACCATCCGTGGATGAGATGTTCTCCTGCCCAAGGCAACGGCC	903
Db	281	PheGluGluIleGlnMetHisProTyrMetGlnAspValIleuLeuProGlnGlnIleuAla	300
Qy	904	GAGATTCACTGCACAGCCTGTGCACCATCACCCAGCAAA	942
Db	301	GluIleHisLeuHisSerLeuSerProGlyProSerTys	313

Search completed: September 22, 2005, 17:46:43
Job time : 184.828 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 22, 2005, 15:59:25 ; Search time 214.949 Seconds
(without alignment)
6203.583 Million cell updates/sec

Title: US-10-705-757-3

Sequence: 1 999atgctctctgtcccaagat.....ggatataaacacagcaccat 1302

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Command line parameters:
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-O=/cgn2.1/USPTO.spool.p/US10705757/runat.22092005.115015.22129/app.query.fasta_1.5333
-DB=uniprot -OPMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -DOPELT=0 -DOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=dlodum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pc -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORNA-ext -HEAPSIZE=500 -MINLEN=200000000
-USER=US10705757@cgn2.1.1.980@runat.22092005.115015.22129 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEJOINT -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Uniprot 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1668	68.3	313	1	P1M1_RAT
2	1638	67.0	313	1	P1M1_FELCA
3	1636	67.0	313	1	P1M1_HUMAN
4	1630	66.7	313	1	P1M1_BOVIN
5	1589	65.0	313	2	O8CFN8
6	1584	64.8	313	1	P1M1_MOUSE
7	1140	46.7	323	1	P1M3_COTVA
8	1136.5	46.4	326	1	P1M3_HUMAN
9	1132.5	46.5	326	1	P1M3_MOUSE
10	1131.5	46.3	326	1	P1M3_RAT
11	1119	45.8	325	2	O611X8
12	1110.5	45.5	318	2	O611I1
13	1104	45.2	323	1	P1M3_XENLA
14	878	35.9	370	1	O6R2B0
15	878	35.9	370	1	P1M2_MOUSE
16	866.5	35.5	311	1	P1M2_HUMAN

17	861	35.2	310	2	O7ZVU5	O7ZVJ5 brachydanio
18	858	35.1	310	2	O8JFW9	O8JFW9 brachydanio
19	853	34.9	310	1	P1M1_BPARB	O9YJN5 brachydanio
20	851	34.8	310	2	O6DI52	O6DI52 brachydanio
21	716.5	29.3	221	2	O8R1Z0	O8R1Z0 mus musculus
22	626	25.6	441	2	O20443	O20443 caenorhabdit
23	485	20.3	378	2	O8T3F1	O8T3F1 caenorhabdit
24	455	20.3	566	2	O17737	O17737 caenorhabdit
25	421	17.2	134	2	O6P2J9	O6P2J9 homo sapien
26	406	16.6	1283	1	P3AK_MOUSE	O8CEE6 mus musculus
27	403	16.5	125	2	O6Q2K5	O6Q2K5 canis famli
28	396	16.2	658	2	O64IK5	O64IK5 mus musculus
29	394	16.1	794	1	K111_HUMAN	O8CDK3 homo sapien
30	387.5	15.9	514	2	O9XFZ5	O9XFZ5 glycine max
31	385	15.8	688	2	O95UP4	O95UP4 ancylostroma
32	385	15.8	776	2	O699J6	O699J6 mus musculus
33	384	15.7	1107	2	O6C310	O6C310 yarowia li
34	381.5	15.6	504	2	P93113	P93113 cucumis sat
35	381.5	15.6	661	1	ARK5_HUMAN	O60285 mus sapien
36	381	15.6	499	2	O8C0V7	m mus muscu
37	380	15.6	535	1	K110_ARATH	O38997 arabidopsis
38	380	15.6	1398	2	O77268	O77268 drosophila
39	380	15.6	1398	2	O9W532	O9W532 drosophila
40	379.5	15.5	432	2	O70XR8	O70XR8 giardia lam
41	379	15.5	1306	2	O6FUT1	O6FUT1 candida gla
42	379	15.5	1336	2	O6FRS7	O6FRS7 candida gla
43	378.5	15.5	698	2	O61298	O61298 halocynthia
44	377.5	15.5	1229	2	O6CKM4	O6CKM4 kluyveromyc
45	374.5	15.3	643	2	O7R0B9	O7R0B9 giardia lam

ALIGNMENTS

RESULT 1
ID P1M1_RAT STANDARD; PRT; 313 AA.
AC P26754;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DB Prote-oncogene serine/threonine-protein kinase Pim-1 (BC 2.7.1.37).
GN Name=Pim1; Synonyms=Pim-1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Testis;
RX MEDLINE=92319652; PubMed=1620615;
RA Wingest D., Reeves R., Magnuson N.S.;
RT "Characterization of the testes-specific pim-1 transcript in rat.";
RL Nucleic Acids Res. 20:3183-3189(1992).
CC 1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC 1- SUBUNIT: Binds to R9 (By similarity).
CC 1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC 1- PTM: Autophosphorylated (By similarity).
CC 1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM subfamily.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage is for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch>).
CC EMBL; X63675; CAA45214.1; -
CC PIR; S26298; S26298.
CC RGD; 3330; Pim1.
CC InterPro; IPR011009; Kinase_like.
CC InterPro; IPR00719; Prot_Kinase.

DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR Pfam: PF00069; Kinase; 1.
 DR ProDom: PD000001; Prot kinase; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Nuclear protein; Phosphorylation; Proto-oncogene;
 KM Serine/threonine-protein kinase; Transferase.
 FT DOMAIN 38 290
 FT NP BIND 44 52
 FT BINDING 67 67
 FT ACT_SITE 167 167
 FT ACT_SITE 167 167
 SQ SEQUENCE 313 AA; 35630 MW; D5757DA9F1821BP9 CRC64;

Alignment Scores:

Pred. No.: 1.63e-99 Length: 313
 Score: 1668.00 Matches: 313
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 68.28% Indels: 0
 DB: 1 Gaps: 0

US-10-705-757-3 (1-1302) x PIM1_RAT (1-313)

QY 4 ATGCTCTGTTCAGATCACTCCCTGCGCCACCTGCGCGACCCCTTTCAGACGACTTG 63
 DB 1 MetLeuLeuSerLysIleAsnSerLeuAlaIleuAlaArgAlaIleuAlaProCysAsnAspLeu 20
 QY 64 CAGGCCCAACAGCTGGCGCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
 DB 21 HisAlaAsnLysLeuAlaProGlyLysGluLysGluProLeuLeuSerGlnLysVal 40
 QY 124 GGGCCCTGTGGGAGAGCGGCTGCTCGGCTCGGCTCTACTCGGGAGATCCGCTGCGCGAC 183
 DB 41 GlyProLeuLeuLysSerGlyGlyPheGlySerValLysSerGlyLysValAlaAsp 60
 QY 184 AACTTGGCGGCTCCATCAAGACGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
 DB 61 AsnLeuProValAlaIleLysValIleGluLysAspArgLysSerAspTrpGlyLeu 80
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 DB 81 ProAsnGlyThrArgValProMetGluValValLeuLeuLysValSerSerGlyPhe 100
 QY 304 TCGGCGCTCATTAAGACTTCTGAGACTGTTGAGAGAGCGGAGTGGTTCGTCGATCTTG 363
 DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleLeu 120
 QY 364 GAGAGCGCCGAGACCCGCTGCAAGACTTCTGACTTATCATCCGAGGAGAGCGCTTCAG 423
 DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
 QY 424 GAGAGACTGGCCCGGAGCTTCTTCTGCGAGGCTGAGAGCGGCTGCGGAGCTTCCCAAC 483
 DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgHisCysHisAsn 160
 QY 484 TCGGCGGCTTCTCAACCGCGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 543
 DB 161 CysGlyValLeuHisArgAspIleLysAspGluAsnIleLeuIleAspLeuAsnArgGly 180
 QY 544 GAACTCAAACTCATCGACTTTCGGGTCGCGGCGCTGCTCAAGAGAGAGAGAGAGAGAGAG 603
 DB 181 GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValLysThrAsp 200
 QY 604 TTTGAGGAGAACCGAGTTCAGTCTCCAGAGTGGATTGCTTACATGGCTTACAGCGGCG 663
 DB 201 PheAspGlyThrArgValLysSerProProGluTrpIleArgLysHisArgLysGly 220
 QY 664 AGGTGCGCTGCTGTTGGTCCCTGCGGAGATCTGCTGATGAGATGGTTCGCGAGATATT 723
 DB 221 ArgSerAlaAlaValIlePheSerLeuGlyLysLeuLeuLysAspMetValCysGlyAspIle 240
 QY 724 CCATTGAGACGACGAGAGAGATGTCAGAGGCGCAAGTGTACTTTAGCGAAAGGCTCTCT 783

DB 241 PropheGluHisAspGluGluIleValLysGlyGlnValLysPheArgGlnArgValSer 260
 QY 784 TCGAATGCGACATCTTATTGATGTCGCTGCTCCGAGACATCGACCGGCGCTCC 843
 DB 261 SerGluCysGlnHisLeuLeuIleArgTrpCysLeuSerLeuArgProSerAspArgProSer 280
 QY 844 TTTGAGAAATCCAGAACCATCCGTGATGACAGATGTTCTCTGCGCGGAGCGCACCGCC 903
 DB 281 PheGluGluIleGlnHisAsnHisProTrpMetGlnAspValLeuLeuProGlnAlaThrAla 300
 QY 904 GAGATTCATTCGACAGCTGTACCATTCACCCAGCAAA 942
 DB 301 GluIleHisLeuHisSerLeuSerProSerProSerLys 313

RESULT 2

PIM1_FELCA STANDARD; PRT; 313 AA.
 ID PIM1_FELCA
 AC Q95LJ0;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
 GN Name=PIM1;
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_Taxid=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fujino Y., Saech H., Hiasue M., Masuda K., Ohno K., Tsujimoto H.,
 RT "The cDNA sequence of the feline pim-1 oncogene."
 RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
 CC -1 CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1 SUBUNIT: Binds to Rps (By similarity).
 CC -1 SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
 CC -1 PTM: Autophosphorylated (By similarity).
 CC -1 SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM subfamily.

CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----

CC EMBL: AB073748; BAB71752.1; -
 CC InterPro: IPR011009; Kinase like.
 CC InterPro: IPR000719; Prot kinase.
 CC InterPro: IPR008271; Ser_thr_pkin_AS.
 DR Pfam: PF00069; Kinase; 1.
 DR ProDom: PD000001; Prot kinase; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Nuclear protein; Phosphorylation; Proto-oncogene;
 KM Serine/threonine-protein kinase; Transferase.
 FT DOMAIN 38 290
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 FT BINDING 67 67
 FT ACT_SITE 167 167
 FT ACT_SITE 167 167
 SQ SEQUENCE 313 AA; 35685 MW; CDBE268D638E967 CRC64;

Alignment Scores:

Pred. No.: 1.41e-97 Length: 313
 Score: 1638.00 Matches: 305
 Percent Similarity: 98.72% Conservative: 4
 Best Local Similarity: 97.44% Mismatches: 4
 Query Match: 67.05% Indels: 0
 DB: 1 Gaps: 0

US-10-705-757-3 (1-1302) x PIM1_FELCA (1-313)

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OY 4 ATGCTCTTTCGAAGATCAACTCCCTGGCCCACTGGCGGAGCCCTTGGCAAGACTCTG 63
DB 1 MetleuSerLeuValLeuSerLeuValLeuSerLeuValLeuSerLeuValLeuSerLeu 20
OY 64 CAGCGCAACAAGCGCGCGCGCGCAAGAGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCG 123
DB 21 H16A1aThrLeuValLeuValLeuValLeuValLeuValLeuValLeuValLeuValLeu 40
OY 124 GCGCCGCTGTGGGACGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 183
DB 41 GlyProleuLeuGlySerGlyGlyPheGlySerAlaGlySerGlyLeuValAlaAsp 60
OY 184 AACTTGGCGGCTGCGCATCAAGACGCTGAGAGAGAGCGGATTTCCGATGGCGGAACTG 243
DB 61 AsnLeuProValAlaAlaIleValLeuValGlyValLeuValLeuValLeuValLeuVal 80
OY 244 CCCAAGGCGACCGCGAGGCGCGCATGGAAGTGGCTGCTGCAAGAGAGAGCGGCGCTTC 303
DB 81 ProAsnGlyThrArgValProMetGlyValValLeuLeuValValSerSerGlyPhe 100
OY 304 TCGGCGCTCATTAAGACTTCTGAGCTGCTGAGAGCGCGCATAGTTTCTGCTGATCTCTG 363
DB 101 SerGlyValIleArgLeuLeuAspTrpPheGlyValArgProAspSerPheValLeuLeu 120
OY 364 GAGAGCGCGCAACCGCTGCAAGACTCTTCTGACTTCATCAACGAGAGAGAGCGCTTCAG 423
DB 121 GlyArgProGlyProValGlyAsnLeuPheAspPheIleThrGlyValAlaLeuGly 140
OY 424 GAGAGCGTGGCGCGGAGCTTCTTCTGCGAGCTGCTGAGAGCGCGCGCGCGCGCGCGCAAC 483
DB 141 GlyGlyLeuValLeuAspSerPhePheTrpGlyValLeuGlyValAlaArgHisCysHisAsn 160
OY 484 TGGCGGCTTCTCCACCGCGCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 543
DB 161 CysGlyValLeuHisAspAspIleValAspGlyAsnIleLeuLeuAspLeuAsnArgGly 180
OY 544 GAACTCAACTCATCGACTTGGGCTGGGCGCGCTGCTCAAGAGACAGCTTACACGAGAC 603
DB 181 GlyLeuValLeuValLeuAspPheGlySerGlyValLeuLeuValAspTrpValTyrThrAsp 200
OY 604 TTGAGCGGAACCGGAGTGTACAGTCTCCAGAGTGTGCTTACCTCCCTACCGAGCGG 663
DB 201 PheAspGlyThrArgValTyrSerProGlyTrpIleArgTyrHisArgTyrHisGly 220
OY 664 AGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723
DB 221 ArgSerAlaAlaValIlePheSerLeuGlyIleLeuLeuValAspPheValCysGlyAspIle 240
OY 724 CCAATTGAGACGAGAGAGATGTGTAAGGCGCGCAAGTGTATTAGCAAAAGGCTCTT 783
DB 241 ProPheGlyHisAspGlyGlyIleIleIleArgGlyGlyValIlePhePheArgGlyValSer 260
OY 784 TCAGATGTCGAACCTTATTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
DB 261 SerGlyCysGlyHisLeuValLeuArgTyrCysLeuValLeuArgProSerAspArgProSer 280
OY 844 TTGGAAGAAATCCGAGACATCCGATGATGAGAGATGTTCTCCGCGCGCGAGCGACCGCG 903
DB 281 PheGlyGlyIleGlyHisAsnHisAspTrpMetGlyHisAspValLeuLeuProGlyGlyHis 300
OY 904 GAGATTGATGTCGACAGCTGTGTCACATCAACCGAGCAAA 942
DB 301 GlyIleHisLeuHisSerLeuSerProGlyProSerLeu 313

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RESULT 3 PIM1_HUMAN STANDARD, PRT; 313 AA.

AC P1309; Q96RG3; 01-JUL-1989 (Rel. 11, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Proto-oncogene serine/threonine-protein kinase pim-1 (BC 2.7.1.37).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90382681; PubMed=2205533; DOI=10.1016/0378-1119(90)90195-W;
 RA Reeves R., Spies G.A., Kiefer M., Barr P.J., Power M.;
 RT "Primary structure of the putative human oncogene, pim-1.";
 RL Gene 90:303-307(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87277423; PubMed=3475233; DOI=10.1016/0378-1119(87)90352-0;
 RA Zakut-Houri R., Hazum S., Givol D., Telexman A.;
 RT "The cDNA sequence and gene analysis of the human pim oncogene.";
 RL Gene 54:105-111(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88217305; PubMed=3329709;
 RA Domen J., von Lindern M., Hermans A., Breuer M., Grosveld G.,
 RA Berns A.;
 RT "Comparison of the human and mouse PIM-1 cDNAs: nucleotide sequence
 and immunological identification of the in vitro synthesized PIM-1
 protein.";
 RL Oncogene Res. 1:103-112(1987).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8815604; PubMed=3429489;
 RA Meeker T.C., Nagarajan L., Ar-Rushdi A., Croce C.M.;
 RT "Cloning and characterization of the human PIM-1 gene: a putative
 oncogene related to the protein kinases.";
 RL J. Cell. Biochem. 35:105-112(1987).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Bowtell M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Tomiyuki S., Carninci P., Prange C.,
 RA Bha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
 RA Besak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra W.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE OF 1-302 FROM N.A.
 RX MEDLINE=21354098; PubMed=11460166; DOI=10.1038/35085586;
 RA Pasqualucci L., Neumeister P., Goossens T., Nandjangu G.,
 RA Chaganti R.S.K., Rupperts R., Dalla-Favera R.;
 RT "Hypermutation of multiple proto-oncogenes in B-cell diffuse large-
 cell lymphomas.";
 RL Nature 412:341-346(2001).
 RN [7]
 RP CHARACTERIZATION.
 RX MEDLINE=88246418; PubMed=2837645;
 RA Telexman A., Amson R., Zakut-Houri R., Givol D.;
 RT "Identification of the human pim-1 gene product as a 33-kilodalton
 cytoplasmic protein with tyrosine kinase activity.";
 RL Mol. Cell. Biol. 8:1498-1503(1988).

RN [8]
 RP FUNCTION
 RX MEDLINE=20130009; PubMed=10664448; DOI=10.1016/S0014-5793(00)01105-4;
 RA Koike N., Maiba H., Taira T., Ariga H., Iguchi-Ariga S.M.M.;
 RT "Identification of heterochromatin protein 1 (HP1) as a
 RT phosphorylation target by Pim-1 kinase and the effect of
 RT phosphorylation on the transcriptional repression function of
 RT HP1(1)."
 RL PNAS Lett. 467:17-21(2000).
 RN [9]
 RP SUBCELLULAR LOCATION.
 RX MEDLINE=22567470; PubMed=12680209;
 RA Ionov Y., Le X., Tunquist B.J., Sweetenham J., Sachs T., Ryder J.,
 RA Johnson T., Lilly M.B., Kraft A.S.;
 RT "Pim-1 protein kinase is nuclear in Burkitt's lymphoma: nuclear
 RT localization is necessary for its biologic effects."
 RL Anticancer Res. 23:167-178(2003).
 CC -1- FUNCTION: Thought to play a role in signal transduction in blood
 CC cells. May affect the structure or silencing of chromatin by
 CC phosphorylating HP1 gamma/CBX3.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SUBUNIT: Binds to R99 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
 CC -1- TISSUE SPECIFICITY: Expressed primarily in cells of the
 CC hematopoietic and germ line lineages.
 CC -1- PTM: Autophosphorylated on tyrosine residues.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
 CC subfamily.
 CC -1- DATABASES: NAMB:Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW=http://www.infobiosgen.fr/services/chromocancer/Genes/PIM1ID261.html".
 CC
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 DR EMBL; M27903; AAA60090.1; -;
 DR EMBL; M16750; AAA60089.1; -;
 DR EMBL; M54915; AAA36447.1; -;
 DR EMBL; M24779; AAA81553.1; -;
 DR EMBL; BC020224; AAH20224.1; -;
 DR EMBL; AF386792; AAK70871.1; -;
 DR PIR; J00327; TYRUP1.
 DR GeneW; HGNC:8986; PIM1.
 DR H-InvDB; HIX005835; -;
 DR MIM; 164960; -;
 DR GO; GO:0005737; C:cytoplasm; TAS.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
 DR GO; GO:0007275; P:development; TAS.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR008271; Ser Thr_pkin_AS.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ATP; 1.
 KM ATP-binding; Nuclear protein; Phosphorylation; Proto-oncogene;
 KM Serine/threonine-protein kinase; Transferase.
 FT DOMAIN 38 290 Protein kinase.
 FT NE_BIND 44 52 ATP (By similarity).
 FT BINDING 67 67 ATP (By similarity).
 FT ACT_SITE 167 167 Proton acceptor (By similarity).
 FT CONFLICT 15 16 AP -> RA (in Ref. 2).
 SQ SEQUENCE 313 AA; 35685 MW; 35BA76D3668B69A3 CRC64;

Alignment Scores: 1.9e-97 Length: 313
 Pred. No.: 1636.00 Matches: 304
 Score:

Percent Similarity: 99.04% Conservative: 6
 Best Local Similarity: 97.12% Mismatches: 3
 Query Match: 66.97% Indels: 0
 DB: 1 Gaps: 0
 US-10-705-757-3 (1-1302) x PIM1_HUMAN (1-313)
 QY 4 ATGCTCTTGTCCAGATGATCCCTGGCCGACCTGCGCGAGCCCTTGACAGCAGT 63
 DB 1 MetLeuSerLysAlaIleHisSerLeuAlaHisLeuArgAlaProCysAlaHisLeu 20
 QY 64 CAGCCCAACAGCTGGCGCGCGGCAAGAGAGAGCCCTGAGTGGAGTACCAAGT 123
 DB 21 HisAlaThrIleLeuAlaProGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 40
 QY 124 GCGCGCGCTGTGGGAGCGGTGGCTTGGCTGGCTACTCGGGACCTCGCGCGAC 183
 DB 41 GlyProLeuLeuGlySerGlyGlyLysSerValTyrSerGlyIleArgValSerAsp 60
 QY 184 AACTTGGCGGTGGCCATCAAGCAGTGGAGAGAGCCGATTTCCGACTGGGGAGACT 243
 DB 61 AsnLeuProValAlaIleLysHisValGlyLysAspArgLysSerThrProLysLeu 80
 QY 244 CCCAAGCGGACCCGAGTGGCCATGAGAGTGTCTGCTGAGAGAGTGAAGTTCG 303
 DB 81 ProAlaGlyThrArgValProMetGlyValLeuLeuLysValSerSerGlyPhe 100
 QY 304 TGGGCGCTATTAGACTTGTGAGCTGTTCGAGAGCCCGAGATGTTGCTGATCTCG 363
 DB 101 SerGlyValIleArgLeuLeuAspTrpPheGlyLysGlyProAspSerPheValLeuLeu 120
 QY 364 GAGAGCCCGAAGCCGCTGCAAGACTTGCATTCATCAAGAGCGAGAGCCCTCAG 423
 DB 121 GlyLysProGlyProValGlnHisLeuPheAspPheIleThrGlyArgGlyAlaLeuGln 140
 QY 424 GAGAGCTGGCCCGAGCTTCTTGTGGAGGTGTGGAGCCGCTGGCGGATTTGCCA 483
 DB 141 GluGlyLeuAlaArgSerPheThrPheGlnValLeuGlnAlaValArgHisCysHisAsn 160
 QY 484 TGGCGGCTTCTCCACCGGACATCAAGAGCGAGAACATTTTAATGACCTGAACCG 543
 DB 161 CysGlyValLeuHisArgAspTrpLeuAspArgGlyLysAlaIleLeuLeuAsnArgGly 180
 QY 544 GAATCAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 603
 DB 181 GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyrThrAsp 200
 QY 604 TTGAAGGAACCGAGTGAAGTCAAGTCTTCAAGAGTGAATGCTTACATGCTACAG 663
 DB 201 PheAspGlyThrArgValTyrSerProGlyIleArgTyrHisArgTyrHisGly 220
 QY 664 AGCTGGCTGCTGTTGGTCCCTGGGAGATCCGCTTAAGATGATGATGATGATGAT 723
 DB 221 ArgSerAlaAlaValTyrSerLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
 QY 724 CCATTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 783
 DB 241 ProPheGlyHisAspGlyGlyIleLeuArgGlyGlnValPhePheArgGlnArgValSer 260
 QY 784 TCAGAAATGCAATCTTATTAATGATGCTGCTGCTGCTGAGACATCGAGCCGCTCC 843
 DB 261 SerGlyCysGlyHisIleLeuIleArgTyrCysLeuAlaLeuArgProSerAspArgProThr 280
 QY 844 TTGAAGAAATCAAGAACATCCGCGAGTGAAGATGTTCTCTGCGCCAGCCAGCCG 903
 DB 281 PheGlyLysIleGlnAsnHisAspTrpMetGlnAspValLeuLeuProGlnGlnThrAla 300
 QY 904 GAGATTCATGTCAGAGCTGTCAACATCAACATCAACATCAACATCAACATCAAC 942
 DB 301 GluIleHisLeuHisSerLeuSerProGlyProSerLys 313
 RESULT 4
 PIM1_BOVIN

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ID P1M1_BOVIN STANDARD; PRT; 313 AA.
AC OGN08;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Proto-oncogene serine/threonine-protein kinase p1m-1 (EC 2.7.1.37).
GN Name=P1M1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2109090; PubMed=1162156; DOI=10.1016/S0165-2427(00)00255-2;
RA Wang Z., Petersen K., Weaver M.S., Magnuson N.S.;
RT "CDNA cloning, sequencing and characterization of bovine p1m-1."
RL Vet. Immunol. Immunopathol. 78:177-195(2001).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBUNIT: Binds to Rps (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC -1- PTM: Autophosphorylated (By similarity).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. P1M
CC subfamily.
CC -----
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CC -----
DR EMBL; AF259078; AAF67200.1; -.
DR HSP; Q63450; 1A06.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR Pfam; PF00069; Kinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00101; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Nuclear protein; Phosphorylation; Proto-oncogene;
KW Serine/threonine-protein kinase; Transferase.
FT DOMAIN 38 290 Protein kinase.
FT NP BIND 44 52 ATP (By similarity).
FT BINDING 67 67 ATP (By similarity).
FT ACT_SITE 167 167 Proton acceptor (By similarity).
FT ACT_SITE 313 AA; 35629 MW; 9EF40229A847AD47 CRC64;
SQ SEQUENCE 313 AA; 35629 MW; 9EF40229A847AD47 CRC64;

Alignment Scores:
Pred. No.: 4,64e-97 Length: 313
Score: 1630.00 Matches: 304
Percent Similarity: 99.04% Conservative: 6
Best Local Similarity: 97.12% Mismatches: 3
Query Match: 66.72% Indels: 0
Gaps: 0

US-10-705-757-3 (1-1302) x P1M1_BOVIN (1-313)

QY 4 ATGCTCTTTCACAGATCACTCCCTGGCCCACTGGCGGAGCCCTTGCACGACCTG 63
DB 1 MetleuenseuSerlySileasnsSerleuAlaHisleuArgAlaAlaProCySseAspIeu 20
QY 64 CAGCCCAACAGCTGGGCGCGGCAAGAGAGAGCCCTGGAGTGGGACGATACAGATG 123
DB 21 HisAlaThrlyBleuAlaProGlylyeGluIuysGluProleuGluuSerGlnIuYrGlnVal 40
QY 124 GGCCCGCTGTGGCAGCGGTGGCTTGGCTGCTACTCGGCGCATCCGCGTCCGCGAC 183
DB 41 GlyProleuGluuGlySerGlyGlyPheGlySerAluYrSerGlyIleArgValAlaAsp 60

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DB 61 AsnuProValAlaIlelyShIsValGluIyAspArgIleSerAspTrpGlyGluIeu 80
QY 244 CCCAAGCGACCCGAGTGGCCATGAGAGATGGTCTCTGAGAGAGGTGAGCTGGCTTC 303
DB 81 ProAnGlyThrArgValProMetGluValIleuIeuIleuIleuIleuIleu 100
QY 304 TCGGGGCTCATTTAGCTTCTGACCTGCTGAGAGCCCGGATAGTTTCTGCTGATCTTC 363
DB 101 SerGlyValIleArgIleuAspTrpPheGluArgProAspSerPheValIleuIleu 120
QY 364 GAGAGCGCCGACCCGCGAAGACCTCTTCACTTCAATCAGCAGGAGGAGCCCTCCAG 423
DB 121 GluArgProGluProValGlnAspIeuPheAspPheIleThrGluArgGlyAlaGluGln 140
QY 424 GAGAGCTGGCCCGGAGCTTCTTCTGAGGTGCTGAGAGCCCGTGGCGCATTCACAC 483
DB 141 GluGluIeuAlaArgSerPhePheTrpGlnValIleuGluAlaValArgHisCySHIsAsp 160
QY 484 TCGGGGCTTCCACCGCCGACATCAAGACGAGAACATTTATGACCTGAAACCGCGG 543
DB 161 CyGlyValIleuHisArgAspIlelyAspGluAsnIleuIleuAspIeuAsnArgGly 180
QY 544 GAACTCAACTCATGACTTCGGGTGGGGGCGCTGCTCAAGGACAGTCTACAGGAC 603
DB 181 GluIeuIyAspIleAspPheGlySerGlyAlaIleuIyAspThrValIyTrnAsp 200
QY 604 TTTGACGGAACCCGAGTGTACAGTCTCCAGAGTGTATTCGATACGATCGTACCAAGC 663
DB 201 PheAspGlyThrArgValIySerProProGluTrpIleArgIyHisArgIyHisGly 220
QY 664 AGGTGGCTGCTGTGTTGTCCTGGGAGATCTGCTCTATGACATGGTCTGGGAGATTT 723
DB 221 ArgSerAlaAlaValIySerIeuGlyIleIeuIeuIyAspMetValCyGlyAspIle 240
QY 724 CCATTTGAGACGACGAGAGATCGTCAAGGGCAGAGTGTACTTGGCAAGAGTCTCT 783
DB 241 ProPheGluHisAspGluGluIleValArgGlyGlnValPhePheArgGlnArgValSer 260
QY 784 TCAGAAATGTCACATCTTATAGATGATGCTGCTGCTGAGACCATCGACCGGCTCTC 843
DB 261 SerGluCyGlnHisIleuIleArgTrpCyBleuAlaIleuArgProSerAspArgProThr 280
QY 844 TTTGAAGAAATCCAGAACCATCGGTGATGACAGATGTTCTCTGCGCCGACCGCCG 903
DB 281 PheGluGluIleGlnAsnHisProTrpMetGlnAspValIleuIeuProGluGlnIuTrAla 300
QY 904 GAGATTCATCTGACGAGCCCTGTCACATCAACCCAGGAA 942
DB 301 GluIleHisIleuHisSerIeuSerProGlyProSerIyS 313

RESULT 5
O8CFN8 PRELIMINARY; PRT; 313 AA.
ID O8CFN8;
AC O8CFN8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Proviral integration site 1.
GN Name=P1m1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=Brain, and Eye;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

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RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer T.E.,
 RA Brownstein M.J., Uddin T.B., Tozhynki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Ffey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
 RA Krzyzanski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Eye;
 RC Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL, BC042885; AAH42885.1; -.
 DR EMBL, BC053019; AAH53019.1; -.
 DR MGI, MGI:97584; Piml.
 DR GO, GO:0005524; P:ATP binding; IEA.
 DR GO, GO:0004674; P:protein serine/threonine kinase activity; IEA.
 DR GO, GO:0016740; P:transferase activity; IEA.
 DR GO, GO:0006681; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR011009; Kinase_Like.
 DR InterPro: IPR000719; Prot_Kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR008271; Ser_thr_kinase.
 DR Pfam: PF00069; Pkinase; I.
 DR Prodom, PD000001; Prot_kinase; 1.
 DR SMART, SM00220; S_TKc; 1.
 DR PROSITE, PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE, PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE, PS00108; PROTEIN_KINASE_ST; 1.
 KM ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SO SEQUENCE 313 AA, 35451 MW, 1294716A03B7CD7 CRC64;

Alignment Scores:
 Pred. No.: 2,07e-94 Length: 313
 Score: 1589.00 Matches: 296
 Percent Similarity: 97.12% Conservative: 8
 Best Local Similarity: 94.57% Mismatches: 9
 Query Match: 65.04% Indels: 0
 DB: 2 Gaps: 0

US-10-705-757-3 (1-1302) x Q8CFN8 (1-313)

QY 4 ATGCTCTTCCAGATCACTCCCTGCGCCACCTGCGGCGACCCCTTGCAACGACTG 63
 DB 1 MetLeuLeuSerIleArgSerIleAlaIleValAlaIleProCysAlaAspLeu 20
 QY 64 CACGCCAACAAGCTGGCGCGGCAAGAGAGAGAGCGCCCTGGAGTGCAGTACAGAGT 123
 DB 21 HIAIAIAIhIyLeuAlaIleProGlyLysGluLysGluProLeuGluSerGlnIlyrGlnVal 40
 QY 124 GGGCCGCTGTGGGCGACGCGTGGCTTGGCTCGGCTACTCGGAGCATCCCGTGGCCGAC 183

DB 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValAlaIleAsp 60
 QY 184 AACCTGGCGGAGTGGCCATCAAGACGATGGAGAGACCGGATTTCCGACTGGGGAGAACTG 243
 DB 61 AaenLeuProValAlaIleIleYehIeValGluLysAspArgIleSerThrPheIlyGluLeu 80
 QY 244 CCCAAGCGGACCCGAGTGGCCCATGGAAGTGTCTCTGTCGAAGAGAGTGAAGTCAAGCTTC 303
 DB 81 ProAlaGlyThrArgValProMetGluValValLeuLeuLysValSerSerAspPhe 100
 QY 304 TGGGCGCTGATTAGACTTCTGCACTGCTTCCAGAGAGCCCGATGATTTGCTGCTGACTCG 363
 DB 101 SerGlyValIleIleArgLeuLeuAspIlePheGluArgProAspSerPheValLeuIleLeu 120
 QY 364 GAGAGCCCGAAGCCGCTGCAAGACCTTCCATTCACCGAGAGAGCCGCTCCAG 423
 DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
 QY 424 GAGAGCTGGCCGAGCTTCTTGGCAGGTGTGAGGCGCCGTGCGGACTTGCACAAAC 483
 DB 141 GluAspLeuAlaIleArgGlyPhePheThrGlnValLeuGluAlaValAlaArgIleCysIleAsn 160
 QY 484 TCGGCGGCTTCTCCACCGGCACTCAAGAGCAACATTTATGACTGATCAAGCGGCG 543
 DB 161 CysGlyValLeuIleArgAspIleLeuYAspGluAsnIleLeuIleAspLeuSerArgGly 180
 QY 544 GAAGTCAACATCATGAGCTTGGGCGGCGGCGCTGCTCAAGAGACAGCTTCAACGAGAC 603
 DB 181 GluIleLeuLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValIlyrThrAsp 200
 QY 604 TTTGACGGAACCCGAGTGTACAGTCCCTCCAGAGTGAATTCGCTACATGCTTACACAGCG 663
 DB 201 PheAspGlyThrArgValTyrSerProProGluIleArgIlyThrIleArgIly 220
 QY 664 AGCTGGCTGCTGTTTGGTCCCTGGGAGATCTGCTCTTATGACATGCTTCGCGAATATT 723
 DB 221 ArgSerAlaAlaValAlaIlePheSerLeuLeuIleLeuLeuIlyrAspMetValCysGlyAspIle 240
 QY 724 CCATTGTAGACAGAGAGATCGCAAGGCGCAAGTGTACTTTAGGCAAGGCTCTCT 783
 DB 241 ProPheGluIleAspGluIleIleLeuLysGlyGlnValPhePheArgGlnThrValSer 260
 QY 784 TCAGATGTCAACATCTTATAGATGTGCTGCTGCTGAGACATCGGACCGGCGCTCC 843
 DB 261 SerGluCysGlnIleLeuIleLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIle 280
 QY 844 TTTGAAGAAATCCAGAAACCATCCGCGATGCGAGATTTCTCTGCGCCGACCGCGC 903
 DB 281 PheGluGluIleArgAsnIleProIlePheGlnGlyAspLeuLeuProGlnAlaIleSer 300
 QY 904 GAGATTGATCTGCACAGCGCTGTCACCATCAGCCAGCAAA 942
 DB 301 GluIleIleLeuIleSerLeuSerProGlySerSerLys 313

RESULT 6
 PIM1 MOUSE STANDARD; PRT; 313 AA.
 ID PIM1 MOUSE
 AC P06803;
 DT 01-JAN-1988 (rel. 06, Created)
 DT 01-JAN-1988 (rel. 06, Last sequence update)
 DT 05-JUL-2004 (rel. 44, Last annotation update)
 DE Proto-oncogene serine/threonine-protein kinase Pim-1 (EC 2.7.1.37).
 GN Name:Pim1; Synonyms:Pim-1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 OX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86272109; PubMed=3015420; DOI=10.1016/0092-8674(86)90886-X;
 RA Sellen G., Guyeys H.T., Boelens W., Robanus-Maandag E., Versteek J.,
 RA Domen J., van Beveren C., Berns A.;
 RT "The primary structure of the putative oncogene pim-1 shows extensive


```

RT      homology with protein kinases." ;
RN      [2]
RL      Cell 46:603-611 (1986).
RP      INTERACTION WITH RP9.
RX      MEDLINE=20389540; PubMed=10931201;
RA      Matsu H., Harada Y., Nagakubo D., Kikura H., Ikeda M., Tamai K.,
RA      Takahashi K., Ariga H., Iguchi-Ariga S.M.M.;
RA      "PAF-1, a novel target protein of phosphorylation by Pim-1 kinase." ;
RL      Eur. J. Biochem. 267:5168-5178 (2000).
CC      -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC      -1- SUBUNIT: Binds to RP9.
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC      -1- PTM: Autophosphorylated (By similarity).
CC      -1- DISEASE: Frequently activated by provirus insertion in murine
CC      leukemic virus-induced T-cell lymphomas.
CC      -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC      subfamily.
CC      -----
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CC      -----
DR      EMBL, M13945; AAA39930.1; -.
DR      PIR, A24169; TVMSPL.
DR      HSRP, Q63450; 1A06.
DR      MGP, MGI:97584; Pim1.
DR      InterPro, IPR011009; Kinase_like.
DR      InterPro, IPR000719; Prot_Kinase.
DR      InterPro, IPR008271; Ser_thr_pkin_AS.
DR      Pfam, PF00069; Pkinase; 1.
DR      ProDom, PD000001; Prot_kinase; 1.
DR      PROSITE, PS00107; PROTEIN_KINASE_DOM; 1.
DR      PROSITE, PS50011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE, PS00108; PROTEIN_KINASE_ST; 1.
KW      ATP-binding; Nuclear protein; Phosphorylation; Proto-oncogene;
KW      Serine/threonine-protein kinase; Transferase.
FT      DOMAIN 38 290
FT      NP BIND 44 52
FT      BINDING 67 67
FT      ACT SITE 167 167
FT      PTM 35536 MM; 79F4779B9DCBD16 CRC64;
SQ      SEQUENCE 313 AA; 35536 MM; 79F4779B9DCBD16 CRC64;
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Alignment Scores:
Pred. No.: 4.36e-94 Length: 313
Score: 1584.00 Matches: 295
Best local Similarity: 96.81% Conservative: 8
Best local Similarity: 94.25% Mismatches: 10
Query Match: 64.84% Indels: 0
DB: 1 Gaps: 0
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US-10-705-757-3 (1-1302) x PIM1_MOUSE (1-313)
OY      4 ATGCTCTGTGTCAGAGATCAATCTCCCTGGCCGACGCGCGAGCCCTTGCAAGACTG 63
Db      1 MetLeuLeuSerLeuValLeuSerLeuAlaHisLeuAlaGalaValProCyAsnAspLeu 20
OY      64 CAGCGCAACAGACTGGCGCGCGCGGACAGAGAGAGAGCCCTGAGATCGCACTACAGAGT 123
Db      21 HisAlaThrLysLeuAlaLafProGlyLysGlyLysGlyLysValTyrSerGlyIleArgValAlaAsp 40
OY      124 GCGCCGCTGTGTGGGCGAGCGGCTTGGCGCTTGGCTGCTACTGCGGAGATCCGCTGCGCGAC 183
Db      41 GlyProLeuLeuGlySerGlyGlyLysValTyrSerGlyIleArgValAlaAsp 60
OY      184 AACTTGGCGGTGGGCATCAAGCAAGTGAGAGAGAGCGGAGATTTCGACCTGGGGGAACTG 243
Db      61 AsnLeuProValAlaIleValIleValAlaGlyValAspArgIleSerAspTrpGlyLysLeu 80
OY      244 CCCAAGCGACCGAGTGCCCATGAGAGATGTGCTCTGTGAAGAGATGAGCTCGGAGCTTC 303

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DB	PROTEIN	SEQUENCE	FUNCTION	LOCUS	GENE	ORGANISM	REFERENCE
Db	81	ProaenglythrArgValProMetGluValIleuLeuLeuLysValSerSerAspPhe					
Qy	304	TCGGGCGTCATTAAGACTTCTGGAGCTGGTTCCAGAGGCGCGATAGATTCCGTGCATCTTG					
Db	101	SerGlyValIleIleArgLeuLeuAspTrpPheGluLysArgProAspSerPheValLeuIleLeu					
Qy	364	GAGAGGCCCGAAACCCGTGCAGAACCTCTTGCATTCATCACCGAGCGAGAGCCCTCCAG					
Db	121	GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln					
Qy	424	GAGAGAGCTGGCCCCGAGCTTCTTCTGGGACGGTGTCTGGAGAGCCGTGGCGCATTCGCAAC					
Db	141	GluAspLeuAlaArgGlyPhePheTrpGlnValIleuGluAlaValArgIleCysHisAsn					
Qy	484	TGCGGGGTTCTCCACCGCGACATCAAGAGCAGAAACATCTTAATGCAGCCGACCGCGG					
Db	161	CysGlyValLeuLeuHisArgAspIleLeuValAspGluAsnIleLeuIleAspLeuSerArgGly					
Qy	544	GAACCTCAACTCATCTGACTTCGGGTCCGGGCGCGCTGCTCAAGAGCACAGTCTTACACGAC					
Db	181	GluIleuLeuIleIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyrThrAsp					
Qy	604	TTTGAACGGAACCCGAGTGTACAGTCTCTCAGAGTGGATTCCGCTACATGGCTTACACGCG					
Db	201	PheAspGlyThrArgValTyrSerProProGluTrpIleArgTyrHisArgTyrHisGly					
Qy	664	AGGTGGGCGTGGTTGGTCCCTGGGGGATCCGCTCTAATGACATGGTCTCGCGGAGATAT					
Db	221	ArgSerAlaAlaValTrpSerLeuLeuLysIleLeuLeuTyrAspMetValCysGlyAspIle					
Qy	724	CCATTGAGCAGCAGCAAGAGATTCGTCAAGGCGCAAGTACTTTAGCGAAAGGGTCTCT					
Db	241	ProPheGluLysIleAspGluGluIleIleLysGlyGlnValPhePheArgGlnThrValSer					
Qy	784	TCAGAAATGCACATCTTATTAGATGATGATGCTGTCCCTGAGACCATCGACCGGCGCTCC					
Db	261	SerGluCysGlnHisIleLeuIleLysTrpCysLeuSerLeuArgProSerAspArgProSer					
Qy	844	TTTGAAGAAATCCAGAACCATCCGCGAGATGCAGAGATGTTCTCTGGCCCGACGCGCC					
Db	281	PheGluGluIleLeuArgAsnHisProTrpPheGlnGlyAspLeuLeuProGlnAlaIleSer					
Qy	904	GAGATTCACTGCACAGCGCTGTCAACCATCACCCAGCAAA 942					
Db	301	GluIleHisIleHisSerLeuSerProGlySerSerLys 313					

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sb-sib.ch).

DR EMBL; AJ130845; CAB62386.1; -
DR HSSP; Q63450; 1A06;
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Phosphorylation; Serine/threonine-protein kinase;
KW Transferase.
FT DOMAIN 40 291 Protein kinase.
FT NE_BIND 46 54 ATP (By similarity).
FT BINDING 69 69 ATP (By similarity).
FT ACT_SITE 168 168 Proton acceptor (By similarity).
SQ SEQUENCE 323 AA; 36597 MW; E2A4FA20B6F6396C CRC64;

Alignment Scores:

Pred. No.:	2,18e-65	Length:	323
Score:	1140.00	Matches:	216
Percent Similarity:	78.48%	Conservative:	43
Best local Similarity:	65.45%	Mismatches:	61
Query Match:	46.66%	Indels:	10
DB:	1	Gaps:	5

US-10-705-757-3 (1-1302) x PIM3_COTUA (1-323)

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QY 4 ATGCTCTGTGCAAGATCACTCCCTGGCCCACTG---CGCGACGCCCTTGCAAGCAG 60
   |||||
Db 1 MetLeuLeuSerIysPheGlySerLeuAlaHisIleCysSerProAlaSerMetAspHis 20

QY 61 CTGCAAGCCCAACAAGCTGGCGCGGCAAA---GAGAAAGAGCCCTGAGTGCAGTAC 117
   |||||
Db 21 LeuProValIysIleLeuProValIysValGlnIleSerIleuProHisPheIysValTyr 40

QY 118 CAGGTGGCGCCGCTGTGGGCAAGCGGTGCTTGGCTCGCTACTCGGCGCATCCGCGTC 177
   |||||
Db 41 GlnValGlySerValIleuGlySerGlyGlyPheGlyThrValTyrAlaGlySerArgThr 60

QY 178 GCGCAACAATTGGCGGTGCATCAAGCAGTGGAGAAGGACCGGATTCGCACTGCGAGG 237
   |||||
Db 61 AlaSerGlyLeuProValIleValIleValIleValIleValIleValIleValIleValIle 80

QY 238 GAATGCCCAACGCAAGCCGATGCGCATGAGAAAGTGCTCTGCTGTAAGAAGTGAAGCTG 297
   |||||
Db 81 ThrIle---GlyGlyValMetValProIleuGlnIleValIleuLeuIysIleValIleSer 99

QY 298 GGGCTTCTGGGCGCTCATTAAGCTTGTGACTGTGTGAGAGGCCCGATAGTTTCTGCTG 357
   |||||
Db 100 GlyPheArgGlyValIleIleValLeuLeuAspTrpTyrGlnArgProAspGlyPheLeuIle 119

QY 358 ATCTGTGAGAGGCGCGCAACCGTGAACACTCTTGCACTTCAACCGGAGGAGGAGCC 417
   |||||
Db 120 ValMetGlnArgProGlnLeuValIysAspLeuPheAspPheIleThrGlnIysGlyAla 139

QY 418 CTCAGAGAGAGCTGGCGCGAGACTTCTTGTGCGAGGTGTGAGAGCGCTGCGGCAATTCG 477
   |||||
Db 140 LeuAspGlnAspHisAlaArgGlyPhePheArgGlnValIleuIleValAlaValAlaGlnHis 159

QY 478 CACAATCGCGGGGTTCTCCACCGGACATCAAGAGCAAGAACTTTAATCGACTGAAC 537
   |||||
Db 160 TyrGlyCysGlyValIleHisArgAspIleIleAspIleuAsnLeuValIleAspLeuArg 179
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QY 538 CGCGGCAACTCAAACTCATGCACTTGGGGTGGGGCGCTGCTCAAGACACAGCTTAC 597
   |||||
Db 180 ThrGlyIleuLeuIleValIleAspPheGlySerGlyAlaIleuLeuIleAspHisThrValTyr 199

QY 598 ACGAATTTGACGGAACCGGAGTGAAGTCTCTCAAGAGTGAATTCGCTTACCATGCTAC 657
   |||||
Db 200 ThrAspPheAspGlyThrArgValIysSerProProGlnTyrIleArgTyrHisArgTyr 219

QY 658 CACGGCAGGTGGCGCTGTGTTGTCCTGGGGGATCTGCTCATGACATGGCTGCGGGA 717
   |||||
Db 220 HisGlyArgSerAlaThrValIysSerLeuGlyValIleuLeuTyrAspMetValCysGly 239

QY 718 GATATTCATTTGACACGACGACGAGATTCGTCAGAGGCGGCAAGTACTTATGAGCAAG 777
   |||||
Db 240 AspIleProPheGlnGlnIleAspIleuIleuLeuArgGlyArgLeuTyrPheArgArgArg 259

QY 778 GTCTCTTCAAGATTCACATCTTATAGATGTCCTGCTGCTGAGACCATCGACCGG 837
   |||||
Db 260 IleSerProGlnCysGlnGlnIleuIleuIysTrpCysLeuSerLeuArgProSerAspArg 279

QY 838 CCTCTCTTGAAGATTCACAGACATCCGTCGATG---CAGGATGTTCTCCTGCGCCGAG 894
   |||||
Db 280 ProThrLeuGlnGlnIlePheAspHisGlnTrpMetHisIysSerGlnValIalIysSer 299

QY 895 GCGACCGCGGCAAGTTCATCTGCACAGCCTGTGACCATCAACCGAATAATGACGCATTC 954
   |||||
Db 300 GlnAspCysAspIleArgLeuArgThrLeuAspThrThrAspValSer----- 314

QY 955 TGTCAAGACCTTCAGGAGAAAGAGAGCTTG 984
   |||||
Db 315 ---SerThrSerSerSerAsnIleuSerIeu 323

RESULT 8
PIM3_HUMAN
ID PIM3_HUMAN STANDARD, PRT, 326 AA.
AC Q86V86;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
GN Name=PIM3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RX Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RX Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RX Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RX Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RX Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RX Raha S.S., Loquellano N.A., Peters G.J., Abrahamson R.D., Mullaly S.J.,
RX Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RX Villardon S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RX Fahreny J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RX Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RX Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RX Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,
RX Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RX Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP IDENTIFICATION FROM ESTS.
RX MEDLINE=22682943; PubMed=12798037; DOI=10.1016/S1476-9271(02)00095-6;
```

RA Chichester C., Nikitin F., Ravarini J.-C., Lisacek F.;
 RT "Consistency checks for characterizing protein forms."
 RL Comput. Biol. Chem. 27:29-35(2003).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
 subfamily.
 CC -----
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 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements/>
 CC or send an email to license@ebi-sib.ch).
 CC -----
 DR EMBL: BC052239; AAS52239.1; ALT_INIT.
 DR InterPro: IPR011009; Kinase like.
 DR InterPro: IPR000719; Prot_Kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000004; Prot_kinase; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Phosphorylation; Serine/threonine-protein kinase;
 KM Transferrase.
 FT DOMAIN 40 293 Protein kinase.
 FT NP_BIND 46 54 ATP (By similarity).
 FT BINDING 69 69 ATP (By similarity).
 FT ACT_SITE 170 170 Proton acceptor (By similarity).
 SQ SEQUENCE 326 AA; 35863 MW; 41FDF9DD2467A162 CRC64;

Alignment Scores:
 Pred. No.: 3,67e-65 Length: 326
 Score: 1136.50 Matches: 224
 Percent Similarity: 77.25% Conservative: 34
 Best Local Similarity: 67.07% Mismatches: 61
 Query Match: 46.52% Indels: 15
 DB: 1 Gaps: 8

US-10-705-757-3 (1-1302) x PIM3_HUMAN (1-326)

QY 4 ATGCTCTTTCGAAGATCAACTCCCTGGCCGCGCAGCCCT-----TGCAAC 57
 DB 1 MetLeuLeuSerIysPheGlySerIleAlaHisLeu---CysGlyProGlyGlyValAsp 19
 QY 58 GACCTTCACCGCAACGACTGCGCGCGCGCAAA---GAGAAGAGCCCTCGAGTCGCG 114
 DB 20 HisLeuProValIleuValIleuGlnProAlaIleuAlaAspIleuSerPheGluValAla 39
 QY 115 TACCAAGTGGGCGCGCTGTGGGAGCGGTGGCTTGGCTCGCTTACTCGGCGATCCGC 174
 DB 40 TyGlnValAlaGlyValAlaValLeuGlySerGlyPheGlyThrValTyralaGlySerArg 59
 QY 175 GTGCGCGCAACACTTGGCGGTGGCGCATCAACGATGAGAGGAGCGGATTCGCACTGG 234
 DB 60 IleAlaAspGlyLeuProValAlaValAlaValValValValValValValValValVal 79
 QY 235 GGGGAACCTGCCCAACGCGACCCGATGCCATGAGTGGTCTCTGCTGAGAGAGTG--- 291
 DB 80 GlySerLeu---GlyGlyAlaThrValProLeuGlnValValLeuLeuArgIleValGly 98
 QY 292 ---AGCTCGGGCTTCTCGGCGCTTACATTGAGCTTGGAGCTGTTGAGAGCGCGATAGT 348
 DB 99 AlaAlaGlyGlyValAlaArgIleValIleArgLeuLeuAspIlePheGluValArgProAspGly 118
 QY 349 TTGCTGTGATCTCGGAGAGAGCGCGCAACCGCTGAGAGAGCTCTTTCGATTCATCACTGAG 408
 DB 119 PheLeuLeuValIleuGlnValArgProGluProAlaGlnAspPheLeuAspPheIleThrGln 138
 QY 409 CGAGAGCCCTTCAGAGAGAGAGCTGCGCGCGAGCTTCTTTCGAGAGGTGCTGAGAGCGCTG 468
 DB 139 ArgGlyAlaLeuAspGluProLeuAlaArgArgPhePheAlaGlnValLeuAlaAlaVal 158

QY 469 CGGATTTGCCAACAATCGCGGGTTCCTCCACCGGAGATCAAGAGAGCAATCATCTTATC 528
 DB 159 ArgHisCysHisSerCysGlyValAlaHisAlaAspIleLeuAspGluLeuLeuVal 178
 QY 529 GACCTGAACCGCGCGCAACTCAAACTCATGACTTCGCGGTGGGCGCGCTCAAGAC 588
 DB 179 AspLeuArgSerGlyGluLeuValLeuIleAspPheGlySerGlyAlaLeuLeuValAsp 198
 QY 589 ACGCTTACACGGAATTTGACGGAACCGGATGATACAGTCTTCAAGATGATTCGCTAC 648
 DB 199 ThrValTyThrAspPheAspGlyThrArgValTySerProGluTyrPheArgTyr 218
 QY 649 CATCGCTACCAAGGAGAGTGGCTGGCTTGGCTCCCTGGAGATCCGCTTATGACATG 708
 DB 219 HisArgTyHisGlyAlaHisSerAlaThrValTyrPheSerLeuGlyValLeuLeuTyrAspMet 238
 QY 709 GTCTGCGAGATATTCATTTGAGCAGCAGAGAGATGCTCAAGGCGCAAGTACTTT 768
 DB 239 ValCysGlyIAspIleProPheGluGlnAlaAspGluGlnIleuArgGlyArgLeuLeuPhe 258
 QY 769 AGGCAAAAGGTCTCTTCAGAAATGTCAACATTTATGATGTGCTGCTCTGAGACCA 828
 DB 259 ArgArgArgValSerProGluCysGlnGlnLeuIleArgTyrCysLeuSerLeuArgPro 278
 QY 829 TCGGACCGCGCTCTTGAAGAAATCCAGAACATCCGCGATG-----CAGAGTGT 882
 DB 279 SerGluArgProSerLeuAspGlnIleAlaHisProTyrPheLeuGlyAlaAspGly 298
 QY 883 CTCCTGCCCCAGGCGCACCGCGCATTCATCTGACAGCTGTCACCATCAGCAGCAAA 942
 DB 299 GlyAlaProGlu---SerCysAspLeuArgLeuCysThrLeuAspPro----- 313
 QY 943 TAGCAGCCATTTCTGTCAACCTTCAGAGGAGAGAGAGCTTG 984
 DB 314 ---AspAspValAlaSerThrThrSerSerSerGluSerLeu 326

RESULT 9
 PIM3_MOUSE
 ID PIM3_MOUSE STANDARD; PRT; 326 AA.
 AC P58750;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
 GN Name=Pim3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon, and Salivary gland;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares J.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Umedin T.B., Toshlyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
 subfamily.
 CC -----
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 CC or send an email to license@1sb-sib.ch).
 CC -----
 DR EMBL: BC017621; AAH17621.1; -.
 DR EMBL: BC026639; AAH26639.1; -.
 DR HSSP: Q03656; 1HOW.
 DR InterPro: IPR011009; Kinase_like.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; Pkinase_1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
 KM ATP-binding: Phosphorylation; Serine/threonine-protein kinase;
 KM Transferrase.
 FT DOMAIN 40 293 Protein kinase.
 FT NE_BIND 46 54 ATP (By similarity).
 FT BINDING 69 69 ATP (By similarity).
 FT ACT_SITE 170 170 Proton acceptor (By similarity).
 SQ SEQUENCE 326 AA; 35970 MW; DD68CBF46354851B CRC64;
 Alignment Scores:
 Pred. No.: 6.66e-65 Length: 326
 Score: 1132.50 Matches: 214
 Percent Similarity: 82.71% Conservative: 30
 Best local similarity: 72.54% Mismatch: 44
 Query Match: 46.36% Indels: 7
 DB: 1 Gaps: 5
 US-10-705-757-3 (1-1302) x PIM3_MOUSE (1-326)
 QY 4 ATGCTCTGTTCGAAGTCAACTGCTGGCCCACTGGCGGAGCCCT-----TGCAC 57
 DB 1 MetLeuLeuSerLysPheGlySerLeuAlaHisLeu---CysGlyProGlyIleValaIaP 19
 QY 58 GACCTGCACCGCAACAAGCTGCGCGCGGCAAA---GAGAGGAGCCCTGAGTGCAG 114
 DB 20 HisLeuProValaIleuValleuGlnProAlaIleuAlaSerPheGlySerIleValaI 39
 QY 115 TACCAAGTGGGCGCGCTGTGGGAGCGGCTTGGCTTGGCTTACTGCGGCGATCCGC 174
 DB 40 TyGlnValaGlyIleValaIleuGlySerGlyIlePheGlyThrValaIleAlaGlySerArg 59
 QY 175 GTGCGCGCAACAATTGCGCGTGCATCAACAGCTGGAAGAAGACCGCGATTCGACATCG 234
 DB 60 IleAlaSerPheIleuProValaIleValaIleValaIleValaIleValaIleValaI 79
 QY 235 GGGGAAGTGCACCGCAACCGGAGTGCATTCAGTGTGCTGCTGTAAGAAGTGT--- 291
 DB 80 GlySerLeu---GlyGlyValaIleValaIleValaIleValaIleValaIleValaIle 98
 QY 292 ---AGCTGGGCTTCTTGGCGGCTGATTGACTTCTGAGCTGTTCGAGAGCCCGATAGT 348
 DB 99 AlaAlaGlyIleValaIleValaIleValaIleValaIleValaIleValaIleValaI 118
 QY 349 TTGCTGTGATCTCTGGAAGAGCCCGCAACCGGTGCAAGACTCTTCCACTTACACCGAG 408
 DB 119 PheLeuLeuValaIleuGlnuArgProGlnProAlaGlnaPheLeuPheSerPheIleTrGln 138
 QY 409 CGAGAGCCCTCCAGAGGAGAGCTGCGCCGAGAGCTTCTTCTGGCAGGTGCTGAGAGCCG 468

DB 139 ArgGlyAlaLeuAspGlyIleProLeuAlaArgArgPhePheAlaGlnValaIleAlaVal 158
 QY 469 CGGATTCGCAACAATGGGGGGTCTCCACCGCGCATCAAGACGAGAACATCTTAATC 528
 DB 159 ArgHisCysHisAspGlySerIleValaIleValaSerPheIleValaSerPheLeuVala 178
 QY 529 GACCTGAACCGCGGGAACCTCAACTGCATTCGATTCGCGTGGGCGCGCTGCTCAAGAC 588
 DB 179 AspLeuArgSerGlyIleuLeuValleuIleAspPheGlySerGlyAlaValaIleuValaP 198
 QY 589 ACGCTTCAACGCACTTTGACGGAACCGAGTGTCACAGTCTTCGAGGTGATTCGCTAC 648
 DB 199 ThrValaIleThrAspPheAspGlyIleThrValaIleYserProGlyIleTrpIleArgTyr 218
 QY 649 CATTCGTCACGAGGAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 708
 DB 219 HisArgTyrHisGlyArgSerAlaThrValaIleTrpSerLeuGlyValaIleuLeuTyrAspMet 238
 QY 709 GTCTCGAGATATTCATTTGAGACGACGAAAGATGCTCAAGGCCCAAGTGTACTTT 768
 DB 239 ValCysGlyAspIlePhePheGlnuArgIleuArgIleuValaIleuArgGlyArgLeuPheP 258
 QY 769 AGGCAAGGGTCTCTTCAGATGTCACATCTTAATGATGCTGCTGCTGCTGACCA 828
 DB 259 ArgArgValaIleSerProGlnCysGlnGlnIleuIleGlnTrpCysLeuSerLeuArgPro 278
 QY 829 TCGACCGCGCCCTCTTGAAGAATCCAGAACCATCCGTCGATG 873
 DB 279 SerGlnuArgProSerLeuAspGlnIleAlaIleAlaHisProTrpMet 293
 RESULT 10
 ID PIM3_RAT STANDARD; PRT; 326 AA.
 AC 070444;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (Protein kinase
 DE Kld-1) (Kinase induced by depolarization).
 GN Name=Pim3; Synonym=Kld1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Konietzko U., Kuhl D.;
 RT "Pim-3 is a member of the pim kinase family";
 RL Submitted (Aug-1998) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=98298176; PubMed=9632723; DOI=10.1074/jbc.273.26.16535;
 RA Feldman J.D., Vician L., Crispino M., Tocco G., Marcheselli V.L.,
 RA Bazan N.G., Baudry M., Herschman H.R.;
 RT "Kld-1, a protein kinase induced by depolarization in brain";
 RL J. Biol. Chem. 273:16535-16543(1998).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- TISSUE SPECIFICITY: Present in a number of unstimulated tissues,
 CC including brain.
 CC -1- INDUCTION: By membrane depolarization or forskolin.
 CC -1- PTM: Autophosphorylated.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
 subfamily.
 CC -----
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CC -----
DR EMBL; AF086624; AAC68900.1; ALT_INIT.
DR EMBL; AF057026; AAC36065.1; -.
DR HSP; Q03656; HKM.
DR RGD; 620462; Pim3.
DR InterPro; IPR011009; Kinase_1like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR InterPro; IPR002290; Ser_Thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Phosphorylation; Serine/threonine-protein kinase;
KW Transferrase.
FT DOMAIN 40 293 protein kinase.
FT NP_BIND 46 54 ATP (By similarity).
FT BINDING 69 69 ATP (By similarity).
FT ACT_SITE 170 170 Proton acceptor (By similarity).
SQ SEQUENCE 326 AA; 36002 MW; DD6C9BF4635F851E CRC64;

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Alignment Scores:
Pred. No.: 7,73e-65 Length: 326
Score: 1131.50 Matches: 214
Percent Similarity: 82.71% Conservative: 30
Best Local Similarity: 72.54% Mismatches: 44
Query Match: 46.32% Indels: 7
DB: 1 Gaps: 5

US-10-705-757-3 (1-1302) x PIM3_RAT (1-326)

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QY 4 ATGCTCTGTGTCAGATCAATCCCTGCGCCAGCCCT-----TGCAC 57
DB 1 MetLeuLeuSerIyPheGlySerLeuAlaHleu---CyGlyProGlyGlyValAap 19
QY 58 GACCTGCACGCCCAACAAAGCTGGCGCGCGGAA---GAGAAGAGAGCCCTGGATGCGAG 114
DB 20 HisLeuProValIyIleLeuGlnProAlaLylValAaSprIySerPheGlyIyVal 39
QY 115 TACAGAGTGGGCGCGCTGTGTGGCAGCGGCGTGGCTGGCTGATCTGAGCATCGC 174
DB 40 TyGlnValGlyIyValIleuGlySerGlyGlyPheGlyThrValIyTralaglySerIy 59
QY 175 GTCCGCGCAACTTGGCGGTCGATCAACAGCATGAGGAAGAGCGGATTTCCAGATG 234
DB 60 IleAlaSprGlyLeuProValIyValIleValIyValIySerGlyIyValIyTrIy 79
QY 235 GGGGAATCGCCCAACGCCGAGCGGCGGATGCGTCTGCGTGAAGAAGTG--- 291
DB 80 GlySerLeu---GlyIyMetAlaValProLeuGlyIyValIleuIyValIyValIy 98
QY 292 ---AGCTCGGAGCTTCTCGGCGTCAATTAAGATTCTGAGCTGTTGAGAGCGCGATAG 348
DB 99 AlaAlaGlyGlyIyAlaArgIyValIleHleGlyLeuIySerPheGlyIyValIy 118
QY 349 TTCGCTGATCTCTGAGAGAGCGCGAAGCCGCGCAAGCATCTTCAATTCACGAG 408
DB 119 PheLeuLeuValIleuGlyIyArgProGlyIyProAlaGlnAapLeuPheIleThrGln 138
QY 409 CGAGAGAGCCCTCAAGAGAGAGCTGGCGCGGAGCTTCTTGGCAGAGTGGAGCGCG 468
DB 139 ArgGlyIyAlaLeuIySerGlyIyProLeuAlaArgIyPheIleAlaIyValIyVal 158
QY 469 CGGCAATTCGCAACAGCTGGGCGTCTCAACCGCGAATCAAGAGAGCAATCTTAATC 528
DB 159 ArgHisGlySerIyValIyValIleHleArgIySerIyValIySerGlyIyValIy 178
QY 529 GACCTGAACCGCGGCAACTCAATCTGAGCTTGGGCGGCGCGCTGCTCAAGAG 588
DB 179 AspLeuArgSerGlyIyGlyIyLeuIyValIleAapPheGlySerGlyIyAlaValIy 198

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QY 589 ACAGCTCAACGAGCTTTGACGGAACCGAGTGTACAGTCTCCAGAGTGTGCTAC 648
DB 199 ThrValIyThrAapPheArgIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 218
QY 649 CATGCTACCAACGAGAGTCTGCTGTTGGCTCCGCGGATCTGCTTAATGACATG 708
DB 219 HisArgTyHisGlyIyArgSerIyAlaThrValIyTrpSerLeuGlyIyValIleuIy 238
QY 709 GTTCGCGAGATTTCTCAATTTGACACAGCAAGATGTCAAGGCCCAAGTACTTT 768
DB 239 ValCyGlyIyAapIleProPheGlyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 258
QY 769 AGGCAAGGCTCTTCAAGATGTCAACATCTTAATGATGTCGCTGCTGAGACCA 828
DB 259 ArgArgIyValSerProGlyIyGlnGlnIleuIyIyIyIyIyIyIyIyIyIyIyIy 278
QY 829 TCGAGCGGCGCTCTTGAAGAAATCAAGAACATCCGTGATG 873
DB 279 SerGlyIyArgProSerLeuIySerGlnIleAlaHleProIyPmet 293

RESULT 11
ID 0811X8 PRELIMINARY; PRT; 325 AA.
AC 0811X8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE KID1.
GN Name=Pim3; Synonyms=Kidl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Yu L.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AT026239; AAK1606.1; -.
DR HSP; Q03656; I099.
DR MGD; MGI:1355297; Pim3.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_1like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 325 AA; 35931 MW; 77DBF8B20F41B3F4 CRC64;

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Alignment Scores:
Pred. No.: 4.96e-64 Length: 325
Score: 1119.00 Matches: 213
Percent Similarity: 82.71% Conservative: 31
Best Local Similarity: 72.20% Mismatches: 43
Query Match: 45.80% Indels: 8
DB: 2 Gaps: 6

US-10-705-757-3 (1-1302) x 0811X8 (1-325)

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QY 4 ATGCTCTGTGTCAGATCAATCCCTGCGCCAGCCCT-----TGCAC 57
DB 1 MetLeuLeuSerIyPheGlySerLeuAlaHleu---CyGlyProGlyGlyValAap 19
QY 58 GACCTGCACGCCCAACAGCTGGCGCGGCAAA---GAGAAGAGAGCCCTGGATGCGAG 114
DB 20 HisLeuProValIyIleLeuGlnProAlaLylValAaSprIySerPheGlyIyVal 39

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Db 117 ILeuMetGluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAla 136
Qy 418 CTCAGAGAGAGAGCTGGGCGGAGCTTCTTCTGGAGAGTGTGGAGGCGCGGCGCATTCG 477
Db 137 LeuGlyGluGluLeuAlaThrAspPheArgGlnValAlaValAlaValArgHisCys 156
Qy 478 CACAACTGCGGGGTTCTCCACCGGACATCAAGAGAGAGAACTATTATGACCTGAC 537
Db 157 HisSerCysAspValValHisArgAspIleLeuAspGluMetIleLeuValAspLeuArg 176
Qy 538 CGCGGCGCAACTCAAACTCATGACTGCGGCGGCGGCGCTGCTCAAGAGACAGTCTAC 597
Db 177 ThrAlaGluLeuLeuLeuIleAspPheGlySerGlyAlaLeuLeuArgAspAlaValIle 196
Qy 598 ACCGACTTTTACCGGAAACCCGAGTGTACAGTCTCCAGAGTGGATTCCTGCTACATCGCTAC 657
Db 197 ThrAspPheAspArgGlyThrArgValIleSerProGluIleThrIleArgPheHisIleTyr 216
Qy 658 CACGCGAGTTCGCTGCTGTTGGTCCCTGGGAGATCCGCTGTATGACATGCTGAGGA 717
Db 217 HisGlyArgSerAlaThrValIleTrpSerLeuGlyIleLeuLeuIleAspMetValCysGly 236
Qy 718 GATATTTCATTGTAGCAGCAGAGAGATGCTCAAGGCGCAAGTGTACTTTAGGCAAGG 777
Db 237 AspIleProPheGluHisLeuAspArgGluIleLeuLeuGlySerGlyIleGlnIleArgCysArg 256
Qy 778 GTCTCTTCAAGATGTCAACATCTTATTAGATGTGCTGCTGCTGCTGAGACCATGAGACGG 837
Db 257 ValSerArgGluCysGlnHisLeuIleGluIleTrpCysLeuSerIleArgProSerAspArg 276
Qy 838 CCGCTCTTGTAGAGAAATCCAGAACCATCCGCGGATG---CAGAGATGTTCTCCG 888
Db 277 ProSerLeuGluGlnIleLeuAlaHisProIleTrpMetSerGlnHisAspPheLeu 294

RESULT 13
PIM3_XENLA STANDARD; PRT; 323 AA.
ID PIM3_XENLA 091832;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (Pim-1).
GN Name=PIM3; Synonym=PIML;
OS Xenopus laevis (African clawed frog).
OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxId=8355;
RN [1]
RX MEDLINE=7236766; PubMed=9096955; DOI=10.1074/jbc.272.16.10514;
RA Palaty C.K., Kaimar G., Tai G., Oh S., Amankawa L., Affolter M.,
RA Nebersold R., Pelech S.L.;
RT "Identification of the autophosphorylation sites of the Xenopus laevis
RT Pim-1 proto-oncogene-encoded protein kinase.";
RL J. Biol. Chem. 272:10514-10521(1997).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- P1M: Autophosphorylated.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC subfamily.
CC -1- CAUTION: Was originally (Ref.1) called Pim-1 but seems to
CC represent the pim-3 isoform.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, L29495; AAA85389.1; -.

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DR InterPro: IPR011009; Kinase like.
DR InterPro: IPR000719; Prot kinase.
DR InterPro: IPR008271; Ser Thr_pkin_AS.
DR Pfam: PF00069; Kinase; 1.
DR ProDom: PD000001; Prot kinase; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP, FALSE_NEG.
DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Phosphorylation; Serine/threonine-protein kinase;
KW Transferase.
FT DOMAIN 40 291 Protein kinase.
FT NP_BIND 46 54 ATP (By similarity).
FT BINDING 69 69 ATP (By similarity).
FT ACT_SITE 168 168 Proton acceptor (By similarity).
FT MOD_RES 4 4 Phosphoserine (by autocatalysis)
FT MOD_RES 4 4 (partial).
FT MOD_RES 190 190 Phosphoserine (by autocatalysis).
FT MOD_RES 205 205 Phosphothreonine (by autocatalysis)
FT MOD_RES 205 205 (partial).
SQ SEQUENCE 323 AA; 36964 MW; AB4DD61E7A99A3BF CRC64;

Alignment Scores:
Pred. No.: 4,62e-63 Length: 323
Score: 1104.00 Matches: 210
Percent Similarity: 76.65% Conservative: 46
Best Local Similarity: 62.87% Mismatches: 60
Query Match: 45.19% Indels: 18
Gaps: 6

US-10-705-757-3 (1-1302) x PIM3_XENLA (1-323)
Qy 4 ANGSTTTGTGCAAGATCAACTCCCTGGCCGACCTGCGGACCCCTTGCAAC----- 57
Db 1 MetLeuLeuSerIleAspPheGlySerLeuAlaHisIle-----CysAspProSer 16
Qy 58 -----GACCTGACCGCAACCAAGCTGGCGCGCGGCAAA---GAGAAAGAGACCCCTG 105
Db 17 AsnMetGluHisIleLeuProValIleLeuGlnProValIleValAspIleValProPhe 36
Qy 106 GAGTCCGAGTACCAAGTGGGCGGCGCTGTGGGAGCGGTGGCTTGGCTGCTGCTACTCG 165
Db 37 GluIleValIleGlnValAlaGlySerValAlaIleSerGlyIleGlyThrValIleTyrSer 56
Qy 166 GCGATCCGCGGTGCCCAACACTTGGCGGTGGCTCATGACGATGAGAGAGACCGGATT 225
Db 57 AspSerArgIleAlaAspArgGlnProValAlaValIleHisValAlaIleAspGluArgVal 76
Qy 226 TCCGACGTGGGAGGAACTGGCCCAAGCGCACCGGACCGGACCGGACGCTGGAAG 285
Db 77 ThrGluTrpGlyThrIleu---AsnGlyValMetValProLeuGluIleValIleLeuLeu 95
Qy 286 AAGGTAGAGTCCGGGCTTCTCGGCGCTCATTAAGCTTCTGAGTGTTCGAGAGCCCGAT 345
Db 96 IlyValProThrAlaPheArgGlyValIleAsnLeuLeuAspTrpTyrGluArgProAsp 115
Qy 346 AGTTTGTGCTGATCTCTGAGAGGCGGCAACCGGTGCAAGACTCTTCACTTCATACC 405
Db 116 AlaPheLeuIleValMetGluArgProGluProValIleAspLeuPheAspTyrIleThr 135
Qy 406 GAGCGAGAGCGCTCCAGGAGAGTGGCGCGGAGCTTCTTCCGAGAGTGTTCGAGAGGC 465
Db 136 GluIleGlyProLeuAspArgIleAspTrpAlaArgGlyPhePheArgGlnValIleGluAla 155
Qy 466 GTGCGGCAATGCAACAAGTGGGCGGTTCTCCACCGGACATCAAGAGAGAGACATCTTA 525
Db 156 ValArgHisCysValArgAsnGlyValValHisArgAspIleLeuAspArgGluMetLeu 175
Qy 526 ATGACCTGACCGCGGCGCAACTCAACTCATGACTTGGGTGGGCGCGCTGCAAG 585
Db 176 ValAspThrArgAsnIleGluLeuLeuIleAspPheGlySerGlyAlaLeuLeu 195
Qy 586 GACACAGTCTTACACGAGCTTTGACGGAACCGAGTGTACAGTCTTCAAGTGTGATTCGC 645

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Db      196 AsptHrValtYrThrAspHeaBglYthrArgValtYrSerProBglUtrpValArg 215
QY      646 TACCATCGCTACACAGCGAGCTGCGTCTGTTGGTCCCTGGAGATCCGCTCTATGAC 705
Db      216 TYNHIArgrYrHtIsgIyAsgSerAlarHValtYrSerLeuDIyValLeuEutYrAsp 235
QY      706 ATGTCGTCGAGATATTCATTCATTTGAGACGACGAAAGAGATCGTCAAGGCGCAAGTAC 765
Db      236 MeVAltYrclYAspIleProHieGluInaBglUglUleValArgValAlaGleuCyS 255
QY      766 TTTAGCGAAAGGCTCTCTTCAGAAATGTCAACATCTTATTAAGATGTGCTGCTCTGAGA 825
Db      256 PheArgrArgrIglIeSerHrGluCySgInglInleuIleYtrpCySleuSerLeuArg 275
QY      826 CCATTCGACCGCGCTCTCTTGAAGAAATTCAGAACCATCCGCTGATG---CAGGATGTT 882
Db      276 ProSerAspArgrProHrleuGluInlIePheAspHrProTrpHecCySlySvCySAsp 295
QY      883 CTCCTGCCCGCCAGCCGCGGAGATTCATCTGACACGCTGTCAACATCAACCCAGCMAA 942
Db      296 LeuValIySerIeUtlAspCySAspLeuArgrleuArgrHrIleAspHeaBglSerSer--- 314
QY      943 TAGCAGCCATTCGTGTGACACCTTCAGGAGAAAGAGAGCTTG 984
Db      315 -----SerThrSerSerSerAsnGluSerLeu 323

RESULT 14
QBR2P0 PRELIMINARY; PRT; 311 AA.
ID      01-JUN-2002 (TREMBlrel. 21, Created)
AC      01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT      01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE      Plm2 protein.
OS      Mus musculus (house).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;

SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA      Altschul S.P., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heien F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA      Brownstein M.J., Udell T.B., Toshitoki S., Carninci P., Prange C.,
RA      Raha S.S., Loeuallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Viallaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whitling R.W., Touchman J.W., Green A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakeley A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Rodriguez A.C., Skalaiba U., Smailus D.B., Schnerch A., Schein J.E.,
RA      Krzyzanski M.I., Skalaiba U., Smailus D.B., Schnerch A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]
RN      SEQUENCE FROM N.A.
RP      STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RC      Straubeberg R.;
RL      Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
CC      1-1 SMILIARITY: Belongs to the Ser/Thr protein kinase family.
DR      EMBL, BC027376; AAH27376.1;..
DR      GO; GO:0005524; P:ATP binding; IEA.
DR      GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR      GO; GO:0016740; P:transferase activity; IEA.
DR      GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

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DR      InterPro; IPR011009; Kinase like.
DR      InterPro; IPR000719; Prot kinase.
DR      InterPro; IPR002290; Ser Thr kinase.
DR      InterPro; IPR008271; Ser_thr_kin_AS.
DR      Pfam; PF00069; Kinase; 1.
DR      ProDom; PD000001; Prot_kinase; 1.
DR      SMART; SM00220; S_TKC; 1.
DR      PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR      PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW      ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ      SEQUENCE 311 AA; 34486 MW; F7B70908D23A710 CRC64;

Alignment Scores:
Pred. No.: 1,856-48 Length: 311
Score: 878.00 Matches: 173
Percent Similarity: 69.93% Conservative: 41
Best Local Similarity: 56.54% Mismatches: 79
Query Match: 35.94% Indels: 13
DB: Gaps: 4

US-10-705-757-3 (1-1302) x QBR2P0 (1-311)
QY      27 CCGGCGCCACCTGCGCGAGCCCTTGCACGACCTGCAGCGCAACGCTGCGCGG 86
Db      10 ProSerProProVal---ThrProThrGlnProPro-----Gly-Gl 22
QY      87 CAAAGAGAGAGAGCCCGCTGAGTCCGACGATACAGAGTGGCGGCTGTTGGAGCGGTG 146
Db      22 YlySAspArgrAlaAlaPheGluAlaGluTyrArgrleuGlyProLeuLeuGlylyl 42
QY      147 CTTGCGCTGCTCTACTCGGCGATCCGCTGCGCGGCAACTTGCGCGTGGCCATCAAGA 206
Db      42 YPheGlyHrValrPheAlaGlyHieArgrValThrAspArgrGlnValAlaIleYrVa 62
QY      207 CGTGAGAAAGAACCGGATTCGAGCTGGGGGAACTGCCAACGGACCGGATGCCAT 266
Db      62 IlleSerArgrAsnArgrValleuGlyTyrSerThrValSerAspSerValThrCySProle 82
QY      267 GGAAGTGTCTCTGAGAAAGAGTG-----AGCTCGAGCTTCTGCGGCTGATTCAGCT 320
Db      82 UglUValAlaUleUtrpLyVaIcYlGluGlyAsnGlyHsProGlyValIleArgrle 102
QY      321 TCTGAGCTGTTCTGAGAGCGCCGATAGTTCTGCTGATCTGAGAGCGCCGACCCGT 380
Db      102 UleuAspTrpPheGluThrProGluGlyPheUleUValleuGluArgrPromerProAl 122
QY      381 GCAAGACTCTTCTGACTTCATCAACGAGCGAGAGCCCTCCAGAGAGAGCTGCCGAG 440
Db      122 agInAspLeuPheAspTyrIleThrGluYsgIleProleuGlyGluSerCySserArgrSe 142
QY      441 CTTCTTCTGAGAGCTGAGCGCGCGGCGGATTCGCAACCTGCGGGGTTCTCCACCG 500
Db      142 rPhePheHrGrInValAlaValAlaValAlaValAlaValAlaValAlaValAlaVal 162
QY      501 CGAGATCAAGAGACGAGACATCTTAATGCACTGAACCGCGGGAATCAAACTCATCGA 560
Db      162 gAspIleYrAspGluAsnIleUleUleAspLeuCySArgrGlySerIleYsleUleAs 182
QY      561 CTTGCGGTGGGGCGCTGCTCAAGAGACAGTTCACGAGACTTTCAGCGAACTTGAGCT 620
Db      182 pPheGlySerGlyAlaLeuUleUleIleAspGluProTyrThrAspPheAspGlyThrArgrVa 202
QY      621 GTTACATCTCTCAGAGATGATTCGATCAAGATCGCTACACGAGAGCTCGGCTGCTTTG 680
Db      202 lYrSerProProGluTrrpIleSerArgrHsGlnTyrHsAlaLeuProAlaHrValtr 222
QY      681 GTCCCTGGGAGATCTGCTATGACATGTGCTGCGAGATATTCATTTGAGACGACGA 740
Db      222 pSerleuGlyValleuUleUleUleUleUleUleUleUleUleUleUleUleUleUle 242
QY      741 AGAGATGTCAAGAGCGCAAGTACTTTAAGCGAAAGGTCCTTCAAAATGTCAACATCT 800

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Db      242  ngulileuGlulabglutueHispheProAlaHisValSerProabpCyScyAlaLe 262
Qy      801  TATTAGATGCTGCTGCTCCCTGAGACCATGACCGCCCTCTTGAAGAATCCAGAA 860
Db      262  uilleaGArxCyaleuAlaProLySpCySerArgProSerLeuGlulLeuLe 282
Qy      861  CCATCCGATGATGAGATGTTCTCCCGCCGAGCCGACCGGAGATTGATCGACAG 920
Db      282  uabpProtpmEgHiser-----ProAlaGlululypProIleamSerSery 299
Qy      921  CCTGTACATCAACCC 936
Db      299  sglYserProThrPro 304

RESULT 15
PIM2_MOUSE
ID      PIM2_MOUSE      STANDARD;      PRT;      370 AA.
AC      Q62070; Q62071; Q62072;
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Serine/threonine-protein kinase Pim-2 (EC 2.7.1.37).
GN      Name=Pim2; Synonyms=Pim-2;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=95300786; Pubmed=7781606;
RA      van der Lugt N.M., Domen J., Verhoeven B., Linders K.,
RT      "Proviral tagging in B mu-myc transgenic mice lacking the Pim-1 proto-
RL      oncogene leads to compensatory activation of Pim-2.";
EMBO J. 14:2536-2544(1995).
CC      -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC      -1- ALTERNATIVE PRODUCTS:
CC      Event=Alternative initiation;
CC      Comment=3 isoforms, 1 (shown here), 2 and 3, are produced by
CC      alternative initiation. Isoform 1 and isoform 2 initiate from
CC      CTG codons;
CC      -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC      subfamily.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@sb-slb.ch).
CC      -----
DR      EMBL; LA1495; AAA98922.1; -
DR      EMBL; LA1495; AAA98923.1; -
DR      FIRM; LA1495; AAA98924.1; -
DR      FIRM; S55333; S55333.
DR      HSSP; Q63450; 1A06.
DR      MGD; MGI:97587; Pim2.
DR      GO; GO:0005515; P:protein binding; IPI.
DR      GO; GO:0004674; P:protein serine/threonine kinase activity; IDA.
DR      GO; GO:0006916; P:anti-apoptosis; IDA.
DR      GO; GO:0006371; P:apoptotic mitochondrial changes; IDA.
DR      InterPro; IPR001109; Kinase-like.
DR      InterPro; IPR000719; Proc_kinase.
DR      InterPro; IPR008271; Ser_thr_kin AS.
DR      InterPro; IPR002290; Ser_thr_kinase.
DR      Pfam; PF00069; Pkinase; 1.
DR      ProDom; PD000001; Proc_kinase; 1.
DR      SMART; SM00220; S_TKc; 1.
DR      PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR      PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR      PROSITE; PS00108; PROTEIN KINASE_SF; 1.
KM      Alternative initiation; ATP-binding; Phosphorylation;

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KW      Serine/threonine-protein kinase; Transferase.
FT      CHAIN      1      370      Serine/threonine-protein kinase Pim-2,
FT      CHAIN      26      370      isoform 1.
FT      CHAIN      60      370      Serine/threonine-protein kinase Pim-2,
FT      CHAIN      60      370      isoform 2.
FT      CHAIN      60      370      Serine/threonine-protein kinase Pim-2,
FT      CHAIN      60      370      isoform 3.
FT      INIT_MET      26      26      For isoform 2.
FT      INIT_MET      60      60      For isoform 3.
FT      DOMAIN      91      345      Protein kinase.
FT      NP_BIND      97      105      ATP (By similarity).
FT      BINDING      120      120      ATP (By similarity).
FT      ACT_SITE      222      222      Proton acceptor (By similarity).
SQ      SEQUENCE      370 AA; 40059 MW; 12BB70BFDD04DBE8A CRC64;

Alignment Scores:
Pred. No.:      1,91e-48      Length:      370
Score:      878.00      Matches:      173
Percent Similarity:      69.93%      Conservative:      41
Best Local Similarity:      56.54%      Mismatches:      79
Query Match:      35.94%      Indels:      13
DB:      Gaps:      4

US-10-705-757-3 (1-1302) x PIM2_MOUSE (1-370)
Qy      27  CCTGCCCACTGCGCGGACGCCCTTGCAACGACTGCACGCCACAGCTGCGCGG 86
Db      69  ProSerProProVal---ThrProThrGlnProPro-----Gly-Gl 81
Qy      87  CAAAGAGAGAGAGCCCTGAGTGCATGACGAGGAGGCGGCTGTGGGAGCGGTG 146
Db      81  ylybaPaPaGAlaAlaPheGluAlaGluTyrArgLeuGlyProLeuLeuGlyGly 101
Qy      147  CTTGCGCTGCTTACTCTCGGAGATCCGCTCGCCGCAACTTGCCCGCATCAAGA 206
Db      101  yPheGlyThrValPheAlaGlyHisArgValThrbaPaPaGAlaAlaLeuVal 121
Qy      207  CGTGAGAGAGACCGGATTTCCGACTGGGGGAGAACTGCCAAGCGACCCGAGTCC 266
Db      121  lIleSerArgAmArgValLeuGlyTyrSerThrValSerArgSerValThrCysPro 141
Qy      267  GGAAGTGTGCTGCTGAAGAAGTG-----AGCTGGGCTTCTGGGGCTATTGACT 320
Db      141  uGluValAlaLeuLeuTyrPlyValGlyGlyLeuGlyHisProGlyValIleArg 161
Qy      321  TCTGAGCTGTTGAGAGGCGCGATGATTGCTGATCTGAGAGGCGCGAACCCT 380
Db      161  uLeuArgTyrPheGlyThrProGluGlyPheMetLeuValLeuGluArgProMetPro 181
Qy      381  GGAAGACTCTTGCACTTCATGACCGAGCGAGAGCCCTCCAGAGAGACTGGCCGAG 440
Db      181  aGlnaPheLeuPheAspTyrIleThrGluPheGlyProLeuGlyGlySerCysSerArg 201
Qy      441  CTTTCTTGGAGAGTGTGAGAGCGGTGGGATTCGCCCAACTGGGGGTTCTCCAC 500
Db      201  rPhePheThrGlnValAlaValAlaValGlnHisCysHisAlaArgGlyValValHis 221
Qy      501  CGACATCAAGAGACGAGACATCTTAATGACCTGAACCGCGGCGAATCAATCTCA 560
Db      221  gAspIleuValaPheGluValaHisIleuLeuAspLeuValaGlySerIleLeuLeu 241
Qy      561  CTTTGGGCTGGGGCGGTGCTCAAGACACAGTTCACGAGACTTTCAGGAACTGGAG 620
Db      241  pPheGlySerGlyAlaIleuLeuHisAspIleuProTyrThrAspPheAspGlyThrArg 261
Qy      621  GTAAGTCTCGAGAGTGGATTCGATACCATGATCAACGCGGAGTGGCTGGTGG 680
Db      261  lTyrSerProProGluTyrPheSerArgHisGlnTyrHisAlaLeuProAlaThrVal 281
Qy      681  GTCCCTGGGAGATCTGCTCTATGACATGCTGCGGAGATATTCATTTGACAGAGCA 740
Db      281  pSerLeuGlyValLeuLeuTyrAspMetValCysGlyAspIleProPheGluArgAsp 301

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus.n2p model

Run on: September 22, 2005, 16:20:36 ; Search time 34.242 Seconds
(without alignments)
5676.828 Million cell updates/sec

Title: US-10-705-757-3

Perfect score: 2443
Sequence: 1 gggatgcctctgcacaaat.....ggattaaaactgacacat 1302

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2.1/USPTO.spool.p/US10705757/runat.22092005.115016.22154/app.query.fasta_1.5333
-DB=Issued_Patents_AA -OFMT=faстан -SUFPTX=n2p.ra1 -MINMATCH=0.1 -LOOPTCL=0
-LOOEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdt
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptco -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10705757@cgn2.1.137 @runat.22092005.115016.22154 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_AA.*
1: /cgn2_6/ptodata/1/1aa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTUS COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1668	68.3	313	3	US-09-237-543-8
2	1668	68.3	313	3	US-09-644-450-8
3	1636	67.0	313	3	US-09-237-543-9
4	1636	67.0	313	3	US-09-644-450-9
5	1623	66.4	313	2	US-08-463-081B-26
6	1623	66.4	313	2	US-08-461-379A-26
7	1623	66.4	313	2	US-08-462-390B-26
8	1623	66.4	313	3	US-08-463-074B-26
9	1623	66.4	313	3	US-08-465-585C-26
10	1623	66.4	313	3	US-08-652-446-26
11	1584	64.8	313	3	US-09-237-543-7
12	1584	64.8	313	3	US-09-644-450-7

13	1304.5	53.4	257	2	US-07-857-224B-41	Sequence 41, Appl
14	1136.5	46.5	326	3	US-09-237-543-2	Sequence 2, Appl
15	1136.5	46.5	326	3	US-09-644-450-2	Sequence 2, Appl
16	1131.5	46.3	345	3	US-09-237-543-5	Sequence 5, Appl
17	1131.5	46.3	345	3	US-09-644-450-5	Sequence 5, Appl
18	1104	45.2	323	3	US-09-237-543-6	Sequence 6, Appl
19	1104	45.2	323	3	US-09-644-450-6	Sequence 6, Appl
20	1083.5	44.4	254	3	US-09-237-543-4	Sequence 4, Appl
21	1083.5	44.4	254	3	US-09-644-450-4	Sequence 4, Appl
22	867.5	35.5	372	4	US-09-949-016-7140	Sequence 7140, Ap
23	392	16.0	778	4	US-10-116-326-2	Sequence 2, Appl
24	392	16.0	778	4	US-10-003-690-2	Sequence 2, Appl
25	374	15.3	1101	3	US-09-770-170-8	Sequence 8, Appl
26	372	15.2	512	4	US-09-633-328B-2	Sequence 2, Appl
27	370.5	15.2	511	4	US-09-633-328B-4	Sequence 4, Appl
28	370.5	15.2	630	4	US-10-355-975A-38	Sequence 38, Appl
29	370.5	15.2	776	4	US-09-523-849-34	Sequence 34, Appl
30	370	15.1	631	4	US-09-579-664B-11	Sequence 11, Appl
31	370	15.1	631	4	US-10-355-975A-11	Sequence 11, Appl
32	366.5	15.0	1323	3	US-09-770-170-2	Sequence 2, Appl
33	366	15.0	1356	3	US-09-770-170-6	Sequence 6, Appl
34	361.5	14.8	668	4	US-09-523-849-32	Sequence 32, Appl
35	360.5	14.8	793	4	US-09-930-181-2	Sequence 2, Appl
36	353.5	14.5	281	4	US-09-248-796A-20512	Sequence 20512, A
37	353	14.4	779	4	US-08-817-832B-31	Sequence 31, Appl
38	349	14.3	703	4	US-10-116-326-6	Sequence 6, Appl
39	347	14.2	1005	3	US-09-770-170-4	Sequence 4, Appl
40	345	14.1	418	4	US-09-248-796A-18441	Sequence 18441, A
41	344	14.1	722	4	US-08-817-832B-32	Sequence 32, Appl
42	343.5	14.1	360	4	US-09-248-796A-20497	Sequence 20497, A
43	343	14.0	722	4	US-09-984-890-4	Sequence 4, Appl
44	343	14.0	722	4	US-10-274-194-4	Sequence 4, Appl
45	342.5	14.0	724	4	US-09-984-890-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-237-543-8
; Sequence 8, Application US/09237543A
; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-237-543-8

Alignment Scores:

Pred. No.: 4.27e-131
Score: 1668.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 68.28%
DB: 3
Gaps: 0

US-10-705-757-3 (1-1302) x US-09-237-543-8 (1-313)
QY 4 AAGCTTTTCAGATGCACTCCCTGGCCGACGAGCCCTTGACAGCAGT 63
DB 1 MetLeuLeuSerIyIleasnSerIleuAlaHsIleuArgAlaIaProCyasnApIleu 20
QY 64 CAGCCCAAGAGCTGGCCGCGGCAAGAAGAGAGAGCCCTGGAGTCGAGTACAGT 123
DB 21 HIsIAshuIyIleuAlaIaProGlyIyIyGluIyGluIyProIeuIuSerIntyIyIyAl 40

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QY      124  GGCCGCGCTGTTGGGAGCCGGTGGCTTGGGCTGGCTGTACTCCGGGACATCCGCGCCGAC 183
DB      41  GLLPRLLEULEUYSERGLYGLYPHEGLYSERVALTYLSERGLYILEARGVALALASP 60
QY      184  AACTTCGCGGTGGCCATCAAGCACTGGAGAAAGAACCGGATTTCTGACTGGGGGAACTG 243
DB      61  AANLEUPROVALALATLEUYSNLSVALGLULYASAPARGILESERAPRTPGLYGLULEU 80
QY      244  CCCAAGCGCAACCCGAGTGGCCATGGAAGTGTCTCTGTAAGAAAGGTGAGCTCGGGCTTC 303
DB      81  PROANGLYTHRARGVALPROMETGLUVALLEULEULYVALSERSEGLYPHE 100
QY      304  TGGGGGCGTATTAAGATTTGGACTGGTTCCAGAGGCGCGGATPAGTTTCGGCTGATCCG 363
DB      101  SERGLYVALILEARGLEULEUMAPRTPRHEGLUARGPROASPSERPHEVALLEULEU 120
QY      364  GAGAGCGCCGAACCCGTGCAAGACTCTTCGACTTATCAACGAGCGAAGCCCTCCAG 423
DB      121  GLUARGPROGLUPROVALGINAPRLEUPRHEPHEILETHGLUARGGLYALALEUGLN 140
QY      424  GAGAGCTGGCCCGGAGCTTTCTTGGCAAGTGTCTGAGGCGCGCTGGCCATTGCCAAGC 483
DB      141  GLUGLULEUALARGSERPHEPHEIHPGINVALLEUGLUALVALARGHISCYNSIASAN 160
QY      484  TGGCGGGTCTCCAGCGCGCATCAAGAGCAAGAAACATCTTAATGACCGCTGAACCGCGGC 543
DB      161  CYSGLYVALLEUNHISARGAPRIILEUYSAPRGLUASNILEULILEAPRLEUMAPRGLY 180
QY      544  GAACCTAAATCATTCGACTTCGGGTCGGGGCGCTGCTCAAGGACACAGTCTTACACGAGC 603
DB      181  GLULEULYLEUNILEAPRHEGLYSERGLYALALEULEULYASPRHVALTYRTHRMAP 200
QY      604  TTTGACGGAACCCGAGTGTACAGTCTCCAGAGTGGATTCGCTACCAATGGCTACACGCGC 663
DB      201  PHEAPRGLYTHRARGVALTYRSEPRPROGLUTPRILEARGTYRHSARGTYRHSGLY 220
QY      664  AGGTGGCTGCTGTTGGTCCCTGGGGATCTGCTCATGACATGGTGTCCGAGATATT 723
DB      221  ARGSERLAIALVALTRPSERLEUNGLYLEULEUNTYRHPMETVALCYSGLYAPRIILE 240
QY      724  CCATTGAGCAGCAGAAAGATGTCAGAGGCGCAAGTGTACTTTAGGAAAGGCTCTCT 783
DB      241  PROPHEGLUNHISAPRGLUINILEVALYSGLYGLINVALTYRPHARGLINARGVALSER 260
QY      784  TCAGATGTCAACATCTTATTAAGATGGCTGCTCCCTGAGACATCGGACCGGCGCTCC 843
DB      261  SERGLUCYSGNLHISLEULILEARGTYRCYLEUSERLEUARGPROSERAPRTRGPROSER 280
QY      844  TTGGAAGAAATCCAGAACCATCCGATGATGATGATGTTCTCTGCGCCAGGCGCACGCGC 903
DB      281  PHEGLUGLULIEGLINAPRHSPTROTTPMETGINAPRVALLEULEUPROGLINALTHRALA 300
QY      904  GAGATTCAATCTGCACAGCCTGTACACATCAACCCAGCAAA 942
DB      301  GLULIEHISLEUNHISERLEUSERPROSERPROSERLYS 313

RESULT 2
US-09-644-450-8
; Sequence 8, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 313
; TYPE: PRT

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; ORGANISM: Rattus norvegicus
US-09-644-450-8
Alignment Scores:
Pred. No.: 4,27e-131
Score: 1668.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 68.28%
DB: 3 Gaps: 0

US-10-705-757-3 (1-1302) x US-09-644-450-8 (1-313)
QY      4  ATGCTCTTGCCAAAGATAACTCCCTGGCGCCACTGGCGGACGCCCTTGCAAGCACTG 63
DB      1  NEULLEUSERLYLEHNSERLEUNHISLEUAPRGLIALAPROCYANAPRLEU 20
QY      64  CAGCCCAACAACTGGCGCCCGGCAAGAAAGAACCCCTGGAATCGCAGTACCAAGTGT 123
DB      21  HISLALANULYBLEUALPROGLYRGLYUGLUPROLEUGLUSERGLINTYRGLINVAL 40
QY      124  GGCCGCGCTGTTGGGAGCGGTGGCTTGGCTGGCTACTCGGGCATCCGCGTCCGCGAC 183
DB      41  GLYPROLEULEUGLYSERGLYGLYPHEGLYSERVALTYRSEGLYILEARGVALALASP 60
QY      184  AACTTCGCGGTGGCCATCAAGCACTGGAGAAAGAACCGGATTTCTGACTGGGGGAACTG 243
DB      61  AANLEUPROVALALATLEUYSNLSVALGLULYASAPARGILESERAPRTPGLYGLULEU 80
QY      244  CCCAAGCGCAACCCGAGTGGCCATGGAAGTGTCTCTGTAAGAAAGGTGAGCTCGGGCTTC 303
DB      81  PROANGLYTHRARGVALPROMETGLUVALLEULEULYVALSERSEGLYPHE 100
QY      304  TGGGGGCGTATTAAGATTTGGACTGGTTCCAGAGGCGCGGATPAGTTTCGGCTGATCCG 363
DB      101  SERGLYVALILEARGLEULEUMAPRTPRHEGLUARGPROASPSERPHEVALLEULEU 120
QY      364  GAGAGCGCCGAACCCGTGCAAGACTCTTCGACTTATCAACGAGCGGACCGCTCCAG 423
DB      121  GLUARGPROGLUPROVALGINAPRLEUPRHEPHEILETHGLUARGGLYALALEUGLN 140
QY      424  GAGAGCTGGCCCGGAGCTTTCTTGGCAAGTGTCTGAGGCGCGCTGGCCATTGCCAAGC 483
DB      141  GLUGLULEUALARGSERPHEPHEIHPGINVALLEUGLUALVALARGHISCYNSIASAN 160
QY      484  TGGCGGGTCTCCAGCGCGCATCAAGAGCAAGAAACATCTTAATGACCGCTGAACCGCGGC 543
DB      161  CYSGLYVALLEUNHISARGAPRIILEUYSAPRGLUASNILEULILEAPRLEUMAPRGLY 180
QY      544  GAACCTAAATCATTCGACTTCGGGTCGGGGCGCTGCTCAAGGACACAGTCTTACACGAGC 603
DB      181  GLULEULYLEUNILEAPRHEGLYSERGLYALALEULEULYASPRHVALTYRTHRMAP 200
QY      604  TTTGACGGAACCCGAGTGTACAGTCTCCAGAGTGGATTCGCTACCAATGGCTACACGCGC 663
DB      201  PHEAPRGLYTHRARGVALTYRSEPRPROGLUTPRILEARGTYRHSARGTYRHSGLY 220
QY      664  AGGTGGCTGCTGTTGGTCCCTGGGGATCTGCTCATGACATGGTGTCCGAGATATT 723
DB      221  ARGSERLAIALVALTRPSERLEUNGLYLEULEUNTYRHPMETVALCYSGLYAPRIILE 240
QY      724  CCATTGAGCAGCAGAAAGATGTCAGAGGCGCAAGTGTACTTTAGGAAAGGCTCTCT 783
DB      241  PROPHEGLUNHISAPRGLUINILEVALYSGLYGLINVALTYRPHARGLINARGVALSER 260
QY      784  TCAGATGTCAACATCTTATTAAGATGGCTGCTCCCTGAGACATCGGACCGGCGCTCC 843
DB      261  SERGLUCYSGNLHISLEULILEARGTYRCYLEUSERLEUARGPROSERAPRTRGPROSER 280
QY      844  TTGGAAGAAATCCAGAACCATCCGATGATGATGATGTTCTCTGCGCCAGGCGCACGCGC 903
DB      281  PHEGLUGLULIEGLINAPRHSPTROTTPMETGINAPRVALLEULEUPROGLINALTHRALA 300

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QY 904 GAGATTCATCTGCACAGCTTGTACCATCCAGCAAA 942
Db 301 GUILIEHLEUHISSERLEUSERPROGILYPROSERLYS 313

RESULT 3

US-09-237-543-9
Sequence 9, Application US/09237543A
Patent No. 6143540
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/237, 543A
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
US-09-237-543-9

Alignment Scores:

Pred. No.:	2,02e-128	Length:	313
Score:	1636.00	Matches:	304
Percent Similarity:	99.04%	Conservative:	6
Best Local Similarity:	97.12%	Mismatches:	3
Query Match:	66.97%	Indels:	0
DB:	3	Gaps:	0

US-10-705-757-3 (1-1302) x US-09-237-543-9 (1-313)

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Db 1 MetLeuLeuSerLySLeaSenSerLeuAlaHISLeuArgAlaAlaProCySaenApleu 20
QY 64 CAGGCCAACAGCTGGCGCCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
Db 21 HIsAlaThrLyLeuAlaProGILyGILyGILyGILyGILyGILyGILyGILyGILy 40
QY 124 GGCCTGCTGTTGGGCGAGCGGTGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 183
Db 41 GlyProLeuLeuLysSerGILyGILyPheGILySerValLySerGILyLeaGILySerPhe 60
QY 184 AACTTCCCGGTGGCCATCAAGACGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
Db 61 AsnLeuProValAlaIleLySHISValGILyAspArgILySerAspTrpGILyGILyLeu 80
QY 244 CCGAAGCGCACCCGAGTGGCCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 303
Db 81 ProAsnGILyThrArgValProMetGILyValValLeuLeuLySValSerSerGILyPhe 100
QY 304 TCGGCGGTCTTGAAGTCTTGAAGTCTTGAAGTCTTGAAGTCTTGAAGTCTTGAAGTCT 363
Db 101 SerGILyValIleArgLeuLeuAspTrpPheGILyArgProAspSerPheValLeuIleLeu 120
QY 364 GAGAGCGCCGAGACCCGTGCAAGACTTCTTGAAGTCTTGAAGTCTTGAAGTCTTGAAG 423
Db 121 GluArgProGILyProValGILyAspLeuPheAspPheIleThrGILyArgGILyAlaLeuGILy 140
QY 424 GAGAGCTGGCCCGGAGACTTCTTGAAGTCTTGAAGTCTTGAAGTCTTGAAGTCTTGAAG 483
Db 141 GluGILyLeuAlaIleArgSerPhePheTrpGILyValLeuGILyAlaValIleArgHISCySHISAsn 160
QY 484 TGGCGGGTCTTGCACCGCGCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 543
Db 161 CySHISValLeuHISArgAspILyLeuAspGILyAsnIleLeuIleAspLeuAsnArgGILy 180
QY 544 GAACTCAAACTCATCGACTTGGGCTGGGGCGCTGCTCAAGAGACAGTCTACAGGAG 603
Db 181 GluLeuLySLeuIleAspPheGILySerGILyAlaLeuLeuLySAspThrValTyTrpAsp 200

QY 604 TTTGAGGAACCCGAGTGTACAGTCTCCAGAGTGTGATTCGTACCATCGACGCG 663
Db 201 PheAspGILyThrArgValLySerProProGILyTrpIleArgTrpHISArgTrpHISGILy 220
QY 664 AGGTGCGTGTCTTGTGCTCCCTGGGATCTCTGCTATGACATGCTTGGAGATATT 723
Db 221 ArgSerAlaAlaValIlePheLeuGILyIleLeuLeuTyAspMetValCySHISArgPhe 240
QY 724 CCAATTGAGCAGCAGAGAGATCTTCAGAGGCGCAAGTGTACTTTAGGCAAGGCTCT 783
Db 241 ProPheGILyHISAspGILyIleIleArgGILyGILyAlaPhePheArgGILyValSer 260
QY 784 TCAGATGTCAACATCTTATGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 843
Db 261 SerGILyGILyHISLeuIleArgTrpCySLeuAlaLeuArgProSerAspArgProTrp 280
QY 844 TTTGAGGAATCCAGAACCATCCGTGAGATGACAGATGTTCTCTGCTCCAGGCGCC 903
Db 281 PheGILyGILyIleGILyHISProTrpMetGILyAspValLeuLeuProGILyTrpAla 300
QY 904 GAGATTCATCTGCACAGCTTGTACCATCCAGCAAA 942
Db 301 GUILIEHLEUHISSERLEUSERPROGILYPROSERLYS 313

RESULT 4

US-09-644-450-9
Sequence 9, Application US/09644450
Patent No. 6383791
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/644, 450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
US-09-644-450-9

Pred. No.:	2,02e-128	Length:	313
Score:	1636.00 <td>Matches:</td> <td>304</td>	Matches:	304
Percent Similarity:	99.04% <td>Conservative:</td> <td>6</td>	Conservative:	6
Best Local Similarity:	97.12% <td>Mismatches:</td> <td>3</td>	Mismatches:	3
Query Match:	66.97% <td>Indels:</td> <td>0</td>	Indels:	0
DB:	3	Gaps:	0

US-10-705-757-3 (1-1302) x US-09-644-450-9 (1-313)

QY 4 ATGCTTTGTCCAGATCACTCCCTGGCCACCTGGCCGAGCCCTTGCACGACTG 63
Db 1 MetLeuLeuSerLySLeaSenSerLeuAlaHISLeuArgAlaAlaProCySaenApleu 20
QY 64 CAGGCCAACAGCTGGCGCCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
Db 21 HIsAlaThrLyLeuAlaProGILyGILyGILyGILyGILyGILyGILyGILyGILy 40
QY 124 GGCCTGCTGTTGGGCGAGCGGTGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 183
Db 41 GlyProLeuLeuGILySerGILyGILyPheGILySerValLySerGILyLeaGILySerPhe 60
QY 184 AACTTCCCGGTGGCCATCAAGACGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
Db 61 AsnLeuProValAlaIleLySHISValGILyAspArgILySerAspTrpGILyGILyLeu 80
QY 244 CCGAAGCGCACCCGAGTGGCCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 303
Db 81 ProAsnGILyThrArgValProMetGILyValValLeuLeuLySValSerSerGILyPhe 100

QY 664 AGGTGGCTGCTGTTTGGTCCCTGGGATCCTGCTATGACATGATGCTGGAGATATT 723
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 Db 221 ATGSerialalalvalttrpserleuglylleuleuetyrasmpevalcysglyaspille 240
 QY 724 CCAATTGAGACGACGAGAGATGCTGACAGGCCAGTGTACTTTAGCAAGGGTCTCT 783
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 Db 241 ProPhetgluhlaaprglugluilleleargglylinalphepheargglinalgvalser 260
 QY 784 TCGAATGTCACATCTTTATTAATGATGGTGCCTGCTCCCTGAGACCATGAGCCGGCTCC 843
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 Db 261 SerGluCyeglhlhlaeuileartrpCyaleuhalaleuarpProserAapArgProthr 280
 QY 844 TTGAAGAATCCAGAACCATCCGATGATGACGAGATGTTCTCCGCGCCGACGACCGCC 903
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 Db 281 PheglugluilleghlnamhlsprottrpmetcglinaspvalleuarpProglnglutnrala 300
 QY 904 GAGATTCATCTGCACAGCCTGTGACCATCAACCAGCAA 942
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 Db 301 GluilehlaeuhiSerleuSerProglyProserlyse 313
 RESULT 6
 US-08-461-379A-26
 / Sequence 26, Application US/08461379A
 / Patent No. 5871961
 / GENERAL INFORMATION:
 / APPLICANT: Smith, Kendall A. & Beadling, Carol
 / TITLE OF INVENTION: Nucleic Acids Encoding CMS Polypeptide,
 / TITLE OF INVENTION: Vector and Transformed Cell Thereof, and
 / NUMBER OF SEQUENCES: 35
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Ratner & Prescila
 / ADDRESS: (B) STREET:One Westlakes-Berwyn
 / CITY: Valley Forge
 / STATE: Pennsylvania
 / COUNTRY: USA
 / ZIP: 19482
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0,
 / SOFTWARE: Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/461,379A
 / FILING DATE: 5-JUNE-1995
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US98 08/330,108; 08/104,736
 / APPLICATION NUMBER: 4 07/796,066
 / FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Viviana Amzel, Ph. D.
 / REGISTRATION NUMBER: 30,930
 / REFERENCE/DOCKET NUMBER: DART-070
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (610)470-0700
 / TELEFAX: (610)470-0701
 / INFORMATION FOR SEQ ID NO: 26:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 313 amino acids
 / TYPE: peptide
 / STRANDEDNESS: n.a.
 / TOPOLOGY: n.a.
 / MOLECULE TYPE: peptide
 / US-08-461-379A-26
 Alignment Scores:
 Pred. No.: 2,46e-127 Length: 313
 Score: 1623.00 Matches: 302
 Percent Similarity: 98.40% Conservative: 5
 Best Local Similarity: 96.49% Mismatches: 6
 Query Match: 66.43% Indels: 0
 DB: 2 Gaps: 0

US-10-705-757-3 (1-1302) x US-08-461-379A-26 (1-313)
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 QY 64 CAGGCCAACAGCTGGCGCGCGGACAAAGAGAGACCCCTTGAGTCCGACGTACAGGT 123
 |||||
 Db 21 HlsalathrllyleuAlaproglylysgluylsgluproleuJubserglntyrGlinal 40
 QY 124 GGCCCGCTGTGGGACGCGGTGCTCGGCTCGGTCTACTCGGGACATCCGCTCGCCGAC 183
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 Db 41 GlyProleuLeucllyserglylypneghlyserValtySercllyleargvalSerasp 60
 QY 184 AACTTCGCGGTGCGCATCAAGCAGTGAAGAAAGAACCGAATTCGATCGGGGAAATG 243
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 Db 61 AenleuProvalAlahlelyshlsValglulysAspArgllSerAsprrpGlyluleu 80
 QY 244 CCGAAGGACCCGAGTCCCATGAGAGTGTCTCTGTAAGAGAGTGAAGTCTGGGCTTC 303
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 Db 81 ProAsnglyThrtrgvalProwetGluvalleuLeuyllyValSerSerGlyphe 100
 QY 304 TCGGCGGTATTAAGACTTCTGACTGCTGAGAGGCGCGATGATTGCTGATCTCTG 363
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 Db 101 SerGlyValilleargleuLeuaprrpneghlualrgProhserPhevalleu 120
 QY 364 GAGAGCGCGAACCCGTGACAGACTTTCGATTCATCAACGAGGAGAGGCGCTTCAG 423
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 Db 121 GluarGProgluprovalGlnleuPheaspPhelethrculnrglylaleuGln 140
 QY 424 GAGAGCTGGCCCGGAGCTTCTTCTGCGAGGTCTGAGGCGCTGGGCAATTGCCACAC 483
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 Db 141 GluGluleuAlarGserPhePetrpGlnvalleuGluAlahlglyshlsAsn 160
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 Db 221 ATGSerialalalvalttrpserleuglylleuleuetyrasmpevalcysglyaspille 240
 QY 724 CCAATTGAGACGACGAGAGATGCTGACAGGCCAGTGTACTTTAGCAAGGGTCTCT 783
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 Db 241 ProPhetgluhlaaprglugluilleleargglylinalphepheargglinalgvalser 260
 QY 784 TCGAATGTCACATCTTTATTAATGATGGTGCCTGCTCCCTGAGACCATGAGCCGGCTCC 843
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 Db 261 SerGluCyeglhlhlaeuileartrpCyaleuhalaleuarpProserAapArgProthr 280
 QY 844 TTGAAGAATCCAGAACCATCCGATGATGACGAGATGTTCTCCGCGCCGACGACCGCC 903
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 Db 281 PheglugluilleghlnamhlsprottrpmetcglinaspvalleuarpProglnglutnrala 300
 QY 904 GAGATTCATCTGCACAGCCTGTGACCATCAACCAGCAA 942
 |||||
 Db 301 GluilehlaeuhiSerleuSerProglyProserlyse 313
 RESULT 7
 US-08-462-390B-26
 / Sequence 26, Application US/08462390B
 / Patent No. 5882894
 / GENERAL INFORMATION:
 / APPLICANT: Smith, K. A., & Beadling, C.

NAME: Viviana Amzel, Ph. D.
 REGISTRATION NUMBER: 30,930
 REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 622-7700
 TELEFAX: (213) 489-4210
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 313 amino acids
 TYPE: peptide
 STRANDEDNESS: n.a.
 TOPOLOGY: n.a.
 MOLECULE TYPE: peptide
 US-08-463-074B-26

Alignment Scores:
 Pred. No.: 2,46e-127 Length: 313
 Score: 1623.00 Matches: 302
 Percent Similarity: 98.40% Conservative: 6
 Best Local Similarity: 96.43% Mismatches: 5
 Query Match: 66.43% Indels: 0
 DB: Gaps: 0

US-10-705-757-3 (1-1302) x US-08-463-074B-26 (1-313)

4 ATGCTCTGTCGAAGATCAACTCCCTGGCCCGGAGAGCCCTTGCAGACGCTG 63
 1 MetLeuLeuSerYylleasenseLeuAlaHisLeuAlaArgAlaCybaanAapLeu 20
 64 CAGCGCAACAGCTGGCGCGGCGCAAGAGAGAGCCCTGAGAGTGCAGTACAGAGT 123
 21 HleAlaThrlyLeuAlaProGlylyGlyLeuGluProLeuGluSerGlnTyrGlnVal 40
 124 GGCCTGCTGGGCGAGCGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 183
 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValSerAap 60
 184 AACCTGGCGGCTGGCATCAAGACGCTGAGAGAGAGAGCCGATTCGAGCGGAGAGCTG 243
 61 AenLeuProValAlaIleYbHsValGluYbAapArgIleSerAapTrpGlyGluLeu 80
 244 CCCAGCGGCAACCGAGTGCATGAGAGTGTCTGCTGAGAGAGAGTGTGAGCTGCTG 303
 81 ProAenGlyThrArgValProMetGluValValLeuLeuYbValSerSerGlyPhe 100
 304 TCGGCGCTCATTAAGCTTCTGAGCTGCTGAGAGCGCGGATAGTTTCTGCTGATCTG 363
 101 SerGlyValIleArgLeuLeuAapTrpPheGluArgProAapSerPheValLeuIleLeu 120
 364 GAGAGCGCGCAACCGCTGCAAGACCTTCTGACTTCACTCAACGAGAGAGAGCGCTCCAG 423
 121 GluArgProGluProValGlnAapLeuPheAapPheIleThrIuArgGlyAlaLeuGln 140
 424 GAGAGCTGGCGCGGAGCTTCTTCTGAGAGTGTGAGAGCGGCTGAGAGCTGCAAC 483
 141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGluAlaValArgHisGlybHsAap 160
 484 TCGGCGCTTCTCCAGCGGCAATCAAGAGAGAGAGATCTTAATTCAGCTGAACTGCGCG 543
 161 CysGlyValLeuHlsArgAapIleYbAapGluAanIleLeuIleAapLeuAanArgGly 180
 544 GAACCTCAACTCATTCAGCTTGGGCTGGGCGGCTGCTCAAGAGACAGCTTCAACGAGAC 603
 181 GluLeuYbLeuIleAapPheGlySerGlyAlaLeuLeuYbAapPheValTyrTrpAap 200
 604 TTGAGCGAAGCCAGAGTGTACAGTCTCCAGAGTGTGATTCGATTCAGCTGCAAGCGG 663
 201 PheAapGlyThrArgValTyrSerProProGluTrpIleArgTyrHisArgTyrHisGly 220
 664 AGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723
 221 ArgSerAlaAlaValTrpSerLeuGlyIleLeuLeuTyrAapMetValCysGlyAapIle 240

QY 724 CCATTGAGCAGCAGAGATGTCAGAGGCGCAAGTGTATTGAGCAAGGCTCT 763
 DB 241 ProPheGluHisAapGluGluIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
 QY 784 TCAGAAATGTCACATCTTATTAGATGCTGCTGCTGAGACCATCGAGCGGCTTCC 843
 DB 261 SerGluGluGlnHisLeuIleArgTyrPcybLeuAlaLeuArgProSerAapArgProThr 280
 QY 844 TTGGAAGAAATCCAGAACCATCTCGTGTGATGACAGAGTGTCTCTGCCCCAGGCGCGCC 903
 DB 281 PheGluGluIleGlnHisAapProTrpMetGlnAapValLeuLeuProGluGlnTrpAla 300
 QY 904 GAGATTCATCTGCAAGCGCTGTCACCATCAACCGAGAA 942
 DB 301 GluIleHisLeuHisSerLeuSerProGlyProSerLys 313

RESULT 9
 US-08-465-585C-26
 Sequence 26, Application US/08465585C
 Patent No. 6027914
 GENERAL INFORMATION:
 APPLICANT: Smith, K. A., & Beadling, C.
 TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vector
 TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
 ADDRESSER: (B) STREET:
 CITY: Los Angeles
 STATE: California
 COUNTRY: USA
 ZIP: 900071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/465,585C
 FILING DATE: 5-JUNE-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USSN 08/330,108
 FILING DATE: 27-OCT-1994
 APPLICATION NUMBER: USSN 08/104,736
 FILING DATE: 10-AUG-1993
 APPLICATION NUMBER: USSN 07/796,066
 FILING DATE: 20-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Viviana Amzel, Ph. D.
 REGISTRATION NUMBER: 30,930
 REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 622-7700
 TELEFAX: (213) 4894210
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 313 amino acids
 TYPE: peptide
 STRANDEDNESS: n.a.
 TOPOLOGY: n.a.
 MOLECULE TYPE: peptide
 US-08-465-585C-26
 Alignment Scores:
 Pred. No.: 2,46e-127 Length: 313
 Score: 1623.00 Matches: 302
 Percent Similarity: 98.40% Conservative: 6
 Best Local Similarity: 96.43% Mismatches: 5
 Query Match: 66.43% Indels: 0
 DB: Gaps: 0
 US-10-705-757-3 (1-1302) x US-08-465-585C-26 (1-313)

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OY      4  TTGCTTTGTTCAGAGTCACTACCTCCCTGGCCCACTCGCGCGAGCCCTTCGAAAGACTG  63
Db      1  MetLeuLeuSerLysIleAsnSerLeuLahIbLeuAlaGAlaCyAAsnAspLeu  20
OY      64  CACGCGCAACAGACTGCGCGCGGCAAGAGAGAGCCCTCGAGTGCAGTACCAAGTG  123
Db      21  HtbaIatThrLysLeuAlaIProGlyLysbGlyLysbGlyProLeuGlnSerGlnTyGlnAl  40
OY      124  GCGCCGCTGTGTGGAGCGCGGTGGCTTCGGGCTCGGCTTACTCGGGCAATCCGGTGCAG  183
Db      41  GlyProLeuLeuGlySerGlyGlyPheGlySerValTyLysSerGlyIleArgValSerAsp  60
OY      184  AACTTGGCGGGTGGCCATCAACACCTGGAGAGAGAGACCCGAGATTTCGACTGGGGGAACTG  243
Db      61  AsnLeuProValAlaIleLysHtIeValGlnLysAspArgIleSerAspTrpGlyLysLeu  80
OY      244  CCCAAGCGGACCCGAGTGGCCATGAGAAATGGTCCGTGAGAGAGTGAAGTGAAGTGGCGCTTC  303
Db      81  ProAsnGlyThrArgValIProMetGlnValIleuLeuLysLysValSerSerGlyPhe  100
OY      304  TCGGCGCTCATTTAGACTTCTGTGAGACTGTGTCAGAGGCGCCGATGATTTCGTGATCTG  363
Db      101  SerGlyValIleArgLeuLeuAspTrpPheGlnArgProAspSerPheValLeuIleLeu  120
OY      364  GAGAGCGCCGAAACCCGTGCAGACCTCTTCGACTTCACTACCGAGCGAGAGCCCTTCAG  423
Db      121  GlnArgProGlnProValGlnAspLeuPheAspPheIleTrpGlnArgGlyAlaLeuGln  140
OY      424  GAGAGAGTGGCGCCGAGCTTCTTCGTGAGAGTGGTGGAGGCGGTGCGGCGCATTTGCGCAAC  483
Db      141  GlnGlnLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgHtLysHtAsn  160
OY      484  TCGCGGGCTTCTCCACCGCGACATCAAGACGAGAAACATCTTAATGACTGAACCGCGCG  543
Db      161  CysGlyValLeuHtAsnArgAspTrpLysAsnArgGlnAsnIleLeuIleAspLeuAsnArgGly  180
OY      544  GAACTCAAACTGACTGCTTGGGCTGGGGGCGCGCTGCAGAGACACAGTTCACAGGAC  603
Db      181  GlnLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyThrAsp  200
OY      604  TTTCAGCGAACCCGAGTGCAGTCCCTCAGAGTGGATTGGCTACATCGCTACACAGCG  663
Db      201  PheAspGlyThrArgValTySerProProGlnTrpIleArgTyHtAsnTyHtGly  220
OY      664  AGGTGGCGTGTGTGGTTCCTCGGGAGTCTGCTCTTATGACATGCTGCGGAGATATT  723
Db      221  ArgSerAlaAlaValTrpSerLeuGlyIleLeuLeuTyLysAsnMetValCysGlyAspIle  240
OY      724  CCAATTTCAGACGAGAAAGATCTCAAGGGCCCAAGTACTTTAGGCAAAAGGCTCTCT  783
Db      241  ProPheGlnHtAsnArgGlnGlnIleIleArgGlnValIlePheAsnArgGlnArgValSer  260
OY      784  TCAGAAATTCAACTTTATTAAGAGTGGCGCTGCTCCCGTGAACCAATCGGACCGCGCTCC  843
Db      261  SerGlnCysGlnHtLysLeuIleArgTyPheValAlaLeuAsnArgProSerAspArgProThr  280
OY      844  TTTCAGAAATTCAGAAACATCCCGTGAATGACAGATGTTCTCTGCGCCAGCGACCGCG  903
Db      281  PheGlnGlnIleGlnAsnHtProTrpMetGlnAspValLeuLeuProGlnGlnThrAla  300
OY      904  GAGATTTCATTCGACAGCGCTGTGACCAATCACCCAGCAAA  942
Db      301  GlnIleHtLeuHtSerLeuSerProGlyProSerLys  313

RESULT 10
US-08-652-446-26
; Sequence 26, Application US/08652446
; Patent No. 6057427
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CRS
; TITLE OF INVENTION: Polypeptide, Vector and Transformed Cell Thereof, and
; TITLE OF INVENTION: Expression Therof

```

```

NUMBER P SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
ADDRESSER: (B) STREET:
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,446
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP APP. # 96921319.8
FILING DATE: 5-JAN-1998
APPLICATION NUMBER: PCT/US/96/09194
FILING DATE: 5-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,108
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,074
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,337
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,390
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,585
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,081
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,379
FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/739,523
FILING DATE: 29-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: FP66 40035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
TYPE: peptide
STRANDEDNESS: n.a.
TOPOLOGY: n.a.
MOLECULE TYPE: peptide
US-08-652-446-26

Alignment Scores:
Pred. No.: 2,46e-127 Length: 313
Score: 1623.00 Matches: 302
Percent Similarity: 98.40% Conservative: 6
Best Local Similarity: 96.49% Mismatches: 5
Query Match: 66.43% Indels: 0
DB: 3 Gaps: 0

US-10-705-757-3 (1-1302) x US-08-652-446-26 (1-313)

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Db      1 MetLeuLeuSerIyEiIleAsnSerIeUaLhIleUaKrgLlaRgLaIaCySaBaAspLeu 20
QY      64 CAGGCCAAACAGCTGGGCGCGGCAAGAGAAGAGCCCTGGAGTGCAGTACAGAGT 123
Db      21 HlaLhIhThrybVleuLaRProGlyLybGluLybGluProLeuGIsuSerGIntYrgLInVal 40
QY      124 GGCCTGGTGTGGGACGGGAGGCTTGGCTCGGCTACTCGGGCACTCCGGCTCGCGAC 183
Db      41 GlyProLeuLeuGIsuSerGlyGlyPheGlySerValYrSerGlyIleArgValSerAsp 60
QY      184 AACTTGGCGGTGGCCATCAAGACAGTGGAGAGAGCCGAGATTTCCGACTGGGGGAACTG 243
Db      61 AsnLeuProValaLaIleIyEhIeValGluLybAspArgIleSerAspTrpGlyGluLeu 80
QY      244 CCCAAGCGGACCCGAGTGGCCATGGAAGTGGTCTGCTGAAGAGTGAAGTGGAGCTTC 303
Db      81 ProAsnGlyThrArgValaPrometGluValaIleuLeuLybValaSerSerGlyPhe 100
QY      304 TGGGGGTCATTAGACTTCTGAGCTGGTGGAGAGCGCGATAGTTTCGTCGATCCCTG 363
Db      101 SerGlyValaIleArgLeuLeuAspTrpPheGluArgProAspSerPheValaIleuLeu 120
QY      364 GAGAGCGCCGACCCGCTGCAAGACCTTCTGACTTCAACCGAGCGAGAGAGCCCTCAG 423
Db      121 GluArgProGluProValaGlnAspLeuPheAspPheIleThrGluArgGlyaIleuGln 140
QY      424 GAGAGAGTGGCCCGGAGCTTCTTCTGGAGCTGTCGAGCGCGCTGGCGCATTCGCAAC 483
Db      141 GluGluLeuValaIaArgSerPhePheTrpGlnValaLeuGlnIleValaArgHisCybHisAsn 160
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QY      544 GAACTCAAACTCATCGACTTCGGGGTCGGGGCGCTGCTCAAGGACACAGTCTACAGGAC 603
Db      181 GluLeuLybLeuIleAspPheGlySerGlyaIleuLeuLybAspPheTrValaYrThrAsp 200
QY      604 TTGAGCGGAACCCGAGTGAACAGTCTCCAGAGTGAATTCGTAACCATCGTAACAGGC 663
Db      201 PheAspGlyThrArgValaYrSerProProGluTrpIleArgTyhIaArgTyhIaGly 220
QY      664 AGGTGGCTGCTGTGGTTCCTGGGGAGTCCGTGATGACATGGCTTCGGAGATATT 723
Db      221 ArgSerAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 240
QY      724 CCATTGAGCAGCAGAGAGATGTCGTCAGAGGCGCAAGTGAATTTAGGCAAGGCTCT 783
Db      241 ProPheGluHlaIaAspGluGluIleIleArgGlyGlnValaPhePheArgGlnArgValaSer 260
QY      784 TCAGAAATGTCACATCTTATTAGATGGTGCCTGCTCCCTGAGACATCGACCGGCTTC 843
Db      261 SerGluCybGlnIleuIleAspIleArgTrpCybLeuValaIleuArgProSerAspArgProthm 280
QY      844 TTTGAAGAATCCAGAACCATTCGTCGATGACAGAGTGTCTCTGGCCCCAGGCGCACCGCC 903
Db      281 PheGluGluIleGlnAsnHisProTrpMetGlnAspValaIleuLeuProGlnIuThrAla 300
QY      904 GAGATTCATCTGACAGAGCTGTACCAACCCAGCAAA 942
Db      301 GluIleHlaIleuHlaSerLeuSerProGlyProSerIyE 313
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; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-237-543-7

Alignment Scores:
Pred. No.:      4,48e-124      Length:      313
Score:          1584.00      Matches:      295
Percent Similarity: 96.81%      Conservative: 8
Best Local Similarity: 94.25%      Mismatches: 10
Query Match:    64,84%      Indels:      0
DB:              3      Gaps:      0

US-10-705-757-3 (1-1302) x US-09-237-543-7 (1-313)

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QY      64 CAGGCCAAACAGCTGGGCGCGGCAAGAGAAGAGCCCTGGAGTGCAGTACAGAGT 123
Db      21 HlaLhIhThrybVleuLaRProGlyLybGluLybGluProLeuGIsuSerGIntYrgLInVal 40
QY      124 GGCCTGGTGTGGGACGGGAGGCTTGGCTCGGCTACTCGGGCACTCCGGCTCGCGAC 183
Db      41 GlyProLeuLeuGIsuSerGlyGlyPheGlySerValYrSerGlyIleArgValaIaAsp 60
QY      184 AACTTGGCGGTGGCCATCAAGACAGTGGAGAGAGCCGAGATTTCCGACTGGGGGAACTG 243
Db      61 AsnLeuProValaLaIleIyEhIeValGluLybAspArgIleSerAspTrpGlyGluLeu 80
QY      244 CCCAAGCGGACCCGAGTGGCCATGGAAGTGGTCTGCTGAAGAGTGAAGTGGAGCTTC 303
Db      81 ProAsnGlyThrArgValaPrometGluValaIleuLeuLybValaSerSerGlyPhe 100
QY      304 TGGGGGTCATTAGACTTCTGAGCTGGTGGAGAGCGCGATAGTTTCGTCGATCCCTG 363
Db      101 SerGlyValaIleArgLeuLeuAspTrpPheGluArgProAspSerPheValaIleuLeu 120
QY      364 GAGAGCGCCGAAACCCGTCGAAGACCTTCTGACTTCAACCGAGCGAGAGAGCCCTCAG 423
Db      121 GluArgProGluProValaGlnAspLeuPheAspPheIleThrGluArgGlyaIleuGln 140
QY      424 GAGAGAGTGGCCCGGAGCTTCTTCTGGAGCTGTCGAGCGCGCTGGCGCATTCGCGCAAC 483
Db      141 GluAspLeuValaIaArgGlyPhePheTrpGlnValaLeuGlnIleValaArgHisCybHisAsn 160
QY      484 TGGGGGGTCTTCCACCGCGCATCAAGAGAGAGAACTTTAATCCACTGGAACCCCGCG 543
Db      161 CybGlyValaIleuHlaRgAspIleLybAspGluAsnIleuLeuIleAspLeuAsnArgGly 180
QY      544 GAACTCAAACTCATCGACTTCGGGGTCGGGGCGCTGCTCAAGGACACAGTCTACAGGAC 603
Db      181 GluIleLybLeuIleAspPheGlySerGlyaIleuLeuLybAspPheTrValaYrThrAsp 200
QY      604 TTGAGCGGAACCCGAGTGAACAGTCTCCAGAGTGAATTCGTAACCATCGTAACAGGC 663
Db      201 PheAspGlyThrArgValaYrSerProProGluTrpIleArgTyhIaArgTyhIaGly 220
QY      664 AGGTGGCTGCTGTGGTTCCTGGGGATCCTGCTGATGACATGGTCTGCGAGATATT 723
Db      221 ArgSerAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 240
QY      724 CCATTGAGCAGCAGAGAGATGTCGTCAGAGGCGCAAGTGAATTTAGGCAAGGCTCT 783
Db      241 ProPheGluHlaAspGluGluIleIleArgGlyGlnValaPhePheArgGlnThrValaSer 260
QY      784 TCAGAAATGTCACATCTTATTAGATGGTGCCTGCTCCCTGAGACATCGACCGGCTTC 843
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Db 261 SerGIuCySGlnHisIleuIleIleYStrCySLeuSerIleuArgProSerAspArgProSer 280
QY 844 TTTGAAGAAATCCAGAACCATCGGTGATGACAGAGATTCTCTGCGCCAGGCGACCGGC 903
Db 281 PheGIuGlnIleArgAsnHisProTrpMetGlnGlyAspIleuLeuProGlnIleAlaSer 300
QY 904 GAGATTTCATCTGCACAGCCCTGTCCACCATCATCCAGCAAA 942
Db 301 GluIleHisIleuHisSerIleuSerProGlnYSerSerIleYs 313

RESULT 12
US-09-644-450-7
; Sequence 7, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; CURRENT FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-644-450-7

Alignment Scores:
Pred. No.: 4,48e-124 Length: 313
Score: 1584.00 Matches: 295
Percent Similarity: 96.81% Conservative: 8
Best Local Similarity: 94.25% Mismatches: 10
Query Match: 64.84% Indels: 0
DB: 3 Gaps: 0

US-10-705-757-3 (1-1302) x US-09-644-450-7 (1-313)
QY 4 ATGCTCTTTCACAAAGTCAACTCCCTGCGCCACCTGCGCGACCCCTTGCAACGACCTG 63
Db 1 MetIleuLeuSerIleYHisIleuSerIleuAlaHisIleuArgAlaArgProCyAsnAspLeu 20
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Db 21 HisIleHisIleuLeuHisIleuArgProGlnYHisIleuArgProGlnYHisIleuArgPro 40
QY 124 GGCCTGCTGTGGGACAGCGGTGCTTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTG 183
Db 41 GlyProIleuLeuGlySerGlyPheGlySerValYIleSerGlyIleArgValAlaAsp 60
QY 184 AACTGCGCGGTGGCGCATCAAGCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
Db 61 AsnLeuProValAlaIleYHisIleuArgProGlnYHisIleuArgProGlnYHisIleu 80
QY 244 CCAAGAGGACCGGAGTGGCGCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 303
Db 81 ProAsnGlyHisIleuArgProGlnYHisIleuArgProGlnYHisIleuArgProGlnYHis 100
QY 304 TCGGCGCTCATTAAGTCTTGAAGTGGTTCGAGAGCGCCGATGATTGCTGATGCTG 363
Db 101 SerGIuValIleArgIleuLeuAspTrpPheGlnArgProAspSerPheValIleuIleu 120
QY 364 GAGAGCGCCGAGACCGGTGCAAGACCTTTGACTTTCACCGAGCGAGAGAGAGAGAGAGAG 423
Db 121 GluArgProGlnProValGlnAspLeuPheAspPheIleHisIleuArgGlyAlaIleuGln 140
QY 424 GAGAGAGTGGCGCGGAGCTTCTTGGAGAGTGGTGGAGAGCGGTGCGGCGATGCGCAAC 483
Db 141 GluAspLeuAlaArgGlyPhePheTrpGlnValIleuGlnValAlaArgHisCysHisAsn 160
QY 484 TGCAGGCTTCCACCGCGCATCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 543

Db 161 CysGIuValIleuHisArgAspIleYHisAspGlnIleuIleAspLeuSerArgGly 180
QY 544 GAATCAAACTCATGACATTCGAGGTGCGGCGCGCTGCTCAAGAGACAGTCTTACACGAC 603
Db 181 GluIleYHisIleuHisAspPheGlySerGlyAlaIleuLeuYHisAspThrValYIleHisAsp 200
QY 604 TTTGACGAGACCGAGTGTATCAGTCTTCGAGAGTGGATTCGCTTACCATCGCTTACACGAC 663
Db 201 PheAspGlyThrArgValYIleSerProProGlnTrpIleArgYHisArgYHisArgYHis 220
QY 664 AGTGGCGCTGCTTGTGCTTCCCTGCGGATCCGCTGCTTGAATGATGTCGCGAGATTT 723
Db 221 ArgSerAlaAlaValTrpSerIleuGlyIleuLeuYHisAspMetValCysGIuAspIle 240
QY 724 CCATTGGACAGCAGAGAGATCGTCAAGGCGCAAGTACTTTAGGCAAGAGTCTCT 783
Db 241 ProPheGlnHisAspGlnGlnIleIleYHisGlyGlnValPhePheArgGlnThrValSer 260
QY 784 TCAGATGTCAACATCTTATTAATGTGTGCTGCTGCTGAGACCATTCGAGCGCGCTTC 843
Db 261 SerGIuCySGlnHisIleuIleYStrCySLeuSerIleuArgProSerAspArgProSer 280
QY 844 TTTGAAGAAATCCAGAACCATCGGTGATGACAGAGATTCTCTGCGCCAGGCGACCGGC 903
Db 281 PheGIuGlnIleArgAsnHisProTrpMetGlnGlyAspIleuLeuProGlnIleAlaSer 300
QY 904 GAGATTTCATCTGCACAGCCCTGTCCACCATCATCCAGCAAA 942
Db 301 GluIleHisIleuHisSerIleuSerProGlnYSerSerIleYs 313

RESULT 13
US-07-857-224B-41
; Sequence 41, Application US/07857224B
; Patent No. 5958784
; GENERAL INFORMATION:
; APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting Folded Structures of Proteins
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Steven A. Benner
; STREET: Hadlaubstrasse 151
; CITY: Zurich
; STATE: none
; COUNTRY: Switzerland
; ZIP: (note: this is an international post code) CH-8092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; FILING DATE: 03/25/92
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA: none
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (International) 41 1 632 2830
; TELEFAX: (International) 41 1 262 2437
; TELEX: none
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: rat
; FEATURE: Protein kinase; Table 8 Column 46
; PUBLICATION INFORMATION:
; AUTHORS:
; AUTHORS: Hanks, S. K.
; AUTHORS: Quinn, A. M.

! AUTHORS: Hunter, T.
! TITLE: The protein kinase family
! JOURNAL: Science
! VOLUME: 241
! PAGES: 42-52
! DATE: 1988
! US-07-857-224B-41

Alignment Scores:	
Pred. No.:	9 47e-101
Score:	1304.50
Percent Similarity:	97.67%
Best Local Similarity:	94.94%
Query Match:	53.40%
DB:	2
Gaps:	2
Length:	25
Matches:	24
Conservative:	7
Mismatches:	3
Indels:	3
Gaps:	2

US-10-705-757-3 (1-1302) x US-07-857-224B-41 (1-257)

Qy	10	TTCCAGATACCAAGGTTGGGCGCGAGTTTGGGCAAGGGTGGCTTCGCTCGCTACTACGGG	168
Db	1	SeGlnTnTglnValGlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGly	20
Qy	169	ATCCGCGTCGCGCAACTTGCCTGGTGGCCATCAAGCAAGTGGAGAGACCGGATTTCC	228
Db	21	IleArgValAlaIleAspIleuProValAlaIleTyrGlnValGlyAspArgIleSer	40
Qy	229	GACTGGGGGGAACTGCCCAACGGCACCCGAGTCCCATGAAAGTGCTCTGCTGAAG	288
Db	41	AspTrpGlyGlu-----AsnGlyThrArgValPrometGluValValLeuLeuTyrLeu	58
Qy	289	GTAGAGCTCCGGGCTTCGCGGCGCATTTACACTTTCGACTGGTTTCGAGAGGCCGGAATG	348
Db	59	ValSerSerAspPheSerGlyValIleArgLeuLeuAspTrpPheGluAspProAspSer	78
Qy	349	TTGCTGCTGATCTCTGGAGAGGCCCGCAACCCGTGCAGAACTCTTCGACTTATCACCGAG	408
Db	79	PheValIleuIleLeuGlnIleArgTrpGlnIleProValGlnIleAspLeuPheAspPheIleThrGlu	98
Qy	409	CGAGAGAGCCCTCCAGAGAGAGCTGGCGCCGGAAGCTTCTTGGCAGAGTGTCTGAGAGCCGTG	468
Db	99	ArgGlyAlaLeuGlnIleGlnIleAspLeuAlaArgGlyPhePheTrpGlnValLeuGluAlaVal	118
Qy	469	CGGCAATTGGCCAAACTGCGGGGTTCTCCACCGCAATCAAGACAGAGAACATCTTAATC	528
Db	119	ArgHisCysHisIleAsnGlySerGlyValLeuHisIleArgAspIleArgAspGlnAsnIleLeuIle	138
Qy	529	GACCTTAACCGCGCGCAACTCAAACTCATCGACTTCGAGTCTGGGGGCGCTGTGCAGAGAC	588
Db	139	AspLeuSerArgGlyIleIleIleTyrLeuIleAspPheGlySerGlyAlaLeuLeuTyrAsp	158
Qy	589	ACAGTGTACACCGGACTTTTGAACGGAACCGGAGTGTACATCTCCAGAGTGGATTCCGTAC	648
Db	159	ThrValTyrThrAspPheAspArgIleThrArgValTyrSerProProGlnTrpIleArgTyr	178
Qy	649	CATCGCTACCAACCGGACAGTCCGCTGCTGTTTGGTCCCTGGAGATCCATGCTATGACATG	708
Db	179	HisArgTyrHisGlyArgSerGlnAlaValAlaTrpSerLeuGlyIleLeuLeuTyrAspMet	198
Qy	709	GTCTCGGAGATATTCATTT--GAGCAACGAAAGATGTCAMGGCGCAAGTGTAC	765
Db	199	ValCysGlyAspIleProPheAspArgIleHisAspArgIleIleTyrGlyGlnValIlePhe	218
Qy	766	TTTAGCGAAAGGCTCTCAGAAATGTCAACACTTATTAAATGATGGCTGTCCCTGTAGA	825
Db	219	PheArgGlnThrValSerSerGlnCysGlnIleValIleTyrGlyTrpCysLeuSerLeuArg	238
Qy	826	CCATCGGACCGGCGCTCTTTGAAGAAATCGGAACCACTCGTGGAGATGAC	876
Db	239	ProSerAspArgProSerPheGlnGlnIleArgAsnHisIleProTrpMetGln	255

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; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapellier, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; PILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 326
;
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-237-543-2

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Alignment Scores:

Pred. No.:	1.4e-86	Length:	326
Score:	116.50	Matches:	224
Percent Similarity:	77.25%	Conservative:	34
Best Local Similarity:	67.07%	Mismatches:	61
Query Match:	46.52%	Indels:	15
DB:	3	Gaps:	8

Oy	4	ATGCTTTGTCGAAGTAAACTCCCTGGCCCACTGGCCGAGACCCCT-----TGCAC	57
Db	1	MetLeuLeuSerIyberhediYserLeuLahSleu---CybgiYProGlyIyValAsp	19
Oy	58	GACCTGCAGCCCAACAGCTGGCCGCCGGGCAAA---GAGAAAGAGCCCTTGAGTCCGAG	114
Db	20	HisLeuProValIybetLeuGInProAlaIySAlaAspIyGblUserPheGluIyAla	39
Oy	115	TACCAAGTGGGCCCGCTGTGGGACACCGGTGCTTCGGCTCGGTACTCCGGCATCCG	17
Db	40	TyGblIyValGlyAlaValLeuGlySerGlyIyPheGlyIyThrAlYyAlaGlySerArg	59
Oy	175	GTGCGCGCAAACTTGGCCGGTGCCTCAAGACACGAGAGAGAGACCCGATTTCCGACTGG	23
Db	60	IleAlaAspGlyIyLeuProAlaIaValIyHisValValIyGblArgValThhGluTrp	79
Oy	235	GGGAAATCGCCCAACCGCACCCGAGTCCCATGCAAGTGTCTCTGTAAGAGGTG---	29
Db	80	GlySerIeu---GlyIyAlaThhAlaProLeuGluValIValLeuLeuArgIyValaGly	98
Oy	292	---AGCTCGGAGCTTCCGGGCGTCAATTGACTTTCGACTGCTCGAGAGGCCCGATAGT	346
Db	99	AlaAlaGlyIyAlaIaArgIyAlaIleArgLeuLeuAspTrpPheGluIyProAspGly	118
Oy	349	TTGCGTGTATCCTGTAGAGAGGCCCGAACCCCGTGCAGACACTTTCGACTTATCAGCCGAG	408
Db	119	PheLeuLeuValIeuGluIyArgProGluProAlaGlnAspLeuPheAspPheIleThnGlu	138
Oy	409	CGAGAGACCCCTCAGAGAGAGAGTGGCCCGGAGACTTCTTGGACAGGTGTGGAGCCGTG	466
Db	139	ArgGlyAlaIeAspAspIyProLeuLiaIaArgArgPhePheAlaGlnIValLeuAlaIaVal	158
Oy	469	CGGCAATTGCSACAACCTGCGGGATTCTCCACCGGCACATCAGACAGAACATCTTAATC	528
Db	159	ArgHisLeuHisSerCybGlyIyAlaValHisArgMerIeIyVAspGlyIaLeuLeuVal	178
Oy	529	GACCTGAACCGCGGAGAACTCAAACTCATCGACTTCGGGTGCGGGCGGCTGCTCAAGAC	588
Db	179	AspLeuArgSerGlyIyLeuIyLeuLeuIleAspPheGlySerGlyAlaLeuLeuIyAsp	198
Oy	589	ACAGTGTACACGGACTTTGACGAGAACCCGAGTGAACAGTCTCCAGAGTGGAATCGGTAC	648
Db	199	ThrValIyThhAspPheAspGlyIyHisArgValIySerTrpProGluIyTrpIleArgTy	218
Oy	649	CATCGTACACCGGACAGTCCGCTGTGTTGGTCCCTGGGGAATCTGCTTATGACATG	708
Db	219	HisArgTyHisGlyIyArgSerAlaThhAlaTrpSerLeuGlyIyAlaLeuLeuTyAspMet	238


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QY 709 GTCTGGAGATATTCATTGTGAGCAGCAAGAGATGCTGACGGGCCAAGTACTTT 768
DB 239 VALCYBGILYASPILEPROPHGILNMBPGLUINLIEUENRGILYARGLEUENPHE 258
QY 769 AGCGAAGGGTCTCTTCAGAAATGTCAACATCTTATTAGATGGTGCCTGCTGAGACCA 828
DB 259 ARGARGARGVALSERPROGLUCYBGILNLEUILLIETRGTCYBUSERLEUENRGPRO 278
QY 829 TCGGACCGGCGCTCTTTGAGAAATCCGAAACCATCCGTGATG-----CAGGATGTT 882
DB 279 SERGLUARGPROSERLEUENBPGLINLIEALAHASPRTOTRPMETLEUENGLYALASPGILY 298
QY 883 CTCCTGCCCCGAGCGCCGCGCATTCATCTGCACAGCCTGTCAACATCACCCAGCAAA 942
DB 299 GLYALAPROGLU---SERCYASBPLEUARGLEUCYSTRHLEUENBP----- 313
QY 943 TAGCAGCCATTCTGTCAACCCCTCCAGGAGAGAGAGAGCTTG 984
DB 314 ---ASPAAPVALALASERTHRTRSERSERGLUSERLEU 326

RESULT 15
US-09-644-450-2
; Sequence 2, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; CURRENT FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-644-450-2

Alignment Scores:
Pred. No.: 1,14e-86 Length: 326
Score: 1136.50 Matches: 224
Percent Similarity: 77.25% Conservative: 34
Best Local Similarity: 67.07% Mismatches: 61
Query Match: 46.52% Indels: 15
DB: 3 Gaps: 8

US-10-705-757-3 (1-1302) x US-09-644-450-2 (1-326)
QY 4 ATGCTCTTGTCCAAATCACTCCCTGGCCCACTGCGGAGCCCT-----TGCAC 57
DB 1 METLEUENSERIYSPHEGLYSERLEUALAHLEU---CYBGILYPROGLYGLYVALASP 19
QY 58 GACCTTCAGCGCAACAAGCTGGCGCGGCGCAA--GAGAGAGAGCCCTGAGTGCAG 114
DB 20 HLEUENPROVALYLRILEUENGLNPROALALYALASBPGLUSERPHEGLULYBALA 39
QY 115 TACCAAGTGGGCGGCTGTGGGACAGCGGTGGCTCGGCTCACTCACTGAGGATCCGC 174
DB 40 TYRGLINVALGLYALALEUENGLYSERGLYPHGLYTHRYALYLAAGLYSERARG 59
QY 175 GTGCGGAGCAACTTGTGCGGATGAGCATCAAGCAGTGAAGAGAGGAGATTTCGAGCTG 234
DB 60 LLEALASBPGLYLEUENPROVALALAVALLYSHISVALVALYBGLUARGVALINRGILTRP 79
QY 235 GGGGAATGCGCCCAACGCGACCCGAGTGCCCATGAAAGTGCTCTGTGAAGAGTG--- 291
DB 80 GLYSERLEU---GLYGLYALATHRYVALPROLEUGLIVALLEUENARGLYSVALGLY 98
QY 292 ---AGCTCGGGGCTTCTCGGGCGTCAATTGACTTGTGAGTGGTTCAGAGAGCCCGATAGT 348
DB 99 ALAALAGLYGLYLAARGLYVALILEARGLEUENASPTRPBPHEGLUARGPROASBPGLY 118

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QY 349 TTGCGTGTATCTTGAGAGAGCCCGAACCCGNGCAAGACCTTCTGACTTCACCCGAG 408
DB 119 PHELEUENVALLEUGLILARGPROGLINPROALAGINMBPHEUENPHEPHEILETHRGIL 138
QY 409 CGAGAGGCCCTTCAGAGAGAGCTGGCCCGGAGCTTCTTCTGCGAGGTGTGAGGCCGTG 468
DB 139 ARGGLYALALEUENBPGLINPROLEUENLARGRGPHEPHEALAGLINVALLEUENLALVAL 158
QY 469 CGGCAATTCGCCCAACTGTGGGGGTTCCTCAGCGCGCATCAAGAGAGAGAACTTAATC 528
DB 159 ARGHLECYSHASERCYBGILYALVALHLSARGASPTLYELYSBPGLINMBLEUENVAL 178
QY 529 GACCTGAACCGCGGCGGAACTCAAACTCATTCGACTTCGGGTCGGGCGCTGTCTCAAGAC 588
DB 179 ASBPLEUARGSERGLYGLILEUENLYSEUILLIENBPHEGLYSERGLYALILEUENLYSAP 198
QY 589 ACAGTCTACACGAGACTTGTGACGGAACCCGAGTGTAACGTCTCTCAAGATGGAATTGGCTAC 648
DB 199 THRVALTYRTHRASBPGLYTHRARGVALTYRSETPROPROGLUTRPILEARGTYR 218
QY 649 CATGCTTACACGCGAGGTCGGCTGTGTTGTGCTCGGGGATGCTGCTATGACATG 708
DB 219 HLSARGTYRHSGLYARGSERALATHRYVALTRPSERLEUGLYVALLEUENUTYRASPHEC 238
QY 709 GTCTCGGAGATATTCATTGTGAGCAGCAAGAGATGCTGCAAGGCGCAAGTGTACTTT 768
DB 239 VALCYBGILYASPILEPROPHGILNMBPGLUINLIEUENRGILYARGLEUENPHE 258
QY 769 AGCGAAGGGTCTCTTCAGAAATGTCAACATCTTATTAGATGGTGCCTGCTGAGACCA 828
DB 259 ARGARGARGVALSERPROGLUCYBGILNLEUILLIETRGTCYBUSERLEUENRGPRO 278
QY 829 TCGGACCGGCGCTCTTTGAGAAATCCGAAACCATCCGTGATG-----CAGGATGTT 882
DB 279 SERGLUARGPROSERLEUENBPGLINLIEALAHASPRTOTRPMETLEUENGLYALASPGILY 298
QY 883 CTCCTGCCCCGAGCGCCGCGCATTCATCTGCACAGCCTGTCAACATCACCCAGCAAA 942
DB 299 GLYALAPROGLU---SERCYASBPLEUARGLEUCYSTRHLEUENBP----- 313
QY 943 TAGCAGCCATTCTGTCAACCCCTCCAGGAGAGAGAGAGCTTG 984
DB 314 ---ASPAAPVALALASERTHRTRSERSERGLUSERLEU 326

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Search completed: September 22, 2005, 17:24:35
 Job time : 42.242 sec

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: September 22, 2005, 15:57:45 ; Search time 170.006 Seconds
(without alignments)
5924.037 Million cell updates/sec

Title: US-10-705-757-3

Perfect score: 2443

Sequence: 1 gggatgcctctgcacagat.....ggatctaaactagacacat 1302

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing:

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-O=/cgn2.1/USPTO.epool.p/US10705757/runat.22092005.115014.22122/app.query.fasta_1.5333
-DB=4.GeneSeq -OPT=fastcan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blonum62 -TRANS=human40.cdi -LIST=45
-DOCALLGN=200 -THR SCORE=pcpt -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=apco -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US10705757 @CGN_1.1_753 @runat.22092005.115014.22122 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELCK=100 -LONGLOG
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

A_GeneSeq_16Dec04:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1668	68.3	313	5	ABG33016
2	1668	68.3	313	7	AAO19789
3	1668	68.3	313	7	ABR62938
4	1636	67.0	313	5	ABP54943
5	1636	67.0	313	5	ABG33017
6	1636	67.0	313	6	AAO19788
7	1636	67.0	313	7	ABU61613
8	1636	67.0	313	7	ABR62939
9	1636	67.0	313	7	ADP55368
10	1636	67.0	313	7	ADP45083

11	1636	67.0	313	8	AD019690
12	1636	67.0	313	8	ADR88370
13	1636	67.0	313	8	ADP24227
14	1623	66.4	313	2	AAW08139
15	1623	66.4	313	3	AAI87959
16	1623	66.4	313	8	AD157202
17	1623	66.4	313	5	ADN03170
18	1584	64.8	313	5	ABG33015
19	1584	64.8	313	6	AAO19790
20	1584	64.8	313	7	ABR62940
21	1584	64.8	313	8	ADN97347
22	1584	64.8	313	8	ADR88371
23	1345	55.1	253	8	AD157241
24	1304.5	53.4	257	2	AAV43942
25	1267.5	51.9	254	8	ADK71853
26	1140	46.7	323	8	ADR88376
27	1138.5	46.6	326	2	AAV06886
28	1136.5	46.5	326	4	AAAB29788
29	1136.5	46.5	326	5	AAE23834
30	1136.5	46.5	326	5	ABG33011
31	1136.5	46.5	326	7	ABR62932
32	1136.5	46.5	326	8	ADU96625
33	1136.5	46.5	326	8	ADU97960
34	1136.5	46.5	382	8	AD020314
35	1136.5	46.5	382	8	ADP55593
36	1132.5	46.4	326	6	AAO19792
37	1132.5	46.4	326	6	ABR62933
38	1132.5	46.4	326	8	AD060032
39	1132.5	46.4	326	8	ADR88375
40	1131.5	46.3	326	5	AAO20524
41	1131.5	46.3	326	6	AAO19791
42	1131.5	46.3	326	7	ABR62936
43	1131.5	46.3	455	5	AAE23836
44	1131.5	46.3	455	5	ABG33013
45	1131.5	46.3	455	7	ADP55366

ALIGNMENTS

RESULT 1	ABG33016	standard; protein; 313 AA.
ID	ABG33016	
XX	ABG33016;	
AC		
XX		
DT	20-DEC-2002 (first entry)	
XX		
DE	Rat protein kinase phosphorylation site #2.	
XX		
KW	HKID-1; serine/threonine kinase; cellular proliferative disorder;	AD019690 Human PRO
KW	differential disorder; cancer; hematopoietic neoplastic disorder;	ADR88370 Human PIM
KW	acute promyeloid leukemia; APLM; Chronic myelogenous leukemia; CML;	ADP24227 PRO polyp
KW	Waldenstrom's macroglobulinemia; WM; rat.	AAW08139 Human CRT
XX		AAI87959 Human CYT
OS	Rattus norvegicus.	AD157202 Human PIM
XX		ADN03170 Human PIM
XX	US2002115120-A1.	ABG33015 Mouse pro
XX		AAO19790 Murine PI
XX		ABR62940 Mouse ser
PD	22-AUG-2002.	ADN97347 Murine PI
XX		ADR88371 Mus muscu
XX	04-OCT-2001; 2001US-00971791.	AD157241 PIM1 dom1
XX		AAV43942 Rat prote
XX		ADK71853 Human kin
XX		ADR88376 Colurrix
XX		AAV06886 HWHU20 P
XX	26-JAN-1999; 99US-00237543.	AAAB29788 Human ser
XX	PR	AAE23834 Human HKI
XX	23-AUG-2000; 2000US-00644450.	ABG33011 Human sex
PA	(MILL-) MILLENNIUM PHARM INC.	ABR62932 Human pro
XX		ADU96625 Human cal
XX		ADU97960 Human PIM
XX	Kapeller-Libermann R, Rudolph-Owen LA, Machbeth K;	AD020314 Human PRO
XX	WPI; 2002-712471/77.	ADP55593 Human PRO
XX		AAO19792 Murine PI
XX		ABR62933 Mouse pro
XX		AD060032 CRH bigna
XX		ADR88375 Mus muscu
XX		AAO20524 Protein s
XX		AAO19791 Rat PIM3
XX		ABR62936 Rat prote
XX		AAE23836 Rat KID-1
XX		ABG33013 Rat prote
XX		ADP55366 Rat Prote
PT	Modulating levels or activity of HKID-1 polypeptides, a member of serine/threonine kinase superfamily, for treating cancer, by contacting	

PT cell expressing the polypeptide with a modulator of the polypeptide.
 XX
 PS Example 3; Page 39-40; 48pp; English.

CC The invention describes a method of modulating the level or activity of
 CC human HKID-1 polypeptide, a member of serine/threonine kinase
 CC superfamily. The method involves contacting a cell expressing the
 CC polypeptide or nucleic acid with an agent to modulate the level or
 CC activity of polypeptide, or level of nucleic acid molecule. The method is
 CC useful for modulating the level or activity of HKID-1 polypeptide or
 CC polynucleotide in a subject having or predisposed to having a disorder
 CC involving cancer. Modulating HKID-1 expression or activity is useful for
 CC therapeutic purposes, for treating cellular proliferative and/or
 CC differentiative disorders including cancer or haematopoietic neoplastic
 CC disorders e.g. Acute promyeloid leukaemia (APML). Chronic myelogenous
 CC leukemia (CML) and Waldenstrom's macroglobulinaemia (WM). This is the
 CC amino acid sequence of a rat protein kinase phosphorylation site

XX Sequence 313 AA;

Alignment Scores:

Pred. No.:	1,09e-128	Length:	313
Score:	1668.00	Matches:	313
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	68.28%	Indels:	0
DB:	5	Gaps:	0

US-10-705-757-3 (1-1302) x ABG3016 (1-313)

QY	4	ATGCTCTTGTCCAGATCACTCCCTGCGCCACCTGCGCGACGCCCTTGCAAGACTTG	63
DB	1	MetLeuLeuSerIySileAenSerLeuAlaHisLeuArgIalAlaProCySaMaApleu	20
QY	64	CAGGCCCAACAGCTGGCGCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	123
DB	21	HisAlaAsnIySleuAlaProGlyIySgluIySgluProLeuIySerGlnTyrgIuAl	40
QY	124	GCGCGCTGTGGGACGCGGTGCTCGGCTCGGCTCACTCGGAGCATCCGCGCGCGAC	183
DB	41	GlyProLeuLeuSerIySgluIySgluIySgluIySgluIySgluIySgluIySgluIy	60
QY	184	AACCTGCGGTGCGCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	243
DB	61	AsnLeuProValAlaIleuIySleuAlaGluIySleuAspArgIleSerAspTrpGlyIuLeu	80
QY	244	CCCAAGCGCACCGGAGTCCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	303
DB	81	ProAsnGlyThyArgValProMetGluValIleuLeuIySleuValSerSerGlyPhe	100
QY	304	TGCGGCGTCACTAGACTTCTGAGCTGGTTCGAGAGGCGCGTTCGCTGATCTTG	363
DB	101	SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleuIleu	120
QY	364	GAGAGCGCCGACCCGTCAGAGACTTCTGAGTTCATCCGAGCGAGAGAGCGCTCAG	423
DB	121	GluArgProGluProValGlnApleuPheAspPheIleThrgIuArgIyAlaLeuGln	140
QY	424	GAGAGCTGGCGCGGAGCTTCTTCTGAGAGTCTGAGAGCGCGTGGCGCATTCGCAAC	483
DB	141	GluGluLeuAlaArgSerPhePheTrpGlnValIleuGlnAlaValArgHisCySHAsn	160
QY	484	TGGGCGGTCTCCACGCGCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	543
DB	161	CysGlyValIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu	180
QY	544	GAACTCAAACTCATGACTTGGGTCGGGGCGCTGCTCAAGAGACAGTTCACGAGAC	603
DB	181	GluLeuLeuLeuIleuAspPheGlySerGlyAlaIleuLeuIySleuAspThrValTyThrAsp	200
QY	604	TTTGAGGAGAACCGGAGTTCAGTCTCCGAGAGTTCGATTCACATCGTACCGAGCG	663
DB	201	PheAspGlyThyArgValTySerProGluTrpIleuArgTyHisArgTyHisArgIy	220

QY	664	AGTGGCTGCTGTTGGTCCCTGGGAGTCTGTCTATGACATGATGTCGCGAGATATT	723
DB	221	ArgSerAlaIleValTrpSerLeuIyIleuLeuTyTrpAspMetValCysGlyAspIle	240
QY	724	CCATTGACGACGAGAGAGAGTCTCAAGGCGCAAGTACTTTAGGCAAGGCTCTT	783
DB	241	ProPheGlnIleAspGluIleValIySgluIySgluIySgluIySgluIySgluIySgluIy	260
QY	784	TGAGATGTCACATCTTATTAGTGGTCCCTGCGAGCAATCGGACCGGCGCTCC	843
DB	261	SerGluCysGlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu	280
QY	844	TTTGAAGAAATCCAGAACCATCCGTGATGAGATGTTCTCTGCGCGAGCGCACCGCC	903
DB	281	PheGluGluIleGlnIleAsnIleProTrpMetGlnAspValIleuLeuProGlnIleThrIle	300
QY	904	GAGATTCATCTGCACAGCCTGTCAACCATCACCAGCAAA	942
DB	301	GluIleHisLeuHisSerLeuSerProSerProSerLys	313

RESULT 2

AA019789
 ID AA019789 standard, protein, 313 AA.

AA019789;

DT 11-AUG-2003 (first entry)

DE Rat PIM1 kinase.

KW Rat; PIM1 kinase; PIM3 kinase; pain; analgesic.

OS Rattus sp.

PN W0200293173-A2.

PD 21-NOV-2002.

PF 13-MAY-2002; 2002MO-BP005234.

PR 11-MAY-2001; 2001DE-01023055.

PA (CHEF) GRUENENTHAL GMBH.

PI Weine E, Schaefer MK;

DR WPI; 2003-120715/11.

DR N-PSDB; ABZ69187.

PT Method for identifying analgesics, useful particularly for treating
 PT chronic pain, by screening compounds for interaction with PIM-1 or -3
 PT kinase, or related compounds.

XX Claim 1; Fig 1D; 97pp; German.

XX The present invention relates to a method of identifying pain-regulating
 CC compounds, involving screening candidate compounds for interaction with
 CC PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are
 CC useful for treating chronic pain, particularly of neuropathic or
 CC inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or
 CC neurodegenerative diseases). The present sequence is rat PIM1 kinase

XX Sequence 313 AA;

Alignment Scores:

Pred. No.:	1,09e-128	Length:	313
Score:	1668.00	Matches:	313
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	68.28%	Indels:	0
DB:	6	Gaps:	0

US-10-705-757-3 (1-1302) x AAO19789 (1-313)

```

QY 4 ATGCTCTTGTCCAAAGATCAACTCCCTGGCCCACTGGCGGACGCCCTTGCAACGACTG 63
DB 1 MetIeuLeuSerIysIleAenSerIeuAlaIleuArgAlaIleProCyAsnAspLeu 20
QY 64 CAGCCCAACAAGCTGGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
DB 21 HisAlaAsnIleuAlaProGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGly 40
QY 124 GGGCCGCTGTGGGCAAGCGGTGGCTTCGCTCGCTTACTCGGAGCATCCGCTCGCCGAC 183
DB 41 GlyProIeuLeuGlySerGlyIleGlyPheGlySerValIleArgValAlaAsp 60
QY 184 AACTTGGCGGTGGCCATCAAGCAGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
DB 61 AsnIleuProValAlaIleIleValIleValIleValIleValIleValIleValIle 80
QY 244 CCGAAGGCGACCGGAGGCGCATGGAAGTGGCTCGTGAAGAGAGAGAGAGAGAGAGAG 303
DB 81 ProAsnGlyThrArgValProMetGluValValIleuLeuIleuValIleuSerGlyPhe 100
QY 304 TCGGCGCTCATTAAGACTTCTGACTGGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 363
DB 101 SerGlyValIleArgIleuLeuAspTrpPheGluArgProAspSerPheValIleuIleu 120
QY 364 GAGAGGCGGACCGGAGGCGCATGCTTCTGACTTCATCACGAGCGAGAGAGAGAGAGAG 423
DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
QY 424 GAGAGACTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 483
DB 141 GluGlnIleuAlaArgSerPhePheTrpGlnValIleuGlnAlaValArgHisCysHisAsn 160
QY 484 TGGCGGAGTCTCCACGCGCAGCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 543
DB 161 CysGlyValIleuLeuHisArgAspIleIleValAspGluAsnIleuIleuLeuAsnAlaGly 180
QY 544 GAACTCAAACTCATTCGACTTCGGGTCGGGCGGCTGTCGAAGAGACAGAGTCAACAGGAC 603
DB 181 GluIleuIleuLeuIleuAspPheGlySerGlyAlaIleuLeuIleuAspTrpValIleu 200
QY 604 TTTGAGCGGAACCGGAGTGTACAGTCTCCAGAGTGGATTGGTACCATCGCTACCAAGGC 663
DB 201 PheAspGlyThrArgValIleuSerProGluTrpIleArgTrpHisArgTrpHisGly 220
QY 664 AGGTCCGCTGCTGTGGTGGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 723
DB 221 ArgSerAlaAlaValIleuSerIleuGlyIleuLeuLeuIleuIleuIleuIleuIleu 240
QY 724 CCATTGGAGCAGCAGAGAGATCGTCAAGAGGCGCAAGTGAATTAGGCAAGAGAGTCTCT 783
DB 241 ProPheGlnIleuHisArgIleuGlnIleuValIleuValIleuValIleuValIleu 260
QY 784 TCGAATGTCAACATCTTATTAGTGTGCTGTCTGCTGAGACCATGAGCCGCGCTCC 843
DB 261 SerGlyCysGlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 280
QY 844 TTTGAAGAATTCAGAGAACCATCCGTGGATGAGAGATTTCTCTGCGCCGAGGCGACCGC 903
DB 281 PheGlnIleuIleuGlnIleuHisArgProTrpMetGlnAspAlaIleuLeuProGlnAla 300
QY 904 GAGATTCATCTGCAAGAGCTGTGACCATCAACGAGCAAA 942
DB 301 GluIleuIleuHisSerIleuSerProSerProSerIleu 313

```

RESULT 3
ABR62938 standard; protein; 313 AA.
XX ABR62938;
AC ABR62938;
XX
DT 04-DEC-2003 (first entry)

```

XX DE Rat serine/threonine protein kinase PIM-1.
XX KM Rat, PIM-1; protein kinase; enzyme.
XX OS Rattus norvegicus.
XX PN W02003060130-A2.
XX PD 24-UTL-2003.
XX PF 20-JAN-2003; 2003MO-EP000492.
XX PR 19-JAN-2002; 2002EP-00001401.
XX PA (AVET ) AVENTIS PHARMA DEUT GMBH.
XX PI Korn M, Mueller G, Schneider R, Teschank G;
XX DR WPI; 2003-598536/56.
XX PT New human or murine PIM-3 DNAs or polypeptides, useful for as a screening
XX PT agent for identifying anti-type 2 diabetes mellitus drugs, or for
XX PT treating insulin resistance or type 2 diabetes mellitus.
XX PS Example 2; Page 39; 40pp; English.
XX CC The present sequence is the protein sequence of the rat serine/threonine
XX CC protein kinase and proto-oncogene, PIM-1. PIM-1 proteins are the
XX CC paralogs of novel human and murine PIM-3 proteins (see ABR62932 and
XX CC ABR62933) of the invention, which are therefore expected to be involved
XX CC in cancer and cell growth regulation. PIM-3 is also involved in the
XX CC development of insulin resistance and type 2 diabetes mellitus. The
XX CC invention relates to the use of PIM-3 nucleic acids and proteins in:
XX CC screening assays for compounds that modulate insulin resistance or type 2
XX CC diabetes mellitus; detection assays for detecting insulin resistance or
XX CC type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing,
XX CC forensic biology); predictive medicine (e.g. diagnostic or prognostic
XX CC assays, monitoring clinical trials, pharmacogenomics); and for the
XX CC preparing a medicament for the treatment of insulin resistance or type 2
XX CC diabetes mellitus
XX SQ Sequence 313 AA;
XX Alignment Scores:
XX Pred. No.: 1.09e-128 Length: 313
XX Score: 1668.00 Matches: 313
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 68.28% Indels: 0
XX DB: 7 Gaps: 0

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US-10-705-757-3 (1-1302) x ABR62938 (1-313)

```

QY 4 ATGCTCTTGTCCAAAGATCAACTCCCTGGCCCACTGGCGGACGCCCTTGCAACGACTG 63
DB 1 MetIeuLeuSerIysIleAenSerIeuAlaIleuArgAlaIleProCyAsnAspLeu 20
QY 64 CAGCCCAACAAGCTGGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
DB 21 HisAlaAsnIleuAlaProGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGly 40
QY 124 GGGCCGCTGTGGGCAAGCGGTGGCTTCGCTCGCTTACTCGGAGCATCCGCTCGCCGAC 183
DB 41 GlyProIeuLeuGlySerGlyIleGlyPheGlySerValIleArgValAlaAsp 60
QY 184 AACTTGGCGGTGGCCATCAAGCAGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
DB 61 AsnIleuProValAlaIleIleValIleValIleValIleValIleValIleValIle 80
QY 244 CCGAAGGCGACCGGAGGCGCATGGAAGTGGCTCGTGAAGAGAGAGAGAGAGAGAGAG 303
DB 81 ProAsnGlyThrArgValProMetGluValValIleuLeuIleuValIleuSerGlyPhe 100

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QY 304 TCGGGCGCTATTGACCTTCTGACCTGATTCGAGAGCCGCGATAGTTCTGCTGATCTTG 363
    |||||
Db 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleu 120
QY 364 GAGAGCCCGGAGCCCGTGCAGAACCTCTTCTGACTTCATCCAGCGAGAGAGCCCTCCAG 423
    |||||
Db 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
QY 424 GAGGAGCTGGCCGGAGCTTCTCTGCGAGGCTGCGAGCCGCTGGCGATTCGCGAAC 483
    |||||
Db 141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgHisAsn 160
QY 484 TGGCGGGTTCTCCACCGCGCATCAAGACGAGAACATCTTAATCCAGCTGAAACCGCGC 543
    |||||
Db 161 CysGlyValLeuHisArgAspIleArgAspGlnAsnIleuIleAspLeuAsnArgGly 180
QY 544 GAACTCAAACTCATGCACTTGGGGTGGGGGCGCTGCTCAAGACACAGTTACAGGAC 603
    |||||
Db 181 GluLeuIleLeuIleAspPheGlySerGlyAlaLeuLeuIleAspThrValTyrThrAsp 200
QY 604 TTGAGAGGAACCGGAGTTACACTCTCCAGAGTGGATTCGCTACCATGCTTACCAACGCG 663
    |||||
Db 201 PheAspGlyThrArgValTyrSerProProGluTrpIleArgTyrHisArgTyrHisGly 220
QY 664 AGGTCCGCTGCTGTTGGTCCCTGGGGAATCTGCTATAGACATGGTCTGCGAGATATT 723
    |||||
Db 221 ArgSerAlaIleValIleTrpSerLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
QY 724 CCATTGAGACACAGAGAGATGCTGACAGGCGCAAGTGTACTTTAGCGAAAGGCTCT 783
    |||||
Db 241 ProPheGlnHisAspGlnGluIleValIleArgGlnValTyrPheArgGlnArgValSer 260
QY 784 TCAGAAATGCAACATCTTATTAGATGGTGTGCTGCTGAGACATCGAGCGGCGCTCC 843
    |||||
Db 261 SerGluCysGlnHisLeuIleArgTrpCysLeuSerLeuArgProSerAspArgProSer 280
QY 844 TTGAGAAATCCAGAACATCCGCTGATGACAGATGTTCTCTGCGCCAGGCGACCGCC 903
    |||||
Db 281 PheGluGlnIleGlnHisAspTrpMetGlnAspValLeuLeuProGlnIleThrAla 300
QY 904 GAGATTCACTGCAACGCTGTGCAACCATCAACCGAA 942
    |||||
Db 301 GluIleHisLeuHisSerLeuSerProSerProSerIle 313

RESULT 4
ABP54943
ID ABP54943 standard; protein; 313 AA.
XX
AC ABP54943;
XX
DT 13-JUN-2003 (first entry)
XX
DE Human Pim1.
XX
KW Pim1; tyrosine threonine kinase; TTK; protein kinase; enzyme;
KM mitotic checkpoint; colon cancer; breast cancer; tumour; cytostatic;
KM human; gene therapy.
XX
OS Homo sapiens.
XX
PN MO200268444-A1.
XX
PD 06-SEP-2002.
XX
PF 21-FEB-2002; 2002MO-US005278.
XX
PR 21-FEB-2001; 2001US-0271254P.
XX
PA (CHIR ) CHIRON CORP.
XX
PI Reinhard C, Jefferson AB, Chan WM,
XX

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DR WPI; 2002-698650/75.
DR N-PSDB; ABV733989.
XX
PT Reducing growth of cancer cells comprises reducing tyrosine threonine
PT kinase (TTK) activity, useful in diagnosing and treating disorders with
PT abnormal expression levels and activity of TTK, such as lung, colon,
PT prostate and ovarian cancer.
XX
PS Disclosure; Page 80-81; 113pp; English.
XX
CC The present sequence is the protein sequence of human Pim1, a protein
CC related to tyrosine threonine kinase (TTK, see ABP54938). TTK
CC polynucleotides and polypeptides of the invention encompass
CC polynucleotides and polypeptides having sequence similarity or sequence
CC identity to human TTK and other genes and gene products related to TTK,
CC such as Pim1. The invention is based on the finding that TTK is
CC differentially expressed in various forms of cancer. It provides methods
CC for the identification of cancerous cells, especially breast cancer and
CC colon cancer cells, by detection of expression levels of TTK, as well as
CC diagnostic, prognostic and therapeutic methods. These methods can be used
CC as the basis of rational therapy. Assays for identifying molecules that
CC modulate the activity of these genes in cancer, as well as methods of
CC inhibiting tumour growth by inhibiting the activity of TTK are also
CC provided
XX
SQ Sequence 313 AA;
XX
Alignment Scores:
Score: 4,75e-126 Length: 313
Perc: 1636.00 Matches: 304
Percent Similarity: 99.04% Conservative: 6
Best Local Similarity: 97.12% Mismatches: 3
Query Match: 66.97% Indels: 0
DB: 5 Gaps: 0

US-10-705-757-3 (1-1302) x ABP54943 (1-313)
QY 4 ATGCTCTTGTCCAGATCACTCCCTGGCCCACTGCGCGACCCCTTGCACGACCTG 63
    |||||
Db 1 MetLeuLeuSerIleValHisAsnSerLeuAlaHisLeuAlaValProCysAsnAspLeu 20
QY 64 CAGGCCAAMAGCTGGCGCGGCGCAAGAGAGAGCCCTGAGTCCGAGTCAACAGGTG 123
    |||||
Db 21 HisAlaThrIleValLeuAlaProGlyArgGluArgProLeuGlnSerGlnTyrGlnVal 40
QY 124 GGGCGGCTGTTGGGAGGCGTGGCTTGGCTCGCTACTGGGGATCCGCGCTCCCGAC 183
    |||||
Db 41 GlyProLeuLeuGlySerIleGlyPheGlySerValTyrSerGlyIleArgValSerAsp 60
QY 184 AACTTGCGGTGGCCATCAAGACGCTGGAAGAGACCGGATTTCCGACTGGGAGAACTG 243
    |||||
Db 61 AsnLeuProValAlaIleIleHisValGluArgAspArgIleSerAspTrpGlyLeu 80
QY 244 CCAGAGCGACCCGAGTGGCCCATGGAAGTGTCTGTCTGAGAGAGGTGAGCTCGGGCTTC 303
    |||||
Db 81 ProAsnGlyThrArgValProMetGlnValValLeuLeuIleValSerSerGlyPhe 100
QY 304 TGGCGGCTCATTAAGCTTCTGACTGTTCCAGAGCCGAGATTTGCTGCTGATTCCTG 363
    |||||
Db 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleu 120
QY 364 GAGAGCCCGGAGCCCGTGCAGAACCTCTTCTGACTTCATCCAGCGAGAGAGCCCTCCAG 423
    |||||
Db 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
QY 424 GAGGAGCTGGCCGGAGCTTCTCTGCGAGGCTGCGAGCCGCTGGCGATTCGCGAAC 483
    |||||
Db 141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgHisAsn 160
QY 484 TGGCGGGTTCTCCACCGCGCATCAAGACGAGAACATCTTAATCCAGCTGAAACCGCGC 543
    |||||
Db 161 CysGlyValLeuHisArgAspIleArgAspGlnAsnIleuIleAspLeuAsnArgGly 180

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QY 544 GAACCTCAACATCGACTTCGGGGCGGCTGCTCAAGACACAGTCTACAGGAC 603
 DB 181 GILUULYALEULIENHSPHEGLYSERGLYALALEULYASAPINRVALTYRTHASP 200
 QY 604 TTGACGGAACCCGAGTGTACAGTCTCCAGAGTGTGCTACCACTGCTACCAAGCC 663
 DB 201 PHEAPGLYTHRARGVALTYRSETPROFGLUTRPRILEARGYRHSARGTYRHSGLY 220
 QY 664 AGGTCCGCTGCTGTTTGGTCCCTGGGATCTGCTCTATGACATGGTCTCGAGATATT 723
 DB 221 ARGSERIALAVALTRPSERLEUGLYILEULYEURYRASPMECTVALCYSGLYASPILE 240
 QY 724 CCATTGACGACGACGAAGATGTCAGAGGCCAAGTGTACTTAGCCAAAGGCTCT 783
 DB 241 PROPHGLUHSAPGLUGLILEIRLEARGLYGINVALPHEPHEARGINARGVALSER 260
 QY 784 TCAGATGTCAACATCTTATAGATGTGCTGCTCCCTGAGACCATCGACCCGCTCC 843
 DB 261 SERGLUCYSEGINHLEULILEARGTRPCYLEULAHLEULARGPROSERAPARGPROTHR 280
 QY 844 TTGGAAGAAATCCAGAACATCCGTGATGCAAGATTTCTCTGCCCAGGCCACCGCC 903
 DB 281 PHEGLUGLULIEGINHSPROTTRPMEGLINAPVALLEULENUPROGLINGLUTRHALA 300
 QY 904 GAGATTCATCTGACAGCCTGTGACCATCAACCAGCAAA 942
 DB 301 GLULIEHLEULHSSERLEUSERPROGLYPROSERLYSE 313

RESULT 5
 ABG33017
 ID ABG33017 standard; protein; 313 AA.
 AC ABG33017;
 DT 20-DEC-2002 (first entry)
 DE Human protein kinase phosphorylation site.
 KW HKID-1, serine/threonine kinase; cellular proliferative disorder;
 KW differentiative disorder; cancer; haematopoietic neoplastic disorder;
 KW acute promyeloid leukaemia; APL; Chronic myelogenous leukaemia; CML;
 KW Waldenstrom's macroglobulinaemia; WM; human.
 OS Homo sapiens.
 XX
 XX US2002115120-A1.
 XX
 XX 22-AUG-2002.
 XX
 XX PD 04-OCT-2001; 2001US-00971791.
 XX
 XX PR 26-JAN-1999; 99US-00237543.
 XX PR 23-AUG-2000; 2000US-00644450.
 XX
 XX PA (MILL-) MILLENNIUM PHARM INC.
 XX
 XX PI Kapeller-Libermann R, Rudolph-Owen LA, Macbeth K;
 DR WPI; 2002-712471/77.
 XX
 XX Modulating levels or activity of HKID-1 polypeptides, a member of
 PT serine/threonine kinase superfamily, for treating cancer, by contacting
 PT cell expressing the polypeptide with a modulator of the polypeptide.
 XX
 XX Example 3; Page 40-41; 48pp; English.
 XX
 XX The invention describes a method of modulating the level or activity of
 CC human HKID-1 polypeptide, a member of serine/threonine kinase
 CC superfamily. The method involves contacting a cell expressing the
 CC polypeptide or nucleic acid with an agent to modulate the level or
 CC activity of polypeptide, or level of nucleic acid molecule. The method is
 CC useful for modulating the level or activity of HKID-1 polypeptide or
 CC polynucleotide in a subject having or predisposed to having a disorder

CC involving cancer. Modulating HKID-1 expression or activity is useful for
 CC therapeutic purposes, for treating cellular proliferative and/or
 CC differentiative disorders including cancer or hematopoietic neoplastic
 CC disorders e.g. Acute promyeloid leukaemia (APL), Chronic myelogenous
 CC leukaemia (CML) and Waldenstrom's macroglobulinaemia (WM). This is the
 CC amino acid sequence of a human protein kinase phosphorylation site
 XX

Sequence 313 AA:
 Alignment Scores:
 Pred. No.: 4,75e-126 Length: 313
 Score: 1636.00 Matches: 304
 Percent Similarity: 99.04% Conservative: 6
 Best Local Similarity: 97.12% Mismatches: 3
 Query Match: 66.97% Indels: 0
 DB: 5 Gaps: 0

US-10-705-757-3 (1-1302) x ABG33017 (1-313)

QY 4 ATGCTCTTGTCCAAATCAATCTCCCTGGCCACCTGCGGACCCCTTGCAACGACTTG 63
 DB 1 MetLeuLeuSerLySileHnsSerLeuAlaHsLeuArgAlaIaProCySaenAspLeu 20
 QY 64 CACGCCAACAGCTGGGCGCGGCAAGAGAGAGCCCTGGAGTCGACGTACCAAGT 123
 DB 21 HsAlaThrLySLeuAlaProGlyLySGLySGLyProLeuLysSerGlnTrVal 40
 QY 124 GGCCTGCTTGGGCAAGCGGTGCTTCCGCTCGGTACTCGGACATCCGCTCGCGAC 183
 DB 41 GLYProLeuLysGlySerGlyPheGlySerValTySerGlyLeuArgValSerAsp 60
 QY 184 AACTTGGCGGTGGCCATCAAGCAGTGAAGAGACCCGATTTCCGACTGGGGGAACTG 243
 DB 61 AsnLeuProValAlaIleLySHisValGluLyAspArgIleSerAspTrpGlyLeu 80
 QY 244 CCCACGGGACCCGAGTGGCCATGAAAGTGCTGCTGAAAGGTGAGCTGGGCTTC 303
 DB 81 ProAsnGlyThrArgValProMetGluValValLeuLeuLySValSerSerGlyPhe 100
 QY 304 TCGGCGGTATTAAGACTTTCGACTGTTGAGAGGCCGAGATGTTTGTGCTGATCTTG 363
 DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspPheValLeu 120
 QY 364 GAGAGGCCGGAACCCGTGCAAGACTCTTCGACTTATCAACGAGGAGAGCCCTTCAG 423
 DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
 QY 424 GAGGAGCTGGCCGGAGCTTTCTTGGAGGTGCTGAGGCGGTGGGCAATTGGCAAC 483
 DB 141 GILUULYALEULIARGSERPHEPHETRPGINVALLEUGLULAVALARIGHISCYSHASAPN 160
 QY 484 TGCAGGTTCTCCACCGGACATCAAGACGAGAACATCTTATCGACCTGAACCGCGCG 543
 DB 161 CySGLYValLeuHsArgAspIleLySAspGlyAsnIleLeuLeuAspLeuAsnArgGly 180
 QY 544 GAACCTCAACATCGACTTCGGGTGCGGCGCTGCTCAAGACACAGTCTACAGGAC 603
 DB 181 GILUULYALEULIENHSPHEGLYSERGLYALALEULYASAPINRVALTYRTHASP 200
 QY 604 TTGACGGAACCCGAGTGTACAGTCTCCAGAGTGTGCTACCACTGCTACCAAGCC 663
 DB 201 PHEAPGLYTHRARGVALTYRSETPROFGLUTRPRILEARGYRHSARGTYRHSGLY 220
 QY 664 AGGTCCGCTGCTGTTTGGTCCCTGGGATCTGCTCTATGACATGGTCTCGAGATATT 723
 DB 221 ARGSERIALAVALTRPSERLEUGLYILEULYEURYRASPMECTVALCYSGLYASPILE 240
 QY 724 CCATTGACGACGACGAAGATGTCAGAGGCCAAGTGTACTTAGCCAAAGGCTCT 783
 DB 241 PROPHGLUHSAPGLUGLILEIRLEARGLYGINVALPHEPHEARGINARGVALSER 260
 QY 784 TCAGATGTCAACATCTTATAGATGTGCTGCTCCCTGAGACCATCGACCCGCTCC 843

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Db      261 SerGluCyseGlnHisLeuIleArgTrpCySLeuAlaLeuArgProSerAspArgProthr 280
QY      844 TTGGAAGAAATCCAGAACCATCCGTGGATGCAGATGTTCTCTGGCCCCAGGCGCACCGCC 903
Db      281 PheGlnGlnIleGlnIleHisProTrpMetGlnAspValIleuLeuProGlnGlnIleAla 300
QY      904 GAGATTCATCTGCACAGCCTGTGCACCATCACCCAGCAAA 942
Db      301 GluIleHisLeuHisSerLeuSerProGlyProSerIlys 313

RESULT 6
AA019788 standard; protein; 313 AA.
XX
XX      AA019788;
AC      11-AUG-2003 (first entry)
XX
XX      11-AUG-2003 (first entry)
XX
XX      Human PIM1 kinase.
DE      Human PIM1 kinase.
XX
XX      Human; PIM1 kinase; PIM3 kinase; pain; analgesic.
XX
XX      Homo sapiens.
OS
XX      MO200293173-A2.
XX
XX      21-NOV-2002.
XX
XX      13-MAY-2002; 2002MO-BP005234.
XX
XX      11-MAY-2001; 2001DE-01023055.
XX
XX      (CHEF ) GRUENENTHAL GMBH.
XX
XX      Weihe E, Schaefer MK;
PI
XX      WPI; 2003-120715/11.
XX
XX      N-PSDB; AB269186.
XX
XX      Method for identifying analgesics, useful particularly for treating
PT      chronic pain, by screening compounds for interaction with PIM-1 or -3
PT      Kinase, or related compounds.
XX
XX      Claim 1; Fig 1B; 97pp; German.
XX
XX      The present invention relates to a method of identifying pain-regulating
CC      compounds, involving screening candidate compounds for interaction with
CC      PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are
CC      useful for treating chronic pain, particularly of neuropathic or
CC      inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or
CC      neurodegenerative diseases). The present sequence is human PIM1 kinase
XX
XX      Sequence 313 AA;
SQ

Alignment Scores:
Pred. No.:      4,75e-126      Length:      313
Score:          1636.00      Matches:      304
Percent Similarity: 99.04%      Conservative: 6
Beet Local Similarity: 97.12%      Mismatches: 3
Query Match:      66.97%      Indels:      0
DB:              Gaps:      0

US-10-705-757-3 (1-1302) x AA019788 (1-313)
QY      4 ATGCTCTTGTCAAGATCAACTCCCTGGCCCACTGGCCGACGCCCTTGCACAGACTG 63
Db      1 MetLeuLeuSerIysIleAsnSerLeuAlaHisLeuArgAlaIleProCySAsnAspLeu 20
QY      64 CAGGCGCAACAAGCTGGCGCGCGGCAAGAGAGAGGCCCTGGAGTGCAGTACCAAGT 123
Db      21 HisAlaThrIlyAsnLeuAlaProGlyLysGlnIlySerIleuProLeuGlnSerGlnIlyrGlnVal 40
QY      124 GAGCCGCTGTGGGACAGCGGTGGCTTCGGCTCGGCTACTCGGACATCCGCGTCCGCGAC 183

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Db      41 GlyProLeuLeuGlySerGlyIlyPheGlySerValIlyrSerGlyIlyLeuArgValSerAsp 60
QY      184 AACTTGGCCGCGTGGCCATCAAGACGTCGAGAAAGACCCGGAATTTCCGACTGGGGGAAACG 243
Db      61 AsnLeuProValAlaIleIlyHisIValGlnIlyAspArgIleSerAspTrpGlyGlnIly 80
QY      244 CCCAAGCGGACCCGAGTGGCCCATGGAAGTGTCTCTGCTAAGAAGGTGAAGTCTCGAGCTTC 303
Db      81 ProAsnGlyThrArgValProMetGlnValIleValLeuLeuIlybIlyValSerSerGlyPhe 100
QY      304 TCGGGGCTGATTGAACCTTGTGAGCTGTGAGAGGCGCGATATGTTCTGTGATCTTG 363
Db      101 SerGlyValIleIleArgLeuLeuAspTrpPheGlnIlyArgProAspSerPheValIleLeu 120
QY      364 GAGAGGCGCGAACCCTGTGAAGACCTCTTCGACTTCAATACCGAGGAGAGAGCCCTCCAG 423
Db      121 GluArgProGlnProValGlnAspLeuPheAspPheIleThrGlnIlyrGlyAlaLeuGln 140
QY      424 GAGAGCTGGCCGAGCTTCTTGTGAGAGTGTGAGAGGCGGTGCGGATTCGCAAC 483
Db      141 GluGlnLeuAlaIlyrSerPheThrGlnIlyValIleuGlnIlyValAlargHisCySAsn 160
QY      484 TCGGGGCTTCTCCACCGCGCATCAAGACGAAACATTTAAATGCACTTGAACCGCGGC 543
Db      161 CySgIlyValLeuHisIleArgAspIleIlyAspArgIlyLeuHisIleuIleAspLeuAspArgIly 180
QY      544 GAACTCAACSTCATGACCTTCGGGTGGGGGGGCGCTGCAAGAGACACATTCACAGAC 603
Db      181 GlnLeuIlyValLeuIleAspPheGlySerGlyAlaLeuIlyAspThrValIlyrThrAsp 200
QY      604 TTGACGGAACCCGAGTGTACAGTCCCTCCAGAGTGTTCGCTACCATCGTACACAGCGC 663
Db      201 PheAspGlyThrArgValIlyrSerProArgIlyrIleArgIlyHisIleArgIlyHisIly 220
QY      664 AGGTGGCTGTGTTGGTCCCTGGGAGATCTGCTGTATGACATGGTCTGGGAGATATT 723
Db      221 ArgSerAlaAlaIlyrIleAspIlyrIleLeuLeuIlyrAspMetValCySgIlyAspIle 240
QY      724 CCAATTGACACGACGAAAGATTCGACAGGCGCAAGTGTATTTAGGAAAGGCTGT 783
Db      241 ProPheGlnIlyAspIlyGlnIlyIleIleArgGlyGlnValIlePheAspGlnIlyrValSer 260
QY      784 TCGAATGTCAACATCTTATTAGATGATGCTGTCCCTGAGACCATCGAGCGGCGCTCC 843
Db      261 SerGluCyseGlnHisLeuIleArgTrpCySLeuAlaLeuArgProSerAspArgProthr 280
QY      844 TTGGAAGAAATCCAGAACCATCCGTGGATGCAGATGTTCTCTGGCCCCAGGCGCACCGCC 903
Db      281 PheGlnGlnIleGlnIleHisProTrpMetGlnAspValIleuLeuProGlnGlnIleAla 300
QY      904 GAGATTCATCTGCACAGCCTGTGCACCATCACCCAGCAAA 942
Db      301 GluIleHisLeuHisSerLeuSerProGlyProSerIlys 313

RESULT 7
ABU61613 standard; protein; 313 AA.
ID      ABU61613;
AC      ABU61613;
XX
XX      11-AUG-2003 (first entry)
XX
XX      Human PIM1 protein.
DE      Human PIM1 protein.
XX
XX      Human; tyrosine threonine kinase; TTK; cancer; cytostatic;
XX      mitotic checkpoint gene; PIM1.
XX
XX      Homo sapiens.
XX
XX      US2003045491-A1.
XX
XX      06-MAR-2003.
PD

```


XX 21-FEB-2002; 2002US-00081119.
 PF
 XX 23-FEB-2001; 2001US-0289813P.
 PR
 XX (REIN/) REINHARD C.
 PA (JEFF/) JEFFERSON A B.
 PA (CHAN/) CHAN V W.
 XX
 PI Reinhard C, Jefferson AB, Chan VW;
 XX
 DR WPI; 2003-45656/43.
 DR N-PSDB; ACA62265.
 XX
 PT Detecting cancer in a subject, by comparing expression levels of tyrosine
 PT threonine kinase polypeptide or polynucleotide in a subject cell and a
 PT normal cell, where an increase in the expression level in the test cell
 PT is indicative of cancer.
 XX
 PS Disclosure; Page 34-35; 79pp; English.
 XX
 CC The invention relates to detecting cancer (other than ovarian cancer) in
 CC a subject, comprising comparing the expression levels of tyrosine
 CC threonine kinase (TRK, a mitotic checkpoint gene) polypeptide or
 CC polynucleotide in a test cell obtained from the subject and in a normal
 CC non-cancer cell, where an increase in the expression level of TRK protein
 CC or nucleic acid in the test cell compared to that in the normal cell,
 CC indicates the presence of cancer other than ovarian cancer. Also included
 CC are reducing growth of a cancerous cell (by contacting a cancerous cell
 CC with an amount of an agent effective to reduce TRK polypeptide activity
 CC in the cell), an assay for identifying a candidate agent that reduces
 CC growth of a cancerous cell (comprising: (i) detecting the activity of a
 CC TRK polypeptide in the presence of a candidate agent; and (ii) comparing
 CC the activity of TRK polypeptide in the presence of a candidate agent
 CC relative to TRK polypeptide activity in the absence of the candidate
 CC agent), identifying an agent that reduces TRK activity (comprising: (i)
 CC contacting a cancerous cell displaying elevated expression of a TRK-
 CC encoding polynucleotide with a candidate agent; and (ii) determining the
 CC effect of the candidate agent on TRK polypeptide activity) and assessing
 CC the prognosis of a cancerous disease other than ovarian cancer in a
 CC subject (comprising: (i) detecting expression of TRK -encoding
 CC polynucleotide in a test cancer cell of a subject; and (ii) comparing a
 CC level of expression of TRK-encoding polynucleotide in the test cancer
 CC cell with a level of expression of the polynucleotide in a control non-
 CC cancer cell, where the level of expression of TRK in the test cancer cell
 CC relative to the level of expression in the control non-cancer cell is
 CC indicative of the prognosis of the cancerous disease). The methods are
 CC useful for detecting cancer (other than ovarian cancer) in a subject,
 CC reducing growth of cancerous cells, identifying a candidate agent that
 CC reduces growth of a cancerous cell, identifying an agent that reduces TRK
 CC activity and assessing the prognosis of a cancerous disease other than
 CC ovarian cancer. The methods are also useful for determining the ability
 CC of a subject to respond to a particular therapy e.g. as a basis of
 CC rational therapy. The present sequence represents a closely related
 CC protein to human TRK, in this case human PIM1 (not defined)
 XX
 SO Sequence 313 AA,
 Alignment Scores:
 Pred. No.: 4,75e-126 Length: 313
 Score: 1636.00 Matches: 304
 Percent Similarity: 99.04% Conservative: 6
 Best Local Similarity: 97.12% Mismatches: 3
 Query Match: 66.97% Indels: 0
 DB: 7 Gaps: 0
 US-10-705-757-3 (1-1302) X ABU61613 (1-313)
 QY 4 ATGCTCTTGTTCAGAGTCAACTCCCTGGCCGACGCTGGCGGACGCTTGCAGACACTG 63
 DB 1 MetLeuLeuSerLysIleAsnSerLeuAlaHisLeuArgIlaIaProCyAsnAspLeu 20
 QY 64 CAGGCCAAGAGCTGGCGCGGCAAGAGAGAGCCCTGGAGTTCGACGTACAGGTG 123

DB 21 HisAlaThrIleuLeuAlaProGlyIlySGuLybGluProLeuGluSerGlnTyrgInVal 40
 QY 124 GGCCTGCTGTGGGACAGCGGTGGCTTCGCTCGGTCTACTCGGGCATCCGCTGCCGAC 183
 DB 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTySerGlyIleArgValSerAsp 60
 QY 184 AACTGCGCGTGGCCATCAAGACGCGGAGAGGACCGGATTCGACCTGGGGGGAACAG 243
 DB 61 AsnLeuProValAlaIleuShIleValGluLybAspArgIleSerAspTrpGlyIleu 80
 QY 244 CCCAGCGACCCGAGTGGCCATGAGAGTGTCTCTGCTGAGAGAGGTGAGCTCGGCTTC 303
 DB 81 ProAsnGlyThrArgValProMetGluValIleuLeuLybValSerSerGlyPhe 100
 QY 304 TCGGCGTCAATTAAGCTTTCGACCTGCTGAGAGGCGCGATAGTTTCTGCTGACTCTG 363
 DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleu 120
 QY 364 GAGAGGCGGACCCGTCGAGACCTTCCTGACTCATGACCGAGGAGGACGCTCCAG 423
 DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
 QY 424 GAGAGCTGGCCCGAGCTTCTTCTGGCAGGTGCTGAGGCGCGGCAATTGCCAACA 483
 DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGluAlaValArgHisCybHisAsn 160
 QY 484 TCGGGGTTCTCCACCGGCACATCAAGACGAGACATCTTAATGACCTGAACCGCGGC 543
 DB 161 CybGlyValIleuHisArgAspIleLybAspGluAsnIleuIleAspLeuAsnArgGly 180
 QY 544 GAACCTCAACTCATGCACTTCGCGGTGGGGGCGCTCTCAAGACCACTTCACAGGAC 603
 DB 181 GluLeuLybLeuIleAspPheGlySerGlyAlaLeuLeuLybAspThrValTyTrpAsp 200
 QY 604 TTGACGGAACCCGAGTGTACAGTCTCCAGAGTGTGATTGCTACCATCGCTCAACGCG 663
 DB 201 PheAspGlyThrArgValTySerProProGluTrpIleArgTyHisArgTyHisGly 220
 QY 664 AGCTCGGCTGCTGTTTGTTCCTCGGGGATCTGCTCTATGACATGGTTCGGAGATATT 723
 DB 221 ArgSerAlaAlaValThrPheTrpLeuGlyIleLeuLeuTyAspMetValCybGlyAspIle 240
 QY 724 CCATTGACACGACGAGAAAGATCGTCAAGGGGCAAGTGTACTTTGGCAAGGCTCTCT 783
 DB 241 ProPheGluHisAspGluIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
 QY 784 TCAGATGTCAACATCTTATTAGATGTGCTGCTGCTGAGACATCGGACCGGCTCTC 843
 DB 261 SerGluCybGlnHisLeuIleArgTrpCybLeuAlaLeuArgProSerAspArgProThr 280
 QY 844 TTGAGAAATTCAGAACCATTCGCGTGAATGACAGATGTTCTCTGCGCCAGGCGCGCT 903
 DB 281 PheGluGluIleGlnAsnHisProTrpMetGlnAspValIleuLeuProGlnGluThrAla 300
 QY 904 GAGATTCATCTGCACAGCTGTGCACATCAACCCAGAAA 942
 DB 301 GluIleHisLeuHisSerLeuSerProGlyProSerLys 313
 RESULT 8
 ID ABR62939 standard; protein; 313 AA.
 AC ABR62939;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Human serine/threonine protein kinase PIM-1.
 XX
 KW Human; PIM-1; protein kinase; enzyme.
 XX
 OS Homo sapiens.
 XX

PN MO2003060130-A2.
 XX 24-UTL-2003.
 XX 20-JAN-2003; 2003MO-EP000492.
 PF 19-JAN-2002; 2002EP-00001401.
 XX (AVER) AVENTIS PHARMA DEUT GMBH.
 PA Korn M, Mueller G, Schneider R, Tschank G;
 PI WPI; 2003-598536/56.
 DR
 XX
 PT New human or murine P1M-3 DNAs or polypeptides, useful for as a screening
 agent for identifying anti-type 2 diabetes mellitus drugs, or for
 PT creating insulin resistance or type 2 diabetes mellitus.
 XX
 PS Example 2; Page 40; 40pp; English.
 CC The present sequence is the protein sequence of the human
 CC serine/threonine protein kinase and proto-oncogene, P1M-1. P1M-1 proteins
 CC are the paralogues of novel human and murine P1M-3 proteins (see ABR62932
 CC and ABR62933) of the invention, which are therefore expected to be
 CC involved in cancer and cell growth regulation. P1M-3 is also involved in
 CC the development of insulin resistance and type 2 diabetes mellitus. The
 CC invention relates to the use of P1M-3 nucleic acids and proteins in:
 CC screening assays for compounds that modulate insulin resistance or type 2
 CC diabetes mellitus; detection assays for detecting insulin resistance or
 CC type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing,
 CC forensic biology); predictive medicine (e.g. diagnostic or prognostic
 CC assays, monitoring clinical trials, pharmacogenetics); and for the
 CC preparing a medicament for the treatment of insulin resistance or type 2
 CC diabetes mellitus
 CC
 XX
 SQ Sequence 313 AA;
 Alignment Scores:
 Pred. No.: 4.75e-126 Length: 313
 Score: 1636.00 Matches: 304
 Percent Similarity: 99.04% Conservative: 6
 Best Local Similarity: 97.12% Mismatches: 3
 Query Match: 66.97% Indels: 0
 DB: 7 Gaps: 0
 US-10-705-757-3 (1-1302) x ABR62939 (1-313)
 QY 4 ATGCTTTGTCAAGATCAACTCCCTGGCCCACTGGCGCAGCCCTTGCAAGACTG 63
 DB 1 MetLeuLeuSerLysIleAenSerLeuAlaHisLeuArgAlaIlaProCyAsnAAspLeu 20
 QY 64 CAGGCCCAACAAGCTGGGGCGGGGCAAGAAGAGACCCCTGGAGTGCAGTCCAGGTG 123
 DB 21 HisAlaThrLysLeuAlaProGlyLysGluLysLeuProLeuGluSerGlnTyrGlnVal 40
 QY 124 GGGCCGCTGTTGGGACAGGGTGGCTTGGCTCGGCTTACTCGGACATCCGCTGCGCAG 183
 DB 41 G1PProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValSerAsp 60
 QY 184 AACTTGGCGGTGGCCATCAAGCAGTGAAGAGAGACCGAATTCGATCGAGGGAGACTG 243
 DB 61 AsnLeuProValAlaIleLysHisValGluLysAspArgLysSerAspTrpGlyGluLeu 80
 QY 244 CCCAAGCGGACCCGAGTGGCCCATGGAAGTGTCTCTGCTGAAGAAGGTGAGACTGGGGCTTC 303
 DB 81 ProAsnGlyThrArgValProMetGluValValLeuLeuLysValSerSerGlyPhe 100
 QY 304 TCGGGCGCTCATTTGACTTGTGACTGTGATGGTGAAGAGCCGATAGTTTGCTGCTGATCTGT 363
 DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluLysTrpAspSerPheValIleLeu 120
 QY 364 GAGAGGCCGAGACCCGTGCAAGACCTTCGACTTCATCAACGAGCAGAGAGCCCTTCAG 423

DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
 QY 424 GAGGAGCTGGCCCGGAGCTTCTTTCGGCAGGTGCTGAGGCGCGTCCGAGATTGCCAAGC 483
 DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGluAlaValArgHisCysHisAsn 160
 QY 484 TCGCGGGTTCTCCACCGCGACATCAAGGACGAGAACATCTTAATGACCTGAGCCGCGC 543
 DB 161 CysGlyValLeuHisArgAspIleLysAspArgIleAsnIleLeuIleAspLeuAsnArgGly 180
 QY 544 GAATCTAATCTCATGACTTCCGGTGGGGGCGCTGCTCAAGACACAGTCTACAGCAGAC 603
 DB 181 GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyrThrAsp 200
 QY 604 TTTGACGGAAACCGAGTGTACAGTCTCCAGAGTGATTCGCTACCATCGCTACCAAGC 663
 DB 201 PheAspGlyThrArgValTyrSerProGluTrpIleArgTyrHisArgTyrHisGly 220
 QY 664 AGCTCGGCTGCTGTTGGTCCCTGGGAGTCCCTGCTATGACATGGTCTGCGAGATATT 723
 DB 221 ArgSerAlaIleValTrpSerLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
 QY 724 CCAATTGACACGACGAGAGAGATCTCAAGGCGCAAGTCTTATGGCAAGGCTCTT 783
 DB 241 ProPheGluHisAspGluGluIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
 QY 784 TCAGAAATGCACATCTTATAGATGGTGCCTGCCCTGAGACCAATCGAGCGGCCCTCC 843
 DB 261 SerGluCysGlnHisLeuIleArgTrpCysValAlaLeuArgProSerAspArgProHis 280
 QY 844 TTTGGAAGAAATCCAGAACCATCCGTGATGACAGATGTTCTCTGCGCCAGGCGCACGCGC 903
 DB 281 PheGluGluIleGlnHisAsnHisProTrpMetGlnAspValLeuLeuProGlnGluThrAla 300
 QY 904 GAGATTCAATCTGCACAGCTGTCCACCATCAACCCAGCAAA 942
 DB 301 GluIleHisLeuHisSerLeuSerProGlyProSerLys 313
 RESULT 9
 AD55368
 ID AD55368 standard, protein; 313 AA.
 XX
 AC AD55368;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein AAA60089, SEQ ID NO 1183.
 XX
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNR; Chung.
 OS Homo sapiens.
 XX
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PF 14-AUG-2002; 2002MO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-033347P.
 XX
 PA (GENO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 DR GENBANK; AAA60089.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for

CC or is modified to contain a reactive group at or near a binding site of
 CC interest, with one or more ligand candidates capable of covalently (C).
 CC bonding to the reactive group thus forming a kinase-(L) conjugate (C).
 CC The method is useful for identifying protein kinase inhibitors that
 CC preferentially bind to inactive conformation of a target protein kinase.
 CC The present sequence is a protein kinase which may be modified via an
 CC amino acid substitution, for use in the method of the invention.

XX Sequence 313 AA;

SO Alignment Scores:

Pred. No.: 4,75e-126 Length: 313
 Score: 1636.00 Matches: 304
 Percent Similarity: 99.04% Conservative: 6
 Best Local Similarity: 97.12% Mismatches: 3
 Query Match: 66.97% Indels: 0
 DB: 7 Gaps: 0

US-10-705-757-3 (1-1302) x ADF45083 (1-313)

QY 4 ATGCTCTTGCCCAAGATCAACTCCCTGGCCCACTGCGCGACGCCCTTGCAACGACCTG 63
 DB 1 MetLeuLeuSerIleAsnSerLeuAlaHisLeuArgAlaAlaProCysAsnAspLeu 20
 QY 64 CAGCCCAACAAAGCTGGCGCGCGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
 DB 21 HisAlaThrIleuLeuAlaProGlyIleGluIleGluProLeuLeuSerGlnIleVal 40
 QY 124 GGGCCGCTGTGGGAGCGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGG 183
 DB 41 GlyProLeuLeuGlySerGlyIlePheGlyIleSerValIleArgValIleSerAsp 60
 QY 184 AACTTGGCCGCTGGCCCAATCAAGACACGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
 DB 61 AsnLeuProValAlaIleIleuShIleValGluIleAspArgIleSerAspIlePheGlyIle 80
 QY 244 CCCAAGCGGACCGGAGAGGCGCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCTTC 303
 DB 81 ProAsnIleThrArgValIleProMetGluValIleLeuLeuIleValIleSerSerGlyPhe 100
 QY 304 TCGGGCGCTGATTAAGCTTCTGAGCTGGTTCGAGAGCGCGCATAGTTTGGTGTGATCTTG 363
 DB 101 SerGlyValIleArgLeuLeuAspIlePheGluIleArgProAspSerPheValIleLeu 120
 QY 364 GAGAGCGGCGGACCGCGGCAAGACCTTCTGACCTTCAACGAGAGAGAGAGAGAGAGAG 423
 DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluIleArgValIleGlu 140
 QY 424 GAGAGCTGGCGCGGAGCTTCTTCTGAGCTGGTTCGAGAGCGCGCATAGTTTGGTGTGATCTTG 483
 DB 141 GluIleLeuAlaArgSerPhePheIlePheGluIleValIleGluIleValIleArgIleSer 160
 QY 484 TGGGGGGTTTCCACCGGACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCTGC 543
 DB 161 CysGlyValIleuHisArgAspIleIleAspGluAsnIleLeuIleAspLeuAsnArgGly 180
 QY 544 GAATCTGAATCTCACTTCGCGTTCGGGGCGCGCTGTCACAGAGACAGCTTCACAGAGAC 603
 DB 181 GluLeuLeuLeuIleAspPheGlySerGlyAlaLeuLeuLeuAspIleValIleThrAsp 200
 QY 604 TTGACCGAAGCCGAGGTGACAGCTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 663
 DB 201 PheAspGlyThrArgValIleIleSerProGluIleIleArgIleThrIleArgIleValIle 220
 QY 664 AGGTGGCTGCTGTTGGTCCCTGGGAGATCTGCTATGACATGCTGCGAGAGATATT 723
 DB 221 ArgSerAlaIleValIlePheSerLeuGlyIleLeuLeuIleAspPheValIleCysGlyAsp 240
 QY 724 CCATTGAGACGACGAGCTCTC 783
 DB 241 ProPheGluIleHisArgGluIleIleArgGlyGlnValIlePhePheArgGlnArgValSer 260
 QY 784 TCAGAAATGTCAACATCTTATTAGATGTGCTGCTGCGTGAAGACATCGAGACCGGCGCTTC 843

DB 261 SerGluCysGlnHisLeuIleArgIleGlyProCysLeuAlaLeuArgProSerAspArgProThr 280
 QY 844 TTGGAAGAAATTCACAAACATCCCGGATGCAAGAGATGTTCTCCGCCCAAGCCACCGCC 903
 DB 281 PheGluGluIleGlnAsnHisProIlePheGlnAspValIleLeuProGluIleThrAla 300
 QY 904 GAGATTCACTGTCACAGCGCTGTCAACCATCAACCCAGCAAA 942
 DB 301 GluIleHisLeuHisSerLeuSerProGlyProSerIle 313

RESULT 11

AD019690
 ID AD019690 strand; protein; 313 AA.

AD019690;

12-AUG-2004 (first entry)

Human PRO polypeptide #308.

Human, PRO, immune related disorder; systemic lupus erythematosus;
 Rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
 systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
 autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
 diabetes mellitus; renal disease; demyelinating disease;
 central nervous system; peripheral nervous system;
 demyelinating polyneuropathy; Guillain-Barre syndrome;
 chronic inflammatory demyelinating polyneuropathy.

Homo sapiens.

MO2004043361-A2.

27-MAY-2004.

06-NOV-2003; 2003WO-US035268.

08-NOV-2002; 2002US-0425235P.

(GENTH) GENENTECH INC.

Fong S, Dennis K, Clark H, Chin H, Schoenfeld J, Williams PW;

Wood WI, Wu TD;

WPI; 2004-420067/39.

N-PSDB; AD019689.

Novel PRO polypeptide e.g., PRO9614, PRO71106, or PRO86388 useful for
 creating an immune related disorder such as systemic lupus erythematosus,
 rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
 spondyloarthritis.

Claim 7; SEQ ID NO 616; 1731pp; English.

The invention relates to human PRO polypeptides and the polynucleotides
 encoding them. The polypeptides and polynucleotides are useful for
 treating and diagnosing immune related disorders in mammals. The immune
 related disorders include systemic lupus erythematosus, rheumatoid
 arthritis, osteoarthritis, juvenile chronic arthritis, systemic
 sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
 haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 mellitus, immune-mediated renal disease, demyelinating diseases of the
 central or peripheral nervous system, demyelinating polyneuropathy,
 Guillain-Barre syndrome and chronic inflammatory demyelinating
 polyneuropathy. This sequence represents a human PRO polypeptide of the
 invention.

SO Sequence 313 AA;

Alignment Scores:

Pred. No.: 4,75e-126 Length: 313
 Score: 1636.00 Matches: 304

Percent Similarity: 99.04%
 Best Local Similarity: 97.12%
 Query Match: 66.97%
 DB: 8
 Gaps: 0

US-10-705-757-3 (1-1302) x ADR88370 (1-313)

```

QY 4 ATGCTCTTGTCCAAAGATCAACTCCCTGGCCCACTGGCCGACGCCCTTGCAACGACCTG 63
DB 1 MetleuenuSerlyslleamSerleuAlahleuArgAlaAlaProCyshamApLeu 20
QY 64 CAGCCCAACAAGCTGGCCGCGGCAAGAGAGAGCCCTGAGTGCAGTACAGAGT 123
DB 21 HleAlaThrlyseuAlaProGlylyseGluylseGluProleuGlySerGlnTyrglnVal 40
QY 124 GGGCCGCTGTGGGACGCGGTGGCTTGGCTGGCTTACTCGGAGCATCCGCTGGCCGAC 183
DB 41 GlyProleuGlySerGlyGlyPheGlySerValTySerGlyIleArgValSerAsp 60
QY 184 AACCTGCGGTGGCCATCAAGACAGTGGAGAGAGCCGCAATTCGACCTGGGGGAACTG 243
DB 61 AsnleuProValAlaIlelyeNlsvalGluylseAspArgIleSerAspTPGlyGluLeu 80
QY 244 CCGCAACGCGACCCGAGTGCATGAGTGGTCTGCTGAGAAAGTGAAGTGGAGCTGGCTTC 303
DB 81 ProhseGlyThrArgValPrometGlyValValleuenuylsValSerSerGlyPhe 100
QY 304 TCGGCGCTCATTTAGACTTCTGAGCTGGTTCGAGAGCCGCAATGCTTCTGCTGATCTG 363
DB 101 SerGlyValIleArgleuLeuAspTTPGheGlyubrgProAspSerPheValIleLeu 120
QY 364 GAGAGGCGCCGACCCGTCGACAGACCTTTCGACTTTCATCACCGAGCGAGAGCCCTTCAG 423
DB 121 GluArgProGlyProValGlnAspLePheAspPheIleThrGlyValAlaLeuGln 140
QY 424 GAGAGGCTGGCCGCGAGCTTCTTTCGAGAGTGTGAGAGCCGCGGCAATGGCCCAAC 483
DB 141 GluGluLeuAlaArgSerPhePheTTPGlnValleuGlnAlaValArgHsCysHlsAsn 160
QY 484 TGGCGGGTTCCTCCACCGCAGATCAAGACGAGAGCAATCTTAATGCACTTGAACCGCGGC 543
DB 161 CysGlyValIleuHlsArgAspIlelyeAspGlyubnHlsleuIleAspLeuAsnArgGly 180
QY 544 GAATCTCAATCTCATCTTCGCGGTTCGCGGCGCTGCTCAAGACAGACAGTCTACACGAC 603
DB 181 GluLeuylsleuIleAspPheGlySerGlyAlaLeuLeuylsAspThrValTyThrAsp 200
QY 604 TTGACGGAACCCGAGTGTACAGTCTTCAGAGTGTGATTCGCTACATCGCTACACGAGC 663
DB 201 PheAspGlyThrArgValTySerPProGlnTTPleArgTyHlsArgTyHlsGly 220
QY 664 AGGTTCGCTGCTGTTGGTCCCTGGGAGATCCTGCTATGACATGATCTCGAGAGATAT 723
DB 221 ArgSerHlsAlaValTTPSerleuGlyIleleuenuylsAspMetValCysGlyAspIle 240
QY 724 CCATTGAGCAGCAGAGAGATGTCAAGGGCCCAAGTGAATTTAGGCAAGGGGTCTT 783
DB 241 ProPheGlyHlsAspGlyGlnIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
QY 784 TCAGAAATGTCAACCTTTAATAGTGGTCTGCTGCTGAGACATCGAGAGCCGCGCTTC 843
DB 261 SerIleuylsGlnHlsleuIleArgTyCysleuAlaLeuArgProSerAspArgProThr 280
QY 844 TTGAGAGAAATCCAGAACATCCGTGATGAGAGATGTTCTCTGCCCAGGCCACGCC 903
DB 281 PheGlyGlyIleGlnAsnHlsProTTPMetGlnAspValleuenuProGlnGlyThrAla 300
QY 904 GAGATTCACTGCGACAGCTTGTACCATCACCCGCAAA 942
DB 301 GlnIleHlsleuHlsSerleuSerProGlyProSerlyys 313

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ID ADR88370 standard; protein; 313 AA.
XX
AC ADR88370;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human PIM 1 protein.
XX
KW Molecular scaffold; nuclear hormone receptor; TNF receptor;
KM G-protein coupled receptor; methyl transferase; ligase; PIM; human.
XX
OS Homo sapiens.
XX
PN US2004171062-A1.
XX
PD 02-SEP-2004.
XX
PF 28-FEB-2003; 2003US-0037268.
XX
PR 28-FEB-2002; 2002US-0360651P.
PR 16-SEP-2002; 2002US-0411398P.
PR 20-SEP-2002; 2002US-0412341P.
PR 02-JAN-2003; 2003US-0437929P.
XX
PA (PLEX-) PLEXIKON INC.
XX
PI Hirsch K, Milburn MV;
XX
DR WPI; 2004-642017/62.
XX
PT Designing a ligand binding to a target molecule, comprises identifying as
PT molecular scaffold compounds binding to members of a molecular family,
PT detecting orientation of scaffolds at a binding site of target, and
PT synthesizing ligand.
XX
PS Disclosure; SEQ ID NO 9; 186bp; English.
XX
XX
CC The present invention relates to a method of designing a ligand binding
CC to a target molecule. The method involves identifying as molecular
CC scaffold compounds binding to members of a molecular family, detecting
CC orientation of scaffolds at a binding site of target, and synthesizing
CC ligand. The invention is useful for designing drug products and for
CC designing ligand binding to target molecules such as nuclear hormone
CC receptors, TNF receptors, G-protein coupled receptors, methyl
CC transferases, ligases, etc. The present sequence is the human PIM 1
CC protein. This sequence is used to illustrate the method of invention.
XX
SQ Sequence 313 AA;
XX
XX
Alignment Scores:
Pred. No.: 4,756-126 Length: 313
Score: 1636.00 Matches: 304
Percent Similarity: 99.04% Conservative: 6
Best Local Similarity: 97.12% Mismatches: 3
Query Match: 66.97% Indels: 0
DB: 8 Gaps: 0

```

```

US-10-705-757-3 (1-1302) x ADR88370 (1-313)
QY 4 ATGCTCTTGTCCAAAGATCAACTCCCTGGCCCACTGGCCGACGCCCTTGCAACGACCTG 63
DB 1 MetleuenuSerlyslleamSerleuAlahleuArgAlaAlaProCyshamApLeu 20
QY 64 CAGCCCAACAAGCTGGCCGCGGCAAGAGAGAGCCCTGAGTGCAGTACAGAGT 123
DB 21 HleAlaThrlyseuAlaProGlylyseGluylseGluProleuGlySerGlnTyrglnVal 40
QY 124 GGGCCGCTGTGGGACGCGGTGGCTTGGCTGGCTTACTCGGAGCATCCGCTGGCCGAC 183
DB 41 GlyProleuGlySerGlyGlyPheGlySerValTySerGlyIleArgValSerAsp 60
QY 184 AACCTGCGGTGGCCATCAAGACAGTGGAGAGAGCCGCAATTCGACCTGGGGGAACTG 243

```

RESULT 12
 ADR88370

```

Db      61 AsnLeuProValAlaIleIysHisValGluIysAspArgIleSerAspTrpGlyGluLeu 80
QY      244 CCCAACGGGACCCGAGTGGCCATGAGAAAGTGTCTGTGTAAGAAAGGAGTGGCTGGCTTC 303
XX      |||
XX      81 ProAsnGlyThrArgValProMetGluValValLeuLeuValValSerSerGlyPhe 100
QY      304 TCGGGCGCTCATTAAGCTTTGAGCTGGTGTGAGAGGCCGATAGTTCTGTGATCTTC 363
XX      |||
XX      101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleLeu 120
QY      364 GAGAGCGCCGACCCGTCGACAACTCTTGAATTCATCCGAGCGAGAGAGCCCTTCAG 423
XX      |||
XX      121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluValGlyAlaLeuGln 140
QY      424 GAGAGCTGGCCGCGAGCTTCTTGTGAGTGTGAGGCCGCTGGGGGACCTTCCCAAC 483
XX      |||
XX      141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgHisCysHisAsn 160
QY      484 TCGGGGTTCTCCACCGCGACATCAAGACGAGAACATCTTAATCGACCTGAACCGCGC 543
XX      |||
XX      161 CysGlyValLeuHisArgAspIleIysAspGluAsnIleLeuIleAspLeuAsnArgGly 180
QY      544 GAACTCAAACTCATTCGACTTCGGGTCGGGGCGCTGCTCAAGACACAGTCTTACAGC 603
XX      |||
XX      181 GluLeuIysLeuIleAspPheGlySerGlyAlaLeuLeuIysAspThrValIleThrAsp 200
QY      604 TTGAGCGGAACCGAGTGTACAGTCCCTCGAGTGGATTCGTGTACATGCTACCGAGC 663
XX      |||
XX      201 PheAspGlyThrArgValIleSerProGluTrpIleArgTyrHisArgTyrHisGly 220
QY      664 AGGTGGCTGCTGTGTTGGTCCCTGGGGATCTGCTCTATGACATGGTCTGCGAGATATT 723
XX      |||
XX      221 ArgSerAlaIleValIlePheSerLeuGlyIleLeuLeuIleAspMetValCysGlyAspIle 240
QY      724 CCATTGAGACGACGAGAAAGATGCTCAAGGGCCAAAGTACTTTAGCGAAAGGCTCTC 783
XX      |||
XX      241 ProPheGluHisAspGluGlnIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
QY      784 TCAGAAATGTCAAATCTTATTAGATGGTGCCTGCTCCCTGAGACATCGAGCGGCGCTCC 843
XX      |||
XX      261 SerGluCysGlnHisLeuIleArgTrpCysLeuAlaLeuArgProSerAspArgProThr 280
QY      844 TTGGAAGAAATCCAGAACCATCCGTGGATGACAGATGTTCTCTGCCCCAGGCCACGCGC 903
XX      |||
XX      281 PheGluGluIleGlnHisAspProTrpMetGlnAspValLeuLeuProGlnGlnThrAla 300
QY      904 GAGATTCAATTCGACAGCTGTGTACCAATCACCCAGCAAA 942
XX      |||
Db      301 GluIleHisIleHisSerLeuSerProGlyProSerLys 313

```

RESULT 13
ADP24227
ID ADP24227 standard; protein; 313 AA.

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XX      AC      ADP24227;
XX      DT      18-NOV-2004 (first entry)
XX      DE      PRO polypeptide SEQ ID NO:1405.
XX      KW      PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
XX      KW      osteopathic; antidiabetic; dermatological; antiporiatic; antiallergic;
XX      KW      antiaesthetic; hepatotropic; respiratory; gene therapy; immune system.
XX      OS      unidentified.
XX      PN      MO2004041170-A2.
XX      PD      21-MAY-2004.
XX      PF      30-OCT-2003; 2003MO-US034312.
XX      PR      01-NOV-2002; 2002US-0423394P.

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XX      XX      (GERTH ) GENENTECH INC.
PA      PA      Clark H, Schenfeld J, Van Lookeren M, Williams PM, Wood WI;
XX      PI      Wu ID;
XX      DR      WPI; 2004-419628/39.
XX      DR      N-PSDB; ADP24226.
XX      PT      New PRO polypeptides and polynucleotides, useful for treating e.g.
XX      PT      erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
XX      PT      renal disease, or demyelinating diseases of the central or peripheral
XX      PT      nervous system.
PS      Claim 7, SEQ ID NO 1405; 2940pp; English.
XX      XX      The invention relates to a novel isolated nucleic acid and the PRO
XX      XX      polypeptide encoded by it. A protein of the invention has
XX      XX      CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
XX      XX      CC osteopathic, antidiabetic, dermatological, antiporiatic, antiallergic,
XX      XX      CC antiaesthetic, hepatotropic, and respiratory activity. A polynucleotide
XX      XX      of the invention may have a use in gene therapy. The PRO polypeptide, its
XX      XX      agonist, antagonist, or antibody that specifically binds to the
XX      XX      CC polypeptide is useful for treating an immune related disorder such as
XX      XX      CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
XX      XX      CC juvenile chronic arthritis, a spondyloarthritis, systemic sclerosis, an
XX      XX      CC idiopathic inflammatory myopathy, Sjogren's syndrome, autoimmune
XX      XX      CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
XX      XX      CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
XX      XX      CC disease, a demyelinating disease of the central or peripheral nervous
XX      XX      CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
XX      XX      CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
XX      XX      CC disease, infectious or autoimmune chronic active hepatitis, primary
XX      XX      CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
XX      XX      CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
XX      XX      CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
XX      XX      CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
XX      XX      CC disease, asthma, allergic rhinitis, atopic dermatitis, food
XX      XX      CC hypersensitivity, urticaria, an immunologic disease of the lung,
XX      XX      CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hyperreactivity
XX      XX      CC pneumonia, a transplantation associated disease, graft rejection or
XX      XX      CC graft-versus-host disease. The present sequence represents a PRO protein
XX      XX      of the invention.
SQ      Sequence 313 AA;

```

Alignment Scores:
Pred. No.: 4,75e-126
Score: 1636.00
Percent Similarity: 99.04%
Best Local Similarity: 97.12%
Query Match: 66.97%
DB: 8
Matches: 313
Conserved: 304
Mismatches: 6
Indels: 0
Gaps: 0

US-10-705-757-3 (1-1302) x ADP24227 (1-313)

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QY      4 ATGCTCTGTTCGAAGATCAACTCCCTGGGCCACCTGGCGGACGCCCTTGAACGACG 63
XX      |||
XX      1 MetLeuLeuSerLysIleHisSerLeuAlaHisIleValGlnAlaProCysAsnAspLeu 20
Db      64 CACGCGCAACAGCTGCGCGCGCGGCAAGAGAGAGCCCTTGAGTTCGAGTACGACGAG 123
XX      |||
XX      21 HisAlaThrIleValLeuAlaProGlyIysGluIysGluIysGluIysGluIysGluIys 40
QY      124 GCGCGCGCTGTTGGGCAAGCGGTGGCTTGGCTGTCTACTCGGGCATCCGCGTCCGAC 183
XX      |||
XX      41 GlyProLeuLeuGlySerGlyIleGlyPheGlySerValIleArgValSerAsp 60
QY      184 AACTTGGCGGTGGCGCATCAAGACGTTGGAGAGACCGGATTTCCGATGGGGGAACTG 243
XX      |||
Db      61 AsnLeuProValAlaIleIysHisValGluIysAspArgIleSerAspTrpGlyGluLeu 80
QY      244 CCCAACGGGACCCGAGTGGCCATGAGATGTGTCTGTGAAGAAAGTGAAGTCTGGGCTTC 303

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Db      81  ProbenGlyThrArgValPrometGluValLeuLeuLeuValSerSerGlyPhe 100
Qy      304  TCGGCGCTCATTAAGCTTCTGAGCTGGTTCGAGAGCCCGATAGTTCTGTCGATCTCTG 363
Db      101  SerGlyValIleArgLeuLeuLeuSerPheGluArgProAspSerPheValIleLeu 120
Qy      364  GAGAGCCCGAACCCTGCAAGACCTCTGCACTTCACTTCAACCGAGGAGGAGCCCTCAG 423
Db      121  GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
Qy      424  GAGAGCTGGCCCGGAGCTTCTTCTGCAAGTGTCTGAGGCGCTGCGGCAATTCGACAAAC 483
Db      141  GluGluLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgHisCysHisAsn 160
Qy      484  TCGGGGGTTCTCCACCCGACATTAAGAGAGAGAAATCTTAATGCACTGAAACCGGCGC 543
Db      161  CysGlyValLeuHisArgAspIleLeuAspGluAsnIleLeuIleAspLeuAsnArgGly 180
Qy      544  GAACCTCAAACTCATGCACTTCGGGTCGGGGGCGCTGCTCAAGGACAGAGCTACACGGAC 603
Db      181  GluLeuLeuLeuIleAspPheGlySerGlyAlaLeuLeuLeuAspTrpValTyrThrAsp 200
Qy      604  TTGACCGGAACCCGAGGTGACAGTCTTCAAGATGATTCGCTACATCCGCTACCAAGCGC 663
Db      201  PheAspGlyThrArgValTyrSerProGluTrpIleArgTyrHisArgTyrHisArgGly 220
Qy      664  AGCTCGCTCTGTTTGGTCCCTGAGGATCTGCTGTATGACATGATGTTCGCGAGATATT 723
Db      221  ArgSerAlaIleValTrpSerLeuGlyIleLeuLeuLeuLeuAspMetValCysGlyAspIle 240
Qy      724  CCAATTGAGCAGCAGAGAGATGTCAGAGGCGCAATGTAATTTAGGCAAGGCTCTCT 783
Db      241  ProPheGluHisAspGluGlnIleIleArgGlyGlnAlaPhePheArgGlnArgValSer 260
Qy      784  TCAGAAATGTCAACATCTTATTAAGATGATGTCCTGCTGAGACCATGAGACCGGCTTCC 843
Db      261  SerGluCysGlnHisLeuIleArgTrpCysLeuAlaLeuArgProSerAspArgProThr 280
Qy      844  TTTGAAAGAAATCCAGAACATCCGTGGATGCAAGATGTTCTCTGCCCCAGGCCACCGGC 903
Db      281  PheGluGlnIleGlnAsnHisProTrpMetGlnAspValLeuLeuProGlnGluTrpAla 300
Qy      904  GAGATTCATCTGACAGCTGTGACCACTCAACCGAAGAA 942
Db      301  GlnIleHisLeuHisSerLeuSerProGlyProSerLeu 313

RESULT 14
AAW08139
ID  AAW08139 standard, protein; 313 AA.
AC  AAW08139,
DT  11-MAR-1997 (first entry)
DE  Human cytokine response protein CR7.
XX
XX  Cytokine response protein; CR7; Interleukin-2; IL-2;
KW  ligand-stimulated gene expression; diagnosis; therapy; proto-oncogene;
KW  p1m1; protein kinase; lymphoma.
XX
XX  Homo sapiens.
OS
XX
XX  WO9639427-A1.
PN
PD  12-DEC-1996.
XX
PF  05-JUN-1996; 96MO-US009194.
XX
PR  05-JUN-1995; 95US-00461379.
PR  05-JUN-1995; 95US-00462337.
PR  05-JUN-1995; 95US-00462390.
PR  05-JUN-1995; 95US-00463074.

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PR 05-JUN-1995; 95US-00463081.
PR 05-JUN-1995; 95US-00465585.
XX
XX (DART-) DARTMOUTH COLLEGE.
XX
XX Smith KA, Beadling C;
XX
XX WPI; 1997-043062/04.
DR N-PSDB; AAT43382.
XX
XX Cytokine response proteins and genes - used in the detection and therapy
PT of diseases caused by a mutation in the CR coding region.
XX
XX Claim 15, Page 32-33; 81pp; English.
XX
XX Cytokine response proteins CR1-CR8 (AAW08133-40) are encoded by genes
CC (see also AAT43376-83) isolated from a thiol-selected interleukin-2-
CC induced human T-cell blast cDNA library. 6 Genes (CR1, 2, 3, 5, 6, 8) are
CC novel. CR7 is a serine/threonine protein kinase involved in T-cell
CC lymphomagenesis. The CR7 gene is identical to the putative proto-oncogene
CC p1m-1, which is over-expressed in about 50% of MuLV-induced T-cell
CC lymphomas. Recombinant CR7 polypeptides can be produced e.g. as GST
CC fusions for use as immunogens and as diagnostic and therapeutic agents
CC
XX
SQ Sequence 313 AA:

Alignment Scores:
Pred. No.: 5,62e-125 Length: 313
Score: 1623.00 Matches: 302
Percent Similarity: 98.40% Conservative: 6
Best Local Similarity: 96.49% Mismatches: 5
Query Match: 66.43% Indels: 0
DB: Gaps: 0

US-10-705-757-3 (1-1302) x AAW08139 (1-313)
Qy 4 ATGCTCTGTGTCGAAGTCAATCCCTGCGCCACCTGCGGAGACCCCTTGCAAGACCTG 63
Db 1 MetLeuLeuSerIleHisSerLeuAlaHisLeuAlaArgAlaCysAsnAspLeu 20
Qy 64 CACGCAACAGCTGCGCGCGGCAAGAGAGAGACCCCTGAGTCCGACATCCAGTACAGTGT 123
Db 21 HisAlaThrIleLeuAlaProGlyIleGluIleGluIleProLeuGlnSerGlnTyrGlnVal 40
Qy 124 GCGCCGCTGTGGAGCGGCGTTCGCGCTGCTACTCGGACATCCGCGTCCGCGAC 183
Db 41 GlyProLeuLeuGlySerGlyIlePheGlySerValTyrSerGlyIleArgValSerAsp 60
Qy 184 AACTTCCCGGTGGCCATCAAGCACGTGGAAGAGACCGGATTTCCGACTGGGGGAACTG 243
Db 61 AsnLeuProValAlaIleLeuHisValGluIleAspArgIleSerAspTrpGluLeu 80
Qy 244 CCAACGAGACCCGAGTGGCCATGGAAGAGTGTCTGCTGAAGAGAGTGAAGCTCGGCTTC 303
Db 81 ProbenGlyThrArgValPrometGluValLeuLeuLeuValSerSerGlyPhe 100
Qy 304 TCGGCGCTCATTAAGCTTCTGAGCTGGTTCGAGAGCCCGATAGTTCTGTCGATCTCTG 363
Db 101 SerGlyValIleArgLeuLeuLeuSerPheGluArgProAspSerPheValIleLeu 120
Qy 364 GAGAGCCCGAACCCTGCAAGACCTCTGCACTTCACTTCAACCGAGGAGGAGCCCTCAG 423
Db 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
Qy 424 GAGAGCTGGCCCGGAGCTTCTTCTGCAAGTGTCTGAGGCGCTGCGGCAATTCGACAAAC 483
Db 141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgHisCysHisAsn 160
Qy 484 TCGGGGGTTCTCCACCCGACATTAAGAGAGAGAAATCTTAATGCACTGAAACCGGCGC 543
Db 161 CysGlyValLeuHisArgAspIleLeuAspGluAsnIleLeuIleAspLeuAsnArgGly 180
Qy 544 GAACCTCAAACTCATGCACTTCGGGTCGGGGGCGCTGCTCAAGGACAGAGCTACACGGAC 603

```


DB 181 GIULEULYLEULILEAPHEPHEGLYSERGLYALALEULEULYASPHRVALTYTHRASP 200
QY 604 TTTGACGGAACCCGAGTGTACAGTCTCCAGAGTGGATTGCTACCATGCTACACGCGC 663
DB 201 PHEASPGLYTHRARGVALTYRSEPRPROGLUTPRILEARGTYRHSARGTYRHSGLY 220
QY 664 AGGTCGGCTGCTGTTTGGTCCCTGGGAGTCCCTGCTATGACATGGTCTGCCGAGATATT 723
DB 221 ARGSERLAIALAVALTPSERLEUGLYILEULEULTYRHPMETVALCYSGLYASPILE 240
QY 724 CCATTGACACGACGAGAGATGTCAGAGGCGCAAGTGTACTTTAGCAAAAGGCTCTT 783
DB 241 PROPHGLUHHISAPGLUGLUILEILEARGLYGLINVALPHEPHARGGLNARGVALSER 260
QY 784 TCGAATGTCACATCTTTATAGTGTGCTGCTCCCTGAGACATCGGACCGGCTTCG 843
DB 261 SERGLUCYSGLINHISLEULILEARGTTCYVLEUALALEUARGPROSERASPRGPROTHR 280
QY 844 TTTGAGGAATCCAGAACCATCCGTGATGACAGATGTTCTCTGCCCGCACGCGCC 903
DB 281 PHEGLUGLUILEGLNHNHSPROTTPMETGLNAPVALLEULPROGLINGLUTHRALA 300
QY 904 GAGATTCACTGACAGACCTGTGACCATCAACCCAGCAA 942
DB 301 GLULIEHLEULHISERLEUSERPROGLYPROSERLYS 313
RESULT 15
AAV87959 standard; protein; 313 AA.
XX AAV87959;
XX
XX
XX 18-SEP-2000 (first entry)
XX
XX Human CR7 protein.
XX
XX CR2; human; antibody; cytokine response gene; cytostratic; anti-allergic;
XX immunosuppressive; antimicrobial; therapy; cell proliferation; treatment;
XX cell differentiation; cancer; immune disease; rheumatologic disease;
XX transplant rejection; anti-infective; CR7.
XX
XX Homo sapiens.
XX
XX US6057427-A.
XX
XX 02-MAY-2000.
XX
XX 05-JUN-1996; 96US-00652446.
XX
XX 20-NOV-1991; 91US-00796066.
XX 10-AUG-1993; 93US-00104736.
XX 27-OCT-1994; 94US-00330108.
XX 05-JUN-1996; 96WO-US008992.
XX
XX (DART-) DARTMOUTH COLLEGE.
XX
XX Beadling C, Smith KA;
XX
XX MPI, 2000-338623/29.
XX
XX N-PSDB; AAA39677.
XX
XX Novel antibody or antibody fragment which selectively binds to a
XX polypeptide encoded by cytokine response gene 2.
XX
XX
XX Example IV; Col 111-114; 66pp; English.
XX
XX This invention describes a novel isolated antibody or antibody fragment
XX (I) which selectively binds to a polypeptide encoded by cytokine response
XX gene 2 (CR2) and modulates CR2 activity. The products of the invention
XX have cyostatic, anti-allergic, immunosuppressive and antimicrobial
XX activity. The antibodies are useful as therapeutic agents for regulating
XX cellular proliferation and differentiation and for treating all kinds of

CC cancer, immune diseases such as allergic, autoimmune, and rheumatologic
CC diseases, transplant rejection, and as anti-infectives for fighting
CC viral, bacterial, parasitic and fungal infections. This sequence
CC represents the human CR7 protein described in the invention

XX Sequence 313 AA;

XX Alignment Scores:

Pred. No.:	5,626-125	Length:	313
Score:	1623.00	Matches:	302
Percent Similarity:	98.40%	Conservative:	6
Best Local Similarity:	96.49%	Mismatches:	5
Query Match:	66.43%	Indels:	0
DB:	3	Gaps:	0

US-10-705-757-3 (1-1302) x AAV87959 (1-313)

QY 4 ATGCTCTGTGTCAGATCACTCTCCGACCACTGCGGACGCCCTTGCAACACTTG 63
DB 1 MetLeuSerLyIleAaNSerLeuAlaHISLeuArgAlaArgAlaCyAsnAspLeu 20
QY 64 CACGCCAACAGCTGCGCGCGGCAAGAGAGAGGCCCTGAGTCCGACGACAGGTT 123
DB 21 HIsAlaThrLyLeuAlaProGlySGInuLySGInuProLeuGlySerGlnTyGlnVal 40
QY 124 GGCCTGCTGTTGGGAGCGGTGGCTTGGCTGCTACTCGGAGCATCCGCTCCGAC 183
DB 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyRserGlyIleArgValSerAsp 60
QY 184 AACCTGCGGTGGCCATCAAGCAGCTGAGAAAGAACCCGAGATTCCGACTGGGGGAACTG 243
DB 61 AenLeuProValAlaIleAysHISValGInuYAsnArgIleSerAspTrpGlyLeu 80
QY 244 CCCAACGGCACCCGAGTCCCAATGGAAGTGTCTGTAAGAGTGAAGTGGCTTCG 303
DB 81 ProAaNGlyThrArgValProMetGlnValLeuLeuLyValSerSerGlyPhe 100
QY 304 TCGGCGCATTAAGACTTCTGAGCTGTTCAGAGAGCCGAGATGTTGCTGCTGCTG 363
DB 101 SerGlyValIleArgLeuLeuAspTrpPheGlnuArgProAspSerPheValLeuLeu 120
QY 364 GAGAGCGCGGAACCCGTGCAAGACTTTCGACTTCATCAACGAGCGAGAGCCCTCAG 423
DB 121 GluArgProGlnProValGlnAspLeuPheAspPheIleThrGlnuArgGlyAlaLeuGln 140
QY 424 GAGAGCTGGCGCGGAGCTTCTTGGAGAGTGTGAGAGCGCGTCCGAGATTGCCAAC 483
DB 141 GluGlnLeuAlaArgSerPhePheTrpGlnValLeuGlnuAlaValArgHISCySHAsn 160
QY 484 TCGGGGGTCTTCCACCGGACATCAAGAGAGAACATCTTAATGACCTGGAACCGCGCG 543
DB 161 CySGlyValLeuHISArgAspIleLyAsnArgIleuAlaLeuIleAspLeuAsnArgGly 180
QY 544 GAACTCAACTCATGACTTCGGGTGCGGGCGCTGCTCAAGACACAGTCTACAGGAC 603
DB 181 GIULEULYLEULILEAPHEPHEGLYSERGLYALALEULEULYASPHRVALTYTHRASP 200
QY 604 TTTGACGGAACCCGAGTGTACAGTCTCCAGAGTGGATTGCTACCATGCTACACGCGC 663
DB 201 PHEASPGLYTHRARGVALTYRSEPRPROGLUTPRILEARGTYRHSARGTYRHSGLY 220
QY 664 AGGTCGGCTGCTGTTTGGTCCCTGGGAGTCCCTGCTATGACATGGTCTGCCGAGATATT 723
DB 221 ARGSERLAIALAVALTPSERLEUGLYILEULEULTYRHPMETVALCYSGLYASPILE 240
QY 724 CCATTGACACGACGAGAGATGTCAGAGGCGCAAGTGTACTTTAGCAAAAGGCTCTT 783
DB 241 PROPHGLUHHISAPGLUGLUILEILEARGLYGLINVALPHEPHARGGLNARGVALSER 260
QY 784 TCGAATGTCACATCTTTATAGTGTGCTGCTCCCTGAGACATCGGACCGGCTTCG 843
DB 261 SERGLUCYSGLINHISLEULILEARGTTCYVLEUALALEUARGPROSERASPRGPROTHR 280

QY 844 TTGAGAAATCCAGAACATCCGTGATGCGAGATGTTCTCTGCCCCAGCCACCGCC 903
Db 281 PheGluGluIleGlnAsnHisProTrpMetGlnAspValLeuLeuProGlnGluThrAla 300
QY 904 GAGATTGATCTGCACAGCCTGTTCACCATCACCGCAAA 942
Db 301 GluIleHisLeuHisSerLeuSerProGlyProSerLys 313

Search completed: September 22, 2005, 16:47:54
Job time : 178.006 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_blue_n2p model

Run on: September 22, 2005, 16:17:56 ; Search time 42.6688 Seconds
(without alignments)
5871.937 Million cell updates/sec

Title: US-10-705-757-3

Perfect score: 2443
Sequence: 1 gggatgctctctgcacagat.....ggattaaacatgacacat 1302

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+n2p.model -DEV=xjp
-Q=/cgr2_1/USPRO.spool_p/US10705757/runat_22092005_115015_22141/app_query.fasta_1.5333
-DB=PIR -OPMT=faetan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPTC=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=bloum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR SCORE=ppct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPRM=ppc -NORM=ext -HEAPEXT=500 -MINLEN=0 -MAXLEN=200000000
-USPR=US10705757_QCGN_1_1_256 @runat_22092005_115015_22141 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1668	68.3	313	1	S26298
2	1636	67.0	313	1	TVHUP1
3	1584	64.8	313	1	TVMSPI
4	878	35.9	370	1	SS5333
5	622.5	25.5	363	2	T22255
6	495	20.3	409	2	T15435
7	381.5	15.6	504	2	T10449
8	380	15.6	512	1	JC1446
9	380	15.6	1398	2	JC13741
10	378	15.5	481	2	I49072
11	374	15.3	1101	2	S66730
12	372	15.2	512	2	T52633
13	370.5	15.2	511	1	AS6009
14	366.5	15.0	887	2	T20941

15	366	15.0	1358	2	S33653	probable serine/th
16	358.5	14.7	512	2	T07788	probable serine/th
17	358.5	14.7	651	2	S52244	p95g3 protein - A
18	358	14.7	798	2	JC7500	gik protein - chic
19	355.5	14.6	469	2	B84644	probable protein k
20	355	14.5	726	2	T33998	hypothetical prote
21	353.5	14.5	513	1	S60304	serine/threonine-s
22	350.5	14.3	414	2	JN0323	Ca2+/calmodulin-de
23	350.5	14.3	504	2	T07415	probable serine/th
24	348	14.2	472	2	B90100	SNF-related kinase
25	338.5	13.9	1518	2	S37928	probable purine nu
26	338	13.8	445	2	T50802	serine/threonine p
27	337.5	13.8	502	2	T02306	probable protein k
28	336.5	13.8	489	2	T04862	probable serine/th
29	336	13.8	713	2	S27966	probable serine/th
30	336	13.8	1558	2	T29253	hypothetical prote
31	334.5	13.7	339	2	S56719	serine/threonine-s
32	334	13.7	435	2	B84707	probable threonine k
33	333.5	13.7	746	2	S62365	SNF1-related prote
34	333	13.6	520	2	G86414	probable protein k
35	331.5	13.6	513	2	S60303	serine/threonine-s
36	330	13.5	461	2	T14822	probable serine/th
37	330	13.5	774	2	I48609	hypothetical prote
38	328	13.4	442	2	T48203	serine/threonine p
39	328	13.4	745	2	G01025	protein kinase - f
40	326	13.3	423	2	T40224	calcium-activated
41	326	13.3	591	2	S54788	protein H39E23.1 (
42	325	13.3	1246	2	G89287	probable serine/th
43	323.5	13.2	713	2	T37886	serine/threonine-s
44	323	13.2	622	1	S44859	serine/threonine-s
45	322.5	13.2	473	1	S59941	

ALIGNMENTS

RESULT 1

S26298

protein kinase (EC 2.7.1.37) pim-1 - rat

N/Alternate names: Kinase-related transforming protein pim-1; pim-1 proto-oncogene prot

C/Species: Rattus norvegicus (Norway rat)

C/Date: 25-Feb-1994 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004

C/Accession: S26298

R/Wingett, D.; Reeves, R.; Magnuson, N.S.

Nucleic Acids Res. 20, 3183-3189, 1992

A/Title: Characterization of the testes-specific pim-1 transcript in rat.

A/Reference number: S26298; MUID:92319652; PMID:1620615

A/Accession: S26298

A/Molecule type: mRNA

A/Residues: 1313 <WIN>

A/Cross-references: UNIPROT:P26794; EMBL:X63675; NID:956902; PIDN:CAA5214.1; PID:95690

A/Experimental source: testis

A/Note: testis-specific transcript is shorter and more stable than the somatic transcript.

C/Comment: Pim-1 autophosphorylates at unknown sites.

C/Function:

A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoni

A/Note: In testis may be involved in signal transduction events of normal germ cell matu

C/Superfamily: Kinase-related transforming protein; protein kinase homology

C/Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogen

F/36-290/Domains: protein kinase homology <KIN>

F/44-52/Region: protein kinase ATP-binding motif

F/67/Active site: Lys #status predicted

Alignment Scores:

Pred. No.: 5.33e-70

Score: 1668.00 Length: 313

Percent Similarity: 100.00% Matches: 313

Beet Local Similarity: 100.00% Mismatches: 0

Query Match: 68.28% Indels: 0

DB: 1 Gaps: 0

US-10-705-757-3 (1-1302) x S26298 (1-313)

QY 4 ATGCTCTTGCAAGATCAATCTCCCTGCGCCACCTGCGCGCAAGCCCTTGCAAGACCTG 63

Db 1 MetLeuLeuSerLysVilLeaSnSerLeuAlaHilVleuAlaTgAlaAlaProCybAenAerLeu 20

Qy 64 CAGCGCAACAAGCTGGCGCCGGGCAAGAGAGAGCCCTGAGTCCAGTACAGATG 123

Db 21 HlValAlaenLybLeuAlaProGilybGilybGilybProLeuGilybSerGlnTyGlnVal 40

Qy 124 GGGCCGCTGTTGGGCGAGCGGTGGCTTGGGCTCCGCTCTACTCGGGCATCCCGGTGCCGAC 183

Db 41 GilyProLeuLeuGilySerGilyGilyPheGilySerValTySerGilyIleArgValAlaAaP 60

Qy 184 AACTTGGCGGTGGGCATGACGACGTTGGAGAAAGGACCGGATTTCCGATCGGGGGAACTG 243

Db 61 AenLeuProValAlaIleLybHilValGilybAaPArgIleSerAaPTrpGilybLeu 80

Qy 244 CCGAAGCGGACCGGAGTGGCCCATGAGAAAGTGGCTCTGTCGAGAAAGTGAAGCTCGGGCTTC 303

Db 81 ProAenGilybHilArgValProMetGilybValValLeuLeuLybValbAlaSerSerGilyPhe 100

Qy 304 TCGGGCGCTCATTTAGACTTCTGAGACTGGTTCGAGAGCGCCGATAGTTCTGTGTCATCTTG 363

Db 101 SerGilyValIleArgLeuLeuAaPTrpPheGilybArgProAaPserPheValLeuIleLeu 120

Qy 364 GAGAGGGCCGGAACCGGTGCAAGACCTCTTGCAGCTTCACTTCAACCGGAGGAGCGCTCCAG 423

Db 121 GilybArgProGilybProValGilybAaPLeuPheAaPTrpPheIleHilGilybArgGilybAlaGln 140

Qy 424 GAGAGAGCTGGCGCCGAGCTTCTTGGCAGGTGGCTGAGGCGCTGCGGACATTCGCAAC 483

Db 141 GilybLeuLeuAlaArgSerPhePheTrpGlnValLeuGilybAlaValAlaGlnbAaP 160

Qy 484 TGGCGGGCTTCTTCACCGGACATCAAGACGAAACCTTAACTACCTGAACCGCGGC 543

Db 161 CybGilyValLeuHilbAaPArgPilyLeuAaPTrpGilybAlaLeuIleLeuIleAaPLeuAaPArgGily 180

Qy 544 GAAGTCAAACTCATGCACTTTCGGGGTGGGGGGCGGTGCTCAAGACAGAGTCTACAGGAC 603

Db 181 GilybLeuLybLeuIleAaPTrpPheGilySerGilyAlaLeuLeuLybAaPTrpValTyTrpAaP 200

Qy 604 TTTGACGGAACCGGAGTGTACAGTCTTCCAGAGTGAATTCGCTACCACTGGTACCAAGGC 663

Db 201 PheAaPTrpHilArgValTybSerProProGilybTrpIleArgTybHilArgTybHilGily 220

Qy 664 AGGTGGCTGCTGTTGGTCCCTGGGGGATCCTGCTCTATGCAAGTGTGTGGGAGATTT 723

Db 221 ArgSerAlaAlaValTrpSerLeuGilyIleLeuLeuTybAaPMetValCybGilyAaPTrp 240

Qy 724 CCATTGAGCAAGAGAGATGCTCAAGGGGCAAGTGACTTAAAGGAGGTCT 783

Db 241 ProPheGilybHilbAaPArgGilybIleValIlybGilybAlaTybPheAaPArgGilybAlaSer 260

Qy 784 TCAGATGTCAACATCTTATTAGATGATGTCCTGTCCTCCAGACCATCGGCGCTCC 843

Db 261 SerGilybCybGilybHilbAaPTrpPheGilybAaPTrpCybLeuSerLeuAaPTrpSer 280

Qy 844 TTTGAAGAAATCCAGAACCATCCGTGATGAGAGATGTTCTCTGTCGCCAGCGCACCGCC 903

Db 281 PheGilybGilybIleGilybAlaHilbProTrpMetGilybAlaValLeuLeuProGilybAlaHilbAla 300

Qy 904 GAGATTCATCTGCACAGCGCTGTCACCAATCACCAGCAAA 942

Db 301 GilybHilbAaPTrpPheGilybAaPTrpSerProSerProSerTyb 313

RESULT 2

TVHDPI

protein kinase (EC 2.7.1.37) p1m-1 - human

NAltternate names: kinase-related transforming protein p1m-1; p1m-1 proto-oncogene protein

Cispecies: Homo sapiens (man)

CDate: 31-Mar-1989 #sequence revision 07-Oct-1994 #text_change 09-Jul-2004

CAccession: J00327; A46554; A27476; I58412

R:Reever, R.; Spies, G.A.; Kiefer, M.; Barr, P.J.; Power, M.

Gene 90, 303-307, 1990

AltTitle: Primary structure of the putative human oncogene, p1m-1.

A:Reference number: J00327, MUID:90382681, PMID:2205533
A:Accession: J00327
A:Molecule type: DNA
A:Residues: 1-313 <RES>
A:Cross-references: UNIPROT:P11309; GB:M27903; NID:G189958; PID:AAA60090.1; PID:G387022
R:Meeker, T.C.; Nagarajan, L.; ar-Ruehdi, A.; Croce, C.M.
J. Cell. Biochem. 35, 105-112, 1987
A:Title: Cloning and characterization of the human PIM-1 gene: a putative oncogene related
A:Reference number: A46554
A:Accession: A46554
A:Molecule type: mRNA
A:Residues: 1-313 <RES>
A:Cross-references: GB:M24779; NID:G1066790; PID:AAA81553.1; PID:G1066791
R:Zakut-Houri, R.; Hazum, S.; Girol, D.; Teitelman, A.
Gene 54, 105-111, 1987
A:Title: The CDNA sequence and gene analysis of the human pim oncogene.
A:Reference number: A27476; MUID:87277423; PMID:3475233
A:Accession: A27476
A:Molecule type: mRNA
A:Residues: 1-14, 'RA', 17-313 <ZAK>
A:Cross-references: GB:M16750; NID:G189956; PID:AAA60089.1; PID:G189957
R:Domen, J.; Von Lindern, M.; Hermans, A.; Breuer, M.; Grosveld, G.; Berns, A.A.
Oncogene Res. 1, 103-112, 1987
A:Title: Comparison of the human and mouse PIM-1 cDNAs: Nucleotide sequence and immunologic
A:Reference number: I58412; MUID:88217305; PMID:3329709
A:Accession: I58412
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-313 <DOM>
A:Cross-references: GB:M54915; NID:G189961; PID:AAA36447.1; PID:G189962
C:Comment: Pim-1 autophosphorylates at unknown sites.
C:Genetics:
A:Gene: GDB:PIM1
A:Cross-references: GDB:119495; OMIM:164960
A:Map position: 6p21.2-6p21.2
A:Introns: 28/2; 63/3; 80/3; 203/1; 262/1
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F:36-290/Domain: protein kinase homology <KIN>
F:44-52/Region: protein kinase ATP-binding motif
F:67/Active site: Lys #status predicted

Alignment Scores:
Pred. No.: 1,59e-68 Length: 313
Score: 1636.00 Matches: 304
Percent Similarity: 99.04% Conservative: 6
Best Local Similarity: 97.12% Mismatches: 3
Query Match: 66.97% Indels: 0
DB: 1 Gaps: 0

US-10-705-757-3 (1-1302) x TVHUP1 (1-313)

QY	4	ATGCTTTGTCCAAAGATCAACTCCCTGGGCCCACTGGCGCAGGCCCTTGCACGACTCG	63
DB	1	MetLeuLeuSerIysIleAsnSerLeuAlaHisLeuAlaAlaProCysAsnAspLeu	20
QY	64	CACGCCAACAGGTGGCGCCGGGCAAGAGAGAGAGGCCCTCGAGTCGACGACGAGG	123
DB	21	HisAlaThrIleValLeuAlaProGlyLysGluLysGluProLeuGluSerGlnIleVal	40
QY	124	GGCCCGCTGTGGGCGAGCGGTGGCTTCGCGCTCGCTTACTCGGCGATCCGCGCCGAC	183
DB	41	GlyProLeuLeuIlyserGlyGlyPheGlySerAlaIlyserGlyIleArgValSerAsp	60
QY	184	AACTTCCCGGTGGCCATCAAGCAGCTGGAGAGAGACCGGATTTCCGACTCGGGGAACTG	243
DB	61	AsnLeuProValAlaIleIleValHisValGluLysAspArgIleSerAspTyrGlyLeu	80
QY	244	CCCAAGGGGACCCGAGATGCCCAAGGAGAGTGGTCTCTGCGAAGAGGTGAGCTCGGGCTTC	303
DB	81	ProAsnGlyThrIlyrGlyAlaProMetGluValValLeuLeuLysValSerSerGlyPhe	100

QY 304 TCGGGCGCATTTAGACTTTCTGAACTGTTTCGAGAGAGCCCGATAGTTTGGTGCATCCCTG 363
 Db 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleLeu 120
 QY 364 GAGAGGCCCGAACCCTGTCAGAGACCTTTGCACTTCATCACCGAGCGAGACCCCTCCAG 423
 Db 121 GluArgProGluProValGlnAspLeuPheAspHeiIeThGluArgGlyAlaLeuGln 140
 QY 424 GAGAGACTGGCCCGGAGCTTTCTTGGCAGGCTGTGAGAGCCGTGGCGCATTTGCCAAG 483
 Db 141 GluGluLeuAlaArgSerPhePheTrpGlnValIleuGlnAlaValArgHisAsn 160
 QY 484 TGGGGGGTCTCCACCCCGACATCAAGAGCAATCTTAATGACTGAAACCGGGC 543
 Db 161 CysGlyValIleuHisArgAspIleuAspGluAsnIleuIleAspLeuAsnArgGly 180
 QY 544 GAACCTCAACATCATGCACTTCGGGTCGGGGCGGCTGTCAAGAGACAGTTCACAGAG 603
 Db 181 GluLeuLeuLeuIleAspPheGlySerGlyAlaLeuLeuLeuAspThrValIlyTrpAsp 200
 QY 604 TTTCAGCGAACCAGAGTGTACGTCCTTCAGAGTGGATTCGTACATCGTATCACAGCG 663
 Db 201 PheAspGlyThrArgValIlySerProGluTrpIleArgIlyHisArgIlyHisGly 220
 QY 664 AGGTGGCTGCTGTTTGGTCCCTGGGAGTCTGCTGTATGACATGCTGTGGAGATATT 723
 Db 221 ArgSerAlaIleValTrpSerLeuGlyIleLeuLeuIyTrpAspMetValCysGlyAspIle 240
 QY 724 CCAATTGAGACGACGAGAGATGTCAGAGGGGCCAAGGTGATCTTAAGCAAGGGCTCT 783
 Db 241 ProPheGluHisAspGluGluIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
 QY 784 TCAGAAATGTCAACATCTTATTAGATGATGCTGTCTCCAGAGCAATCGAGCCGGCTCC 843
 Db 261 SerGluCysGlnIleuIleuIleArgTrpCysLeuAlaLeuArgProSerAspArgProThr 280
 QY 844 TTGGAAGAAATCCAGAACCATCGGTGATGACAGATGTTCTCTGCCCCAGGCCACCGCT 903
 Db 281 PheGluGluIleGlnAsnHisProTrpMetGlnAspValIleuLeuProGlnIleThrAla 300
 QY 904 GAGATTCATGCGACAGCGCTGTCAACATCACCACCGCAAA 942
 Db 301 GlnIleHisLeuHisSerLeuSerProGlyProSerIys 313

RESULT 3
 TVMSPI
 protein kinase (EC 2.7.1.37) p1m-1 - mouse
 N/AInteract names: Kinase-related transforming protein p1m-1; p1m-1 proto-oncogene prote
 C/Species: Mus musculus (house mouse)
 C/Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
 C/Accession: A24169
 R/Setlen, G.; Cuypers, H.T.; Boelens, W.; Robanus-Manday, E.; Verbeek, J.; Domen, J.; V
 Cell 46, 603-611, 1986
 A/TITLE: The primary structure of the putative oncogene p1m-1 shows extensive homology w
 A/Reference number: A24169; MUID:86272109; PMID:3015420
 A/Accession: A24169
 A/Molecule type: DNA
 A/Restrict: 1-313 <SBL>
 A/Cross-references: UNIPROT:P06803; GB:M13945; GB:M13946; NID:9200352; PTDN:AAA39930.1;
 C/Comment: P1m-1 autophosphorylates at unknown sites.
 C/Genetics:
 A/Gene: p1m-1
 A/Intron: 28/1; 63/3; 80/3; 203/1; 262/1
 C/Function:
 A/Description: catalyzes the formation of peptidyl-L-serine-phosphate or peptidyl-L-threonin
 C/Superfamily: kinase-related transforming protein; protein kinase homology
 C/Keywords: ATP; autophosphorylation; phosphotransferase; proto-oncogene; serine/threonin
 P.136-290/Domain: protein kinase homology <KIN>
 P.146-52/Region: protein kinase ATP-binding motif
 P.167/Active site: Lys #status predicted

Alignment Scores:

Pred. No.:	3,94e-66	Length:	313
Score:	1584.00	Matches:	295
Percent Similarity:	96.81%	Conservative:	8
Best Local Similarity:	94.25%	Mismatches:	10
Query Match:	64.84%	Indels:	0
DB:	1	Gaps:	0
US-10-705-757-3 (1-1302) x TWMSPI (1-313)			
QY	4 ATGCTCTTGTCCAGATCAACTCTCCCTGGCCCACTGGCGGCAAGCCCTTGGAACGACTTG	63	
DB	1 MetleuleuSerIylelleasnSerleuAlaHleuAArgProCysaaenAerleu	20	
QY	64 CAGGCGCAACAACCTGGCGCGGCGCAAGAGAGAGACCCCTGGAGTCGCACTGCGAGTG	123	
DB	21 HlsAlaThrLyseAenAlaProGlyuysGlyuysGluProleuInduSerGlnTyGlnVal	40	
QY	124 GGGCCGCTGTGTGGAGCGAGTGGCTTCCGCTGGCTACTCGGGCACTCCGCTCGCGAC	183	
DB	41 GlyceroleuLeuGlySerDyGlyPheGlySerValTySerDyGlyleAArgValAlaAsp	60	
QY	184 AACTTGGCGGTGGCCATCAAGCAAGCTGGAGAAAGAACCGGATTTCCACTGGGGGAACTG	243	
DB	61 AsnleuProvalAlaIlelyeHlsValGluysAspArgIleSerAspTrpGlyGluLeu	80	
QY	244 CCGAAGCGAACCCGAGTCCCATGGAAAGTGCCTGTGAAGAAGGTGAGCTGGGCTTC	303	
DB	81 ProaenGlyThrAArgValaPrometGlnValleuLeuLyseValSerSerAspPhe	100	
QY	304 TCGGCGCTCATTAAGACTTCTGGACTGGTTCGAGAGGCGCCGATAGTTTCGTGCTGATCTTG	363	
DB	101 SerGlyVallelleArgleuLeuAspTrpPheGlnuAArgProAspSerPheValleuIleu	120	
QY	364 GAGAGCGCCGAAACCCGTGCAAAACTCTTGCACTTATCAACGAGCGAGAGCCCTCAG	423	
DB	121 GluAArgProGluProValGlnAspPheAspPheIleThrGluAArgGlyAlaLeuGln	140	
QY	424 GAGGAGCTGGCGCGGAGCTTCTTGCGAGAGTGCCTGGAGCGCTGGGGCACTTGCACAAC	483	
DB	141 GluAspLeuAlaArgGlyPhePheTrpGlnValleuGlnAlaValArgHlsCysHlsAsn	160	
QY	484 TCGGGGGTCTTCCACCGCGACATCAAGGACGAACTTTAATCGACCTGGAACCGCGGC	543	
DB	161 CysGlyValleuHlsAArgAspTrleuysAspGluAenIleuHlsAerleuSerAArgGly	180	
QY	544 GAACTCAAATCATGACTTGGGGTGGGGGGCGCTGCTCAAGGACACAGCTTACAGCGAC	603	
DB	181 GluIleuLyseuIleAspPheGlySerGlyAlaIleuLeuLyAspPheArgValTyTrpAsp	200	
QY	604 TTTGACGGAACCCGAGTGAAGCTCTCCAGAGTGAGTTGCGTACCATGGTATCCAGCGGC	663	
DB	201 PheAspGlyThrAArgValTySerProArgGluTrpIleArgGlyTrHlsArgGly	220	
QY	664 AGGTGGCGTGTGTGGCTCCCTGGGGAACTCTGCTATAGACATGGCTGCGGAGATATT	723	
DB	221 ArgSerAlaAlaValTrpSerleuGlyIleleuLeuTyAspMetValCysGlyAspIle	240	
QY	724 CCATTGAGACAGAGAAAGATCGTCAAGGGCCAAAGTACTTTAGGCAAGGGTCTCT	783	
DB	241 PropheGluHlsAAspGluGluIleTrleuysGlyGlnValPheAspPheArgGlnThrValSer	260	
QY	784 TCAGAAATGCAACATTTATTAAGATGGTGGCTGGCTCCGAGACATCGGACCGGCGCTGC	843	
DB	261 SerGluCysGlnHlsleuIleuysTrpCysAspSerleuAArgProSerAspArgProG	280	
QY	844 TTTGAAGAAATCCAGAACATCCGTGTGAATGCAAGATGTTTCTGCTGGCCGAGCGCACCGC	903	
DB	281 PheGluGluIleuIleAArgAsnHlsProTrpMetGlnGlyAspLeuLeuProGlnAlaAlaSer	300	
QY	904 GAGATTATCTGCACAGGCTGTACACCATACCCACAGAA 942		
DB	301 GluIleHlsleuHlsSerleuSerProGlySerIleys 313		


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Db      235 lylleuProPheargEngluileGluileCylleuGlyAbaVallyPheProAap 254
Qy      778 GTGTCCTTCAGAAAGTCAACATCTTATTAAGTGGCTGCTCCCTGAGACATCGGACCG 837
Db      255 LeuSerlyGelValValCysGluLeuVallySerCysLeuThrThrSerThrSerAlaArg 274
Qy      838 CCTCTCTTCAGAAATTCAGAACCATCCCTGGATGCAG----- 876
Db      275 AlaSerLeuAlaGluLeuLeuAlaAlaHleProTPrMetGluThrAspLysProPheNegly 294
Qy      877 ---GATGTCCTCTGCCCCAGCCGACCCGCAAGATT 909
Db      295 GlyAspLeuThrPheGluGluValAlaLeuMetGluile 306

RESULT 7
T10449
probable serine/threonine-specific protein kinase (EC 2.7.1.-) - cucumber
N:Alternate names: SNF1-related protein kinase
C:Species: Cucumis sativus (cucumber)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10449
R:Gimpel, N.J.
submitted to the EMBL Data Library, December 1996
A:Reference number: Z17020
A:Accession: T10449
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-504 <GUM>
A:Cross-references: UNIPROT:P91113; EMBL:Y10036
A:Experimental source: cv. Maeterpiece; cotyledon
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C:Keyword: AMP-activated protein kinase; protein kinase homology
F:6-260/Domain: protein kinase homology <KIN>

Alignment Scores:
Pred. No.:      8.69e-11      Length:      504
Score:          381.50      Matches:     124
Percent Similarity: 46.39%      Conservative: 69
Best Local Similarity: 29.81%      Mismatches: 165
Query Match:      15.62%      Indels:      58
DB:              2          Gaps:      16

US-10-705-757-3 (1-1302) x T10449 (1-504)
Qy      115 TACCAAGTGGCGCGCTGTGGGAGCGGTGGCTGGCTGCTTACTCGGCAATCGC 174
Db      8 TyltylLeuGluGlyThrLeuGlyLeuGlySerPheGlyVallyValleAlaGluHis 27
Qy      175 GTGGCGCAACATTCGCCGCGGCATCAAGCAGTGGAGAACGCGGATTCGCACTGG 234
Db      28 AlaLeuThrGlyHisVallyValleAlaLeuValleLeuAsnArgArglyValleValan--- 46
Qy      235 GGGGAATTCGCCCAACGCGACCCGAGTGCCTGAGAAAGTGGCTGAAGAAAGTGAAC 294
Db      47 -----LeuAspMetGluGluVallyValArgArgGluLeuValleLeuAsnArgLeuPheMet 64
Qy      295 TCGGGGCTTCTCGGCGCTGATTGACTTGTGGAAGTGTTCGAGAGCGCGGATGCTTCG 354
Db      65 -----HisProHislelleArgLeuValleValleGluThrProSerAspIleTy 82
Qy      355 CTGATCTGTGAGAGCGCCGCAACCGGTGCAAGACTCTTCGACTTCATCCGACCGAGGA 414
Db      83 ValValMetGluVallySer---GlyGluLeuPheAspTyrlleValGluValy 101
Qy      415 GCCCTCCAGAGAGAGCGCCGAGGCTTCTTCGAGCGGTGGAGCGCGTGGCGGACT 474
Db      102 ArgLeuGluGluValArgValleAlaArgAsnPheGluGluLeuIleleSerGlyValGluTy 121
Qy      475 TGGCCAAACTGCGGGGTTCTTCACCGCGACATCAAGAGCAGAGAACTTAAATGACTG 534
Db      122 CysHisArgAsnMetValValHisArgAspLeuLysProGluLeuLeuLeuAsp--- 140

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Qy      535 AACCGGGCAACTCAATCATGACTTCGAGGTGGGGCGCTGCTCAAGACAGATC 594
Db      141 SerLysCysAbaVallylelleAlaAspPheGlyLeuSerAsnIleMetArgAspGlyHis 160
Qy      595 TACACGAGCTTTGAC---GGAACCCGAGTGAACAGTCTCCAGAGTGAATTCGTAACAT 651
Db      161 PheLeuLysThrSerCysGlySerProAsnTyrlaAlaProGluValleleSerGlyLys 180
Qy      652 CGCTACCAACGAGAGTGGCTGCTGTTGGTTCCTCGGAGATCTGCTGTAACATGATC 711
Db      181 LeuTyrlaGlyProGluValaAspValIlySerCysGlyVallelleuTyrlaLeuLeu 200
Qy      712 TCGCAGATATTCATTGAGCAGCAGAAAGATC-----GTCAAG 753
Db      201 CysGlyThrLeuProPheAsp---AspGluAbaNlleProAbaLeuPheLysIleLys 219
Qy      754 GGCCAAGTGTAC---TTTAAAGCAAGGCTCTTTCAGAAATGCAACATTTATTAGATGC 810
Db      220 GlyGlyIleTyrlThrLeuProSerHisLeuSerSerGlyAlaArgGluLeuIleProSer 239
Qy      811 TGCCTGCTCCCTAGAACATCGGACCGGCTCTTGAAGAAATCCAGAACCATCGGTG 870
Db      240 MetLeuValaAspProMetLysArgIleThrIleProGluIleArgGluHisProTyr 259
Qy      871 ATGCAAGATGTTCTCTGCCCCAGCCGACCGGAGATCATCTGCACAGCCTGTCAACCA 930
Db      260 PheGlu-----AlaHisLeuProArgTyrlleuAlaValPro 271
Qy      931 TCACCCAGCAATAGACGACCATCTGTGACAGCCCTCCAGAGAAAGAGAGCTTGTCTGT 990
Db      272 ProPro-----AspThrMetGluGluAlaLysValleAspGlu 284
Qy      991 GGCCTTCACAGACACCTGCTTACAGATGACAGGACAGAAAGACAACTCATTCAGAGT 1050
Db      285 AspIleLeuGluGluVallyVallyMetGlyPheAspArgAsn-----GluLeu 300
Qy      1051 CCGGGGCTCCCTGAGACAACTCCCTCAAGAGAAAGATTAAGTCA-----CTCGTCT 1104
Db      301 ValGluSerLeuArg-AsnArgIleGluAsnGluAlaThrValaAlaTyrlleuLeu 320
Qy      1105 GGAACCCGCTTGGCCCTTCACAGACTCACTGAGCGTTCAGTGGCTGCGCTCGCAAGT 1164
Db      320 AspAsnArgPhe-----ArgValSerSerGlyTyrlleGluAlaGluPheG 336
Qy      1165 CCGGGGTGTGGGGGGGAGAGTGGAGTGGGTTCAGAGCCCTGATGAACTTAAGTCA 1224
Db      336 nGluThrMet-----GluThrGlyPheAsnArgMetHisProSerAspProth 352
Qy      1225 CATGAGACTGTGGTCAACCA-----GATGGGCGCCAGGTAGGAG----- 1264
Db      352 AsnProAlaValGlyHisArgLeuProGlyTyrlMetAspTyrlGluGlyMetGlyLeuArg 372
Qy      1265 -----AAAAACATTTGGGGGTTGGGATTTAAAAACT 1294
Db      372 GAlaGluPheProValGluArgLysTrpAlaLeuGlyLeuGluIns 387

RESULT 8
JCI446
serine/threonine-specific protein kinase (EC 2.7.1.-) AR21 - Arabidopsis thaliana
N:Alternate names: protein kinase SNF1 homolog
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JCI446; S58266; S66334
R:Leguen, L.; Thomas, M.; Blanch, M.; Halford, N.G.; Kreis, M.
Gene 120, 249-254, 1992
A:Title: Structure and expression of a gene from Arabidopsis thaliana encoding a protei.
A:Reference number: JCI446; MUID:93013041; PMID:1339373
A:Accession: JCI446
A:Molecule type: DNA
A:Residues: 1-512 <LEGS>
A:Cross-references: UNIPROT:Q38997; GB:M93023; NID:g166599; PIDN:AAA3236.1; PID:g16660
R:Thummler, F.; Kirchner, M.; Teuber, R.; Dietrich, P.

```



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Db      84 GluValValGluThrProSerAspIleTy-ValValMetGluTyValIleSer---Gly 102
Qy      385 GACCTCTTGCATTGCACCGGAGGAGCCCTTCAGAGAGAGCGGCCCGAGCTTC 444
      103 GluLeuPheApyrTylValGluValArgLeuIndIlePheGluValAaGlyPhe 122
Qy      445 TTTCGAGGTTGTCGAGGCGGCGATTTCGACAACTCGGGGTTCTCAACCGGAG 504
      123 PheGlnIndIleIleSerGlyValGluTy-CyHisArgAsnMetValIleHisArgAsp 142
Qy      505 ATCAAGACGAGAAATCTTAAATGACGTGAACCGCGCGCAACTCAATCATGACTTC 564
      143 LeuLeuProGluLeuLeuLeuLeuAsp---SerIleTyrAsnValIleValIleAspPhe 161
Qy      565 GGGTCGGGGCGCTGCTCAAGACACAGTCTACAGCACTTTGAC---GGAACCCGAGTG 621
      162 GlyLeuSerAsnIleMetArgAspGlyHisPheLeuIleTyHisSerCysGlySerProAsn 181
Qy      622 TACAGTCTCTCAGAGTGGATTTCGCTACATCGCTACACGCGAGTGCGGCTGGTTTG 681
      182 TyrAlaIleProGluValIleSerGlyLeuLeuTyraGlyProGluValAspValTyr 201
Qy      682 TCCCTGGGAGTCTGCTCTATGACATGCTGTCGAGATATTCATTGACAGCAAC--- 738
      202 SerCysGlyValIleLeuTyraIleLeuLeuCysGlyThrLeuProPheAspArgIleAsn 221
Qy      739 -----GAAAGATCTGTCAGGCGGCAAGTGTACTTAAAGCAAGGCTCT 783
      222 IleProAsnLeuPheLeuValIleGlyGlyMetIleSerLeuProSerHisLeuSer 241
Qy      784 TCAGAAATGTCACATCTTATTAGATGTCGCTGCTCCAGACATCGAGCGCCCTGC 843
      242 AlIGlyAlaArgAspLeuIleProArgMetLeuIleValAspProMetIleValArgMetTyr 261
Qy      844 TTGAGAAATTCAGAACATCCGTCGATGACAGATGTTCTCTGCGCCGAGCCAGCCG 903
      262 IleProGluIleArgMetHisProTyrPheGln-----Ala 273
Db      904 GAATTCATCTGCACAGCCCTGTCACTCAACCCAGCAATAGACCATTTCTGCAGACC 963
      274 HisLeuProArgTyrIleValAlaValProProPro-----AspThr 286
Qy      964 CTCGAGGAGAGAGAGATGTCGTGTCGTCGCTCAACAGACCCCTGCTTACGATGACG 1023
      287 MetGlnHisAlaValIleValIleAspGluAspIleLeuGlnIleValIleValArgGlyPhe 306
Qy      1024 GACAGAAATGAC-----AATCATTTCCAGGCTCCGCGGCTCCCTG 1062
      307 AspArgAsnSerLeuValAlaSerLeuCysAsnArgValGlnAsnGluGlyThrVal 325
Db

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RESULT 14
T20941
hypothetical protein F15A2.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T20941
R:category: J.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19349
A:Accession: T20941
A:status: preliminary; translated from GB/EMBL/DBJ
A:molecule type: DNA
A:releases: 1-887 <MIL>
A:cross-references: UNIPROT:Q19469; EMBL:Z70207; PIDN:CAA94127.1; GSPDB:GN00028; CESP:F1
A:experimental source: clone F15A2
C:genetics:
A:gene: CESP:F15A2.6
A:map position: X
A:features: 32/1; 63/3; 92/2; 139/2; 189/3; 328/2; 448/2; 516/3; 604/2; 684/3; 735/2; 777

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Alignment Scores:      3,92e-10      Length:      887
Pred. No.:      366.50      Matches:      119
Score:

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Query Match: 15.00%      Indels: 71
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Qy      175 GTGCGCGCAACAATTGCGCGGTCATCAAGACAGTGAAGAAGACCGGATTTTCCAGTGG 234
      40 CysIleThrGlyArgValHisAlaIleValIleValAsnValGluIleValSerGlu--- 58
Qy      235 GGGAAATGCCCAACGCGACCCGAGTCCCATGAAGATGGCTCTGCTGAAGAGTGAAC 294
      59 -----SerValLeuGlnIleValGluArgGluIleAlaIleMetIleValIleGlu 75
Db      295 TCGGGCTTCGGGCGCTCATTAAGATTTTGCATGCTGTTGAGAGGCGCGATTTTCGTG 354
      76 -----HisProHisValIleHisIleValTyrAspValTyrGluAsnValIleValTyr 93
Qy      355 CTGATCTGAGAGAGCGCCGACCCGACCTTCTGACAGTGTGAGAGCGCGGAT 474
      94 LeuLeuLeuGluIleHisValIleSerGly---GlyGlyLeuPheAspTyrLeuValArgGly 112
Db      415 GCGCTCAGAGAGAGCTGGCGCGAGCTTCTTGGCAGGTGTGAGAGCGCGGAT 474
      113 ArgLeuMetSerIleGluIleAlaArgIlePhePheArgGlnIleIleSerHisLeuAspPhe 132
Qy      475 TGCCCAACATGCGCGGTTCTCCACCGCGACATACAGAGAGAAATCTTATATGACCTG 534
      133 CysHisAlaHisValAsnIleCysHisArgAspLeuIleProGluAsnLeuLeuAsp--- 151
Qy      535 AACCGGCGGCAATCAATCAATCAATCGAGTTCGGGTCGGGCGCGT---CTCAAGACACA 591
      152 GluArgAsnAsnIleValIleValAlaAspPheGlyMetAlaSerLeuGlnValIleGlySer 171
Db      592 GTCTACACGAACTTTGACGGAACCCGAGTGTACAGTCTTCAGAGTGTGCTACAT 651
      172 MetLeuGluIleHisSerCysGlySerProHisTyrAlaCysProIleValIleArgGlyGlu 191
Qy      652 CGTCAACAGGACGAGGTCGCTGTTTGTGCTCCGAGGATCTGCTTATGACAGTGC 711
      192 LysTyrAspGlyArgValIleAspValIleTyrSerCysGlyValIleLeuTyraIleLeu 211
Qy      712 TCGGAGATTAATTCATTGAGCAGCAGC-----GAAAGATCGTCAAG 753
      212 ValGlyAlaLeuProPheAspPheAspValAsnValGluValIleValValIleValArg 231
Db      754 GCGCAAGTACTTTAGGCAAGAGTCTCTTCAGAAATGCAATCTTATTAGATGTCG 813
      232 GlyValPheHisIleLeuHisPheValProHisAspValGlnSerLeuAspArgLamet 251
Qy      814 CTGTCCTGACAGCATCGAGCGGCTCTTGAAGATACAGAAACATCGCTGAGATG 873
      252 IleGluValAspProGlyLysValTyrSerLeuAlaAspValPheLeuHisProTyrVal 271
Qy      874 CAGGATGTTCTGCTGCCAGGCGACCGGCGGATTCATCTGACAGCTGTACACATCA 933
      272 SerGlyThr-----ThrValAsnProGluIleLeu----- 283
Db      934 CCCAGCAATAGACAGCATTTGTGCAGCCTTCAG-----GGAAGAGAG 978
      284 -----PrometSerGlnValValGlnThrHisValIleProGlyGluAsp 298
Qy      979 AGTTTCTGCTGCGC---CTCCACAGACCCCTGCTTACATGC---AGGACAGAAAT 1032
      299 SerIleAspProAspValLeuArgHisMetAsnCysValGluGlyCysPheLysAspLys-Gl 318
Db      1033 GACAACTATTCAGGCTCCGCGGCTCCGAGCAACCTC----- 1072
      318

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Db 318 nlyslleuileanlululeuSerProlyshlsaenthrGlulymetValtyr-Phele 338
 QY 1073 -----CCTCAAGAGAAAGACTAGTACTGTCCTG-- 1105
 Db 338 ulleuAapArglysaArgArgArgProhlaaglnuAapPThGluileValleuAr 358
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 Db 358 gglYlaAlaAlaGlnAenAenAapProProlYslYsaArgThraPseSerArgThSer-- 377
 QY 1147 GCGTCGCGTCCCAAGAGTCCCGGCTGGGGGGAGGTGGAGTGGGTCAAGCCCTG 1206
 Db 378 -----ArgTyrProMetGlySerIleAlaAepGlySerProIleasnPro-- 392
 QY 1207 TCATGAACCTTAGTACCATGAGACTGTGGGTCAACAGATGGCCAGGTAGAGGAA 1266
 Db 393 -----ArglyserThryGlyArg-AenGlnYsSerGlyArgHlas 406
 QY 1267 AAACATTTGGGGGG 1280
 Db 406 erSerleuclYgly 410

RESULT 15

S33653

probable serine/threonine protein kinase (EC 2.7.1.-) - Yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein YAL002; protein YAL017W; secretory protein SPD138
 C:Species: Saccharomyces cerevisiae
 C>Date: 30-Sep-1993 #sequence_revision 02-Aug-1994 #text_change 16-Aug-2004
 C:Accession: S33653; S36717; S36732; JH0486
 R:Clark, M.W.; Zhong, W.W.; Keng, T.; Storme, R.K.; Ouellette, B.F.F.; Barton, A.; Kabac
 Yeast 9, 543-549, 1993
 A>Title: The YAL017 gene on the left arm of chromosome I of Saccharomyces cerevisiae enc
 A:Reference number: S33653; MID:93311122; PMID:8322517

A:Accession: S33653
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-1358 <CL>

A:Cross-references: UNIPROT:P31374; EMBL:L05146
 R:Ouellette, F.; Clark, M.W.; Keng, T.; Storme, R.K.; Zhong, W.; Zeng, B.; Fortin, N.; D
 Submitted to the EMBL Data Library, January 1993

A:Description: Sequencing of Chromosome I from Saccharomyces cerevisiae: analysis of a 3
 A:Reference number: S36711
 A:Accession: S36717
 A:Molecule type: DNA
 A:Residues: 1-864,867-1358 <ONE>

A:Cross-references: EMBL:L05146; MID:g171851; PIDN:AAC04940.1; PID:g171858; MIPS:YAL017W
 R:Clark, M.W.; Zhong, W.W.; Keng, T.; Storme, R.K.; Barton, A.; Kaback, D.B.; Bussey, H.
 Yeast 8, 133-145, 1992
 A>Title: Identification of a Saccharomyces cerevisiae homolog of the SNF2 transcriptiona
 A:Reference number: S22266; MID:92221690; PMID:1561836

A:Accession: S36732
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-862 <CL2>

A:Cross-references: EMBL:S93805
 R:Sidhu, R.S.; Mathewes, S.; Bollon, A.P.
 Gene 107, 111-118, 1991

A>Title: Selection of secretory protein-encoding genes by fusion with PHOS in Saccharomy
 A:Reference number: JH0483; MID:92077420; PMID:1743509
 A:Accession: JH0486
 A:Molecule type: DNA
 A:Residues: 1-72, 'E', 74-154 <SID>

C:Genetic:
 A:Gene: SGD:FUN31; SSP138
 A:Cross-references: SGD:S0000015; MIPS:YAL017W
 A:Map position: 1L

C:Superfamily: protein kinase homology
 C:Keywords: ATP; glycoprotein; phosphotransferase; serine/threonine-specific protein kin
 F:1096-1356/domain: protein kinase homology <KIN>
 F:1104-1112/region: protein kinase ATP-binding motif
 F:8,128/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:1232/Active site: Asp #status predicted

Alignment Scores:
 Pred. No.: 3,886-10 Length: 1358
 Score: 366.00 Matches: 86
 Percent Similarity: 55.04% Conservative: 56
 Best Local Similarity: 33.33% Mismatches: 100
 Query Match: 14.98% Indels: 16
 DB: 2 Gaps: 6

US-10-705-757-3 (1-1302) x S33653 (1-1358)

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 QY 193 GTGGCCATCAAGACAGTGGAGAGACCGGATT-----TCGACTGGGGGAGACTGGCC 246
 Db 1124 ValValIleYMetIlePheYseGlnYrGlyIleValAspThrTrrValArgAspArg 1143
 QY 247 AACGCGACCCGAGTCCCATGAGAGTGGTCTGTGTAAGAAAGTAGC--TCGGGCTTC 303
 Db 1144 LysLeuGlyThrIleProSerGlnIleGlnIleMetAlaThrLeuAsnYlyAspProHls 1163
 QY 304 TCGGCGCTCATTAAGACTTGTGACTGTGTCCAGAGCCCGATGTTGTGCTGATCCG 363
 Db 1164 GluAenIleLeuArgLeuAspPhePheGlnAspAspTyrTyrIle----- 1181
 QY 364 GAGAGCCCGAACCCGTGCA-----GACCTTCGACTTCATTCACC 405
 Db 1182 -----GlnThrProValHlsGlyGlnTyrGlyCyHleAspLeuPheAspIleGln 1199
 QY 406 GAGCGAGAGCCCTCAGAGAGAGTGGCCCGGACTTCTTGTGCAAGTGTGAGAGCC 465
 Db 1200 PheYsThrAsnMetThrGlnPheGlnAlaYlyLeuIlePheYsGlnValValAlaGly 1219
 QY 466 GTGGCGCTTGGCCACACTCGCGGGTTCCTCCAGCCGACATTAAGAGAGAAACTTTA 525
 Db 1220 IleYshIleYHlsAspGlnGlyIleValHlsArgAspIleYAspGlnAsnValIle 1239
 QY 526 ATCGACCTGAACCGCGGAGAACTCAAACTCACTCGACTCGGGTGGGGCGCTGCTCAG 585
 Db 1240 ValAsp---SerYsGlyPheValYsIleIleAspPheGlySerAlaAlaTyrValYls 1258
 QY 586 GACACAGTCTACACGCACTTTGACCGAAACCGAGGTACAGTCTTCAGAGTGAATCGC 645
 Db 1259 SerGlyProPheAspValPheValGlyThrIleAspTyrAlaAlaProGluValIleugly 1278
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 Db 1299 ValValPheYsGlnAsnProPheYrAsnIleAspGlnIleGlnGlnYlyAspLeuYls 1318
 QY 766 TTTAGG-----CAAGGGTCTCTTCAGAAATCAACTTTATTAGATGTCCTGTCC 819
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 QY 820 CTGAACCATCGGACCGGCTCTTGAAGAAATCCAGAACCATCCGATG 873
 Db 1339 ArgCyValProYsArgProThrIleAspAspIleAenAsnAspYsTrpLeu 1356

Search completed: September 22, 2005, 17:20:31
 Job time : 58.6688 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 22, 2005, 16:20:36 ; Search time 24.7742 Seconds

(without alignments)
5676.828 Million cell updates/sec

Title: US-10-705-757-5

Perfect score: 1749
Sequence: 1 atgcctcctgcacagatcaaa.....caccggagatccagcaagtag 942

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Ygapop 10.0 , Ygapext 0.5	
Fgapext 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1668	95.4	313	3	US-09-237-543-7
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3	1584	90.6	313	3	US-09-237-543-8
4	1584	90.6	313	3	US-09-237-543-8
5	1582	90.5	313	3	US-09-237-543-9
6	1582	90.5	313	3	US-09-237-543-9
7	1580	90.3	313	2	US-08-463-3908-26
8	1580	90.3	313	2	US-08-463-3908-26
9	1580	90.3	313	3	US-08-463-3908-26
10	1580	90.3	313	3	US-08-463-3908-26
11	1580	90.3	313	3	US-08-465-585C-26
12	1580	90.3	313	3	US-08-652-446-26

13	1355.5	77.5	257	2	US-07-857-224B-41	Sequence 41, Appl1
14	1122.5	64.2	455	3	US-09-237-543-5	Sequence 5, Appl1
15	1122.5	64.2	455	3	US-09-237-543-5	Sequence 5, Appl1
16	1119	64.0	326	3	US-09-237-543-2	Sequence 2, Appl1
17	1119	64.0	326	3	US-09-237-543-2	Sequence 2, Appl1
18	1113	63.6	323	3	US-09-237-543-6	Sequence 6, Appl1
19	1113	63.6	323	3	US-09-237-543-6	Sequence 6, Appl1
20	1065.5	60.9	254	3	US-09-237-543-4	Sequence 4, Appl1
21	1065.5	60.9	254	3	US-09-237-543-4	Sequence 4, Appl1
22	856	48.9	312	4	US-09-949-016-7140	Sequence 7140, Ap
23	379	21.7	1101	3	US-09-770-170-8	Sequence 8, Appl1
24	377.5	21.6	776	4	US-09-523-849-34	Sequence 34, Appl1
25	372	21.3	1356	3	US-09-770-170-6	Sequence 6, Appl1
26	371	21.2	778	4	US-10-116-326-2	Sequence 2, Appl1
27	371	21.2	778	4	US-10-116-326-2	Sequence 2, Appl1
28	371	21.2	1333	3	US-09-770-170-2	Sequence 2, Appl1
29	370	21.2	511	4	US-09-633-328B-4	Sequence 4, Appl1
30	367	21.0	512	4	US-09-633-328B-2	Sequence 2, Appl1
31	361.5	20.7	281	4	US-09-248-796A-20512	Sequence 20512, A
32	359.5	20.6	630	4	US-10-355-975A-38	Sequence 38, Appl1
33	359.5	20.6	631	4	US-09-579-664B-11	Sequence 11, Appl1
34	359.5	20.6	631	4	US-10-355-975A-11	Sequence 11, Appl1
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37	345	19.7	722	4	US-08-817-832B-32	Sequence 32, Appl1
38	344	19.7	722	4	US-09-884-890-4	Sequence 4, Appl1
39	344	19.7	722	4	US-10-274-194-4	Sequence 4, Appl1
40	344	19.7	1005	3	US-09-770-170-4	Sequence 4, Appl1
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42	343	19.6	724	4	US-10-274-194-2	Sequence 2, Appl1
43	342	19.6	602	4	US-09-949-016-7417	Sequence 7417, Ap
44	342	19.6	602	4	US-09-949-016-7417	Sequence 7418, Ap
45	341	19.5	504	4	US-09-954-726A-10	Sequence 10, Appl1

ALIGNMENTS

RESULT 1
US-09-237-543-7
; Sequence 7, Application US/09237543A
; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-237-543-7

Alignment Scores:

Pred. No.: 4.9e-144
Score: 1668.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 95.37%
DB: 3
Gaps: 0

US-10-705-757-5 (1-942) x US-09-237-543-7 (1-313)
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QY 61 CACGCCACCAAGCTGCGCGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 21 HisAlaThrIleuAlaIleuProGlySerGlyuGluProLeuGluSerIleuTrpVal 40

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QY      181  AACTGGCCGGTGGCCATTAAAGCAACGGGAGAAAGACCGGAATTTCCGATTGGGGAGAACTG 240
DB      61  AsneuProvalaIalleuYshIvalGIuYaaPaGIIeSePaPrPGLyGIIeu 80
QY      241  CCCAAATGGCAACCGAGTGGCCCAATGGAAGTGTCTGTGAAGAAAGTGAAGCTTGCAGATTG 300
DB      81  ProhsmGIyhrnIatgValPrometGIuValIleuYblyValIseSerAaPhe 100
QY      301  TCGGGGCTCAATTGACTCTTGGACTGGTGTGGAAGAGCCCGATAGTTTGTGTCTGATCTTG 360
DB      101  SerGIYallIleatgIleuYaaPrTrPheGIuaIaGrPaadSerPheValIleuIleu 120
QY      361  GAGAGGCGCGAACCGGTGGCAAGACCTCTTGACTTATACCGAAACGAGAGCCCTACAG 420
DB      121  GIuIaPrProGIuProValGIuIaPheYaaPrPheIIeIhGIuaIaGGLyalaIeGIh 140
QY      421  GAGAGCTTGGCCCGAGAGATTCTTCTGGCAAGTGTCTGAAGGCGGTGGCCGATTTGSCAAC 480
DB      141  GIuIaPheYaaPrIaIatgIyPhePheTrGIuValIeGIuIaIaIaIaIaIaIaIaIaIa 160
QY      481  TGGGGGGTTTCCACCGGCAACATCAAGGACGAGAAACATTTATATGACCTTGAAGCCGGG 540
DB      161  CyedIYalIeuhIaIatgAaPrIleuYaaPrGIuIaIaIeIuIleIaPheYaaPrGIy 180
QY      541  GAAATCAAACTCATGCACTTCGGGATCGGGGGCGCTGCTCAAGACACAGTCTACACGAC 600
DB      181  GIuIleYaaPrIleuYaaPrPheGIYserGIYalaleuIeYaaPrThValIyThIaPr 200
QY      601  TTGATGAGAACCCGAGTGAACAAGTCTCCAGAGTGAATTCCGTACACGCTACACGAC 660
DB      201  PheaPrGIYhrnIatgValIyIserPrProGIuTrIleatgIYhIaIatgIYhIaIa 220
QY      661  AGGTGGGCACTGTCTGATCCCTTGGGATCCGCTTATGACATGCTGTGGGAGATATT 720
DB      221  AAgSerIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 240
QY      721  CCGTTTGAAGCAGATGAGAGATCATCAAGGCGCAAGTGTCTTTCAGGCAAACTGTCT 780
DB      241  ProheGIuIaIaPrGIuIaIeIuIleIuYbGIuIaIaIaIaIaIaIaIaIaIaIaIaIa 260
QY      781  TCAAGTGTCAAGCACTTATTAATGTGTCTGTCCCTGAAGACGCTCAAGTCGGCCTCC 840
DB      261  SerGIuYbGIhIaIeIuIleYbTrCyIeIaSerIeIaIaIaIaIaIaIaIaIaIaIaIa 280
QY      841  TTTGAAGAAATCCGGAACCATCGGTGAAGAGGAGTCACTTCGCCCAAGCAAGCTTCT 900
DB      281  PheGIuIaIeIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 300
QY      901  GAGATTCATGTGCAAGTCTGTCAACGGGATCCAGCAAG 939
DB      301  GIuIleIaIeIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 313

RESULT 2
US-09-644-450-7
; Sequence 7, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HK1D-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; CURRENT FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 313
; TYPE: PR

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	ORGANISM: Mus musculus
US-09-644-450-7	
Alignment Scores:	
Pred. No.:	4.9e-144
Score:	1668.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	95.37%
DB:	3
US-10-705-757-5 (1-942) x US-09-644-450-7 (1-313)	
QY	1 ATGCTCTGTCCAGATGAATCTCCCTGGCCCACTGGCGGCCGCCCTTGCAACGACTTG 60
DB	1 MetLeuLeuSerLySIIeAsnSerLeuAlaHisLeuArgAlaIaArgProCySAsnSerLeu 20
QY	61 CACGGCAACCAAGCTGGCGCCGGGCAAAAGAGAAAGAGAGCCCTGGAGAGTCGAGTACCAAGCTG 120
DB	21 HisAlaIaTrpVbLeuAlaProGlyArgGlyVbGluProLeuGlnSerGlnTrpAlaSer 40
QY	121 GGGCCGCTGTTGGGCGAGCGGTGGCTTCGGCTCGCTCTACTCGCATCCGCGTCGCCGAC 180
DB	41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValAlaIaSer 60
QY	181 AACTTGGCGGTGGCCATTAAAGCAGCTGGAGAAAGACCCGATTTCCGATTGGGGAGAACTG 240
DB	61 AsnLeuProValAlaIleIleYbHisValGluYbAspArgIleSerAspTrpGlyGluLeu 80
QY	241 CCCAATGGCAACCCGAGTGGCCCTTGAGAGAGTGTCTGTTGAAAGAGGTGAGCTCGGACTTC 300
DB	81 ProAsnGlyTrpArgValProMetGluValIleLeuLeuYbLysValIleSerAspPhe 100
QY	301 TCGGGCGCTCATTTGACTTCTGGACTGTGTTCGAGAGCGCCGATAGTTTCGTCTGATCTTG 360
DB	101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleLeu 120
QY	361 GAGAGCGCCGGAACCGGTGCAAGACTCTTCGACTTATACCGAAGAGAGCGCCCTACAG 420
DB	121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
QY	421 GAGGACTGGCCCGAGAGATTTCTTCTGGCAGGTGCTGAGAGCCGTGCGGACTTGGCCAAAC 480
DB	141 GluAspLeuAlaArgGlyPhePheTrpGlnValLeuGluAlaValAlaArgHisCybHisAsn 160
QY	481 TCGGGGTTCTTCACCCGCGACATCAAGACGAAGAACTTTATGACTGACTGAGCCGGCG 540
DB	161 CybGlyValLeuHisArgAspTrpIleYbAspGluAsnIleLeuIleAspLeuSerArgGly 180
QY	541 GAAATCAAACTCATGACTGGGGTGGGGGGCGGTCAAGAGACACATGTACACAGGAC 600
DB	181 GluIleYbLeuIleAspPheGlySerGlyAlaLeuLeuYbAspTrpValTyrTrpAsp 200
QY	601 TTGTATGGGACCCGAGTGTACAGTCTCCAGAGTGAGATTCCGTACCATCGCTACCAACGAG 660
DB	201 PheAspGlyTrpArgValTyrSerProProGluTrpIleArgTyrHisArgGlyTrpHisGly 220
QY	661 AGGTGGGAGCTGTCTGGTCCCTTGGGACTCTGCTCTATGACATGCTTGGCGAGATATT 720
DB	221 ArgSerAlaAlaValTrpSerLeuGlyIleLeuLeuTyrAspMetValCybGlyAspPhe 240
QY	721 CCGTTTGAAGCAAGATGAAGAGATCATCAAGGGCCAAAGTGTCTTTCAGGCAAACTGATCTT 780
DB	241 ProPheGluHisAspGlnGlnIleIleYbGlyGlnValPhePheArgGlnTrpAlaSer 260
QY	781 TCAGAGTGCAGACCTTATTAATGATGTGCTGCTCCCTGAGACCGTCAAGTCGGCCCTCC 840
DB	261 SerGluCybGlnHisLeuIleYbTrpCybLeuSerLeuArgProSerAspArgProSer 280
QY	841 TTTGAAGAAATCCGGAACATCTCCGTGATGACAGGGGTGACCTCTGGCCCAAGGAGCTTCT 900
DB	281 PheGlnGlnIleArgAspHisArgProTrpMetGlnGlyAspLeuLeuProGlnAlaAlaSer 300


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QY 301 TCAGGCGTCATTAGACTTCTGACCTGGTTGAGAGGCGCCGATGTTCTGCTGATCTTG 360
| | | | |
Db 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleLeu 120
QY 361 GAGAGGCCCGACCCGGTGCAGAACCTCTTGACTTTATCCGAGACGAGAGCCCTACAG 420
| | | | |
Db 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
QY 421 GAGAGCTGGCCGAGGATCTCTGTCGACGTGTCGAGGCGCTGGGCGCATTCGCAAC 480
| | | | |
Db 141 GluGluLeuAlaArgSerPheThrGlnValLeuGlnAlaValArgHisCysHisAsn 160
QY 481 TGGCGGGTTCTCCACCGCGCATCAAGACGAGAACATCTTAATCGACTGACCGCGC 540
| | | | |
Db 161 CysGlyValLeuHisArgAspIleLeuAspGluAsnIleLeuIleAspLeuAsnArgGly 180
QY 541 GAAATCAAACTCATCCGACTTCGGGTCGGGGCCGCTGTCAGAGACACAGTCTACAGGAC 600
| | | | |
Db 181 GluLeuValLeuIleAspPheGlySerGlyAlaLeuLeuValAspThrValTyrThrAsp 200
QY 601 TTTGATGGGACCCGAGTGTACAGTCCCTCCAGAGTGGATTGCTACACATGCTACAGCGC 660
| | | | |
Db 201 PheAspGlyThrArgValTyrSerProGluTrpIleArgTyrHisArgIleVal 220
QY 661 AGGTCCGACAGCTGTCTGTCCCTTGAGATCTGCTATGACATGCTGTCGAGAGATATT 720
| | | | |
Db 221 ArgSerHisAlaValIleTrpSerLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
QY 721 CCGTTGAGACGACATGAGAGATCATCAAGGCCCAAGTGTCTTTCAGGCAAACTGTCTCT 780
| | | | |
Db 241 ProPheGluHisAspGluGluValIleValGlyGlnValTyrPheArgGlnArgValSer 260
QY 781 TCAGAGTGTACAGACCTTATTAATGATGCTGCTGCCCTGAGACCGTACAGATCGACCTCC 840
| | | | |
Db 261 SerGluCysGlnHisAspLeuIleArgTyrCysLeuSerLeuArgProSerAspArgProSer 280
QY 841 TTGAGAAATCCGGAACCATCCGTCGATGACAGGTGACCTCTGCGCCGAGCAGCTTCT 900
| | | | |
Db 281 PheGluGluIleGlnIleAsnHisProTrpMetGlnAspValLeuLeuProGlnAlaThrAla 300
QY 901 GAGATCCATCTGCACAGTCTGTCAACGGGATCCAGCAG 939
| | | | |
Db 301 GluIleHisLeuHisSerLeuSerProSerProSerIys 313

RESULT 5
US-09-237-543-9
; Sequence 9, Application US/09237543A
; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-237-543-9

Alignment Scores:
Pred. No.: 3,57e-136 Length: 313
Score: 1582.00 Matches: 294
Percent Similarity: 97.12% Conservative: 10
Best Local Similarity: 93.93% Mismatches: 9
Query Match: 90.45% Indels: 0
DB: 3 Gaps: 0

US-10-705-757-5 (1-942) x US-09-237-543-9 (1-313)
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QY 1 ATGCTCTGTCTCCAGATCAACTCCCTGGCCACCTGCGGCGCCGCCCTGCAACGACTG 60
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Db 1 MetLeuLeuSerIysIleAsnSerLeuAlaHisLeuArgAlaIleProCysAsnAspLeu 20
QY 61 CACGCCACCAACTGGCCGCGCGGCAAGAGAACCCCTTGAGTCCGAGTACCAAGTGG 120
| | | | |
Db 21 HisAlaThrIleValLeuAlaProGlyIleValGluProLeuGlnSerGlnTyrGlnVal 40
QY 121 GGCCTGCTTTGGGAGCGGAGCTTGGGCTTGGCTGCTACTGAGCATCCGCTGCGCGAC 180
| | | | |
Db 41 GlyProLeuLeuGlySerGlyIlePheGlySerValTyrSerGlyIleArgValSerAsp 60
QY 181 AACCTGCGGTCGACATTAAAGCAGTGAAGAACCCGATTTCCGATTTGGGAGAACTG 240
| | | | |
Db 61 AsnLeuProValAlaIleValHisValGluValAspArgIleSerAspTrpGlyGluLeu 80
QY 241 CCCAATGGACCCGAGTGGCCCATGGAAGTGTCTCTTGAAGAAGTGAAGTCCGACTTC 300
| | | | |
Db 81 ProAsnGlyThrArgValProMetGluValIleLeuValValSerSerGlyPhe 100
QY 301 TCAGGCGTCATTAGACTTCTGACCTGGTTGAGAGGCGCCGATGTTCTGCTGATCTTG 360
| | | | |
Db 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleLeu 120
QY 361 GAGAGGCCCGAACCGGTGCAGAACCTCTTGACTTTATCCGAGACGAGAGCCCTACAG 420
| | | | |
Db 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
QY 421 GAGACCTGGCCCGAGAGATCTTCTGACGAGTGTCTGAGGCGCTGGCGGATTTGCCAAC 480
| | | | |
Db 141 GluGluLeuAlaArgSerPheThrGlnValIleGluAlaValArgHisCysHisAsn 160
QY 481 TGGCGGGTTCTCCACCGCGCATCAAGACGAGAACATCTTAATCGACTGACCGCGC 540
| | | | |
Db 161 CysGlyValLeuHisArgAspIleLeuAspGluAsnIleLeuIleAspLeuAsnArgGly 180
QY 541 GAAATCAAACTCATCCGACTTCGGGTCGGGGCCGCTGTCAGAGACACAGTCTACAGGAC 600
| | | | |
Db 181 GluLeuValLeuIleAspPheGlySerGlyAlaLeuLeuValAspThrValTyrThrAsp 200
QY 601 TTTGATGGGACCCGAGTGTACAGTCCCTCCAGAGTGGATTGCTACACATGCTACAGCGC 660
| | | | |
Db 201 PheAspGlyThrArgValTyrSerProGluTrpIleArgTyrHisArgIleVal 220
QY 661 AGGTCCGACAGCTGTCTGTCCCTTGAGATCTGCTATGACATGCTGTCGAGAGATATT 720
| | | | |
Db 221 ArgSerHisAlaValIleTrpSerLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
QY 721 CCGTTGAGACGACATGAGAGATCATCAAGGCCCAAGTGTCTTTCAGGCAAACTGTCTCT 780
| | | | |
Db 241 PhePheGluHisAspGluGluIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
QY 781 TCAGAGTGTACAGACCTTATTAATGATGCTGCTGCCCTGAGACCGTACAGATCGACCTCC 840
| | | | |
Db 261 SerGluCysGlnHisAspLeuIleArgTyrCysLeuAlaLeuArgProSerAspArgProTrp 280
QY 841 TTGAGAAATCCGGAACCATCCGTCGATGACAGGTGACCTCTGCGCCGAGCAGCTTCT 900
| | | | |
Db 281 PheGluGluIleGlnIleAsnHisProTrpMetGlnAspValLeuLeuProGlnAlaThrAla 300
QY 901 GAGATCCATCTGCACAGTCTGTCAACGGGATCCAGCAG 939
| | | | |
Db 301 GluIleHisLeuHisSerLeuSerProGlyProSerIys 313

RESULT 6
US-09-644-450-9
; Sequence 9, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
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/ CURRENT APPLICATION NUMBER: US/09/644,450
/ CURRENT FILING DATE: 2000-08-23
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 9
/ LENGTH: 313
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-644-450-9

Alignment Scores:
Pred. No.: 3,576-136 Length: 313
Score: 1582.00 Matches: 294
Percent Similarity: 97.12% Conservative: 10
Best Local Similarity: 93.93% Mismatches: 9
Query Match: 90.45% Indels: 0
Gaps: 0

US-10-705-757-5 (1-942) x US-09-644-450-9 (1-313)

QY 1 ATGCTCTGTCCAAAGTCAATCCCTGGCCACCTGGCGCCGCCCTTGCAACGACTTG 60
DB 1 MetLeuLeuSerIysIleAenSerLeuAlaHleuAArgAlaIaProCysAenAArgLeu 20
QY 61 CAGCCCAACCAAGTGGCGCCGCCCAAGAGAGAGCCCTGGAGTCCGACGTAACGACTG 120
DB 21 HlaIaIaThryLeuAlaProGlyIyGAluIyGAluProLeuIuSerGlnIyGAluVal 40
QY 121 GGGCCGCTGTGGGAGCGGCTGGCTTCGCTCGATCTAGTCACTCGGCTCGCGAG 180
DB 41 GlyProLeuLeuSerIyGAluIyGAluIyGAluIyGAluIyGAluIyGAluIyGAluIy 60
QY 181 AACTTCCCGGTGGCCATTGAAGACGTGGAGAGAGACCGGATTTCCGATTGGGAGAACTG 240
DB 61 AenLeuProValAlaIleIyGAluIyGAluIyGAluIyGAluIyGAluIyGAluIyGAluIy 80
QY 241 CCCAATGGGACCCGAGTGGCCATGAAGTGTCTGTGAAGAGAGTGGAGTGGACTTC 300
DB 81 ProAenGlyThryrGAluIyGAluIyGAluIyGAluIyGAluIyGAluIyGAluIyGAluIy 100
QY 301 TCGGGGCTGTAGACTTCTGAGACTGGTTGAGAGGCGCGATAGTTTGGCTGATCTTG 360
DB 101 SerGlyValIleIyGAluIyGAluIyGAluIyGAluIyGAluIyGAluIyGAluIyGAluIy 120
QY 361 GAGAGGCGCCGAGACCGGTGCAAGACTTCTTGAATTAATCAACGAGAGAGGCTTACG 420
DB 121 GluAryProGluProValGlnAArgLeuPheAArgPheIleThryGlnIyGAluIyGAluIy 140
QY 421 GAGGAGCTGGCCGAGAGATCTTCTGGCAGGTCTGAGAGGCGCTGGCGGCTTCCACAC 480
DB 141 GluGlnLeuAlaIyGAluIyGAluIyGAluIyGAluIyGAluIyGAluIyGAluIyGAluIy 160
QY 481 TGGGGGTTTCTCAGCGCGACATCAAGAGAGAGAACTTAAATCAAGCTGAGCGCGG 540
DB 161 CysGlyValIleuHleAArgAArgIleIyGAluIyGAluIyGAluIyGAluIyGAluIyGAluIy 180
QY 541 GAAATCAAACTCATCGACTTCGGGTCGGGGCGCTGCTCAAGAGACAGTCTACAGGAC 600
DB 181 GluLeuIySerLeuIleAArgPheGlySerGlyAlaIleuLeuIyAArgPheIyThryrAArg 200
QY 601 TTTGATGGGACCCGAGGTGATCACTCTCCAGAGTGGATTTGGTACCACTGCTACAGCGC 660
DB 201 PheAArgPheIyThryrGAluIyGAluIyGAluIyGAluIyGAluIyGAluIyGAluIyGAluIy 220
QY 661 AGGTGGGACGCTGTCTGCTGCTGGATCTGCTGATGACATGAGTCTGCGAGAGATTT 720
DB 221 ArgSerAlaIaIyAlaIyIyPheSerLeuGlyIleuLeuIyThryrAArgPheIyCysGlyAArgPhe 240
QY 721 CCGTTTGAGACGAGTGAAGAGATCATCAAGAGGCGCAAGTGTCTTCAAGCAAACTGCTCT 780
DB 241 ProPheGlnIyHleAArgPheGlnIyIleIyGAluIyGAluIyGAluIyGAluIyGAluIyGAluIy 260
QY 781 TCAGAGTGTGACGACCTTATTAATGATGCTGCTGCTGAGACCGTCAAGTCCGCGCTTC 840
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DB 261 SerGlnIyCysGlnIleuLeuIleAArgIyThryCysLeuAlaIleuAArgProSerAArgProThr 280
QY 841 TTTGAAGAATCCGAGACCATCCGTGGATGACAGGAGTACCTCTGCGCCAGGACGACTTCT 900
DB 281 PheGlnIyGlnIyGAluIyGAluIyGAluIyGAluIyGAluIyGAluIyGAluIyGAluIyGAluIy 300
QY 901 GAGATCCATGTGACGACGCTGTCAACCGGATCCAGCAAG 939
DB 301 GluIleIleIySerLeuIySerProGlyProSerIyS 313

RESULT 7
US-08-463-081B-26
/ Sequence 26, Application US/08463081B
/ Patent No. 5871960
/ Patent No. 5871960 5837487
/ GENERAL INFORMATION:
/ APPLICANT: Smith, Kendall A. & Beadling, Carol
/ TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
/ TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof
/ NUMBER OF SEQUENCES: 35
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: PRETTY, SCHROEDER & POPAWSKI
/ STREET: 444 South Flower St. - Suite 1900
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: USA
/ ZIP: 90071
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0,
/ SOFTWARE: Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/463,081B
/ FILING DATE: 5-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/104,736
/ FILING DATE: 10-AUG-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/796,066
/ FILING DATE: 20-NOV-91
/ ATTORNEY/AGENT INFORMATION:
/ NAME: VAVIANA Amzel, Ph. D.
/ REGISTRATION NUMBER: 30,930
/ REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 622-7700
/ TELEFAX: (213) 489-4210
/ INFORMATION FOR SEQ ID NO: 26:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 313 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: n.a.
/ TOPOLOGY: n.a.
/ MOLECULAR TYPE: peptide
/ US-08-463-081B-26

Alignment Scores:
Pred. No.: 5,446-136 Length: 313
Score: 1580.00 Matches: 294
Percent Similarity: 97.12% Conservative: 10
Best Local Similarity: 93.93% Mismatches: 9
Query Match: 90.34% Indels: 0
Gaps: 0

US-10-705-757-5 (1-942) x US-08-463-081B-26 (1-313)

QY 1 ATGCTCTGTCCAAAGTCAATCCCTGGCCACCTGGCGCCGCCCTTGCAACGACTTG 60
DB 1 MetLeuLeuSerIysIleAenSerLeuAlaHleuAArgAlaIaProCysAenAArgLeu 20
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61 CACGGCACAACAGCTGGCGCGCGGCGCAAGAAAGAAAGAACCCCTGGAGGTGCGACGTACCAAGGTG 120
 21 HhSalatmLyLeuLdLaProGlyLysGluLysGlnProLeuLdLserGlnTyGlnVal 40
 121 GGCCTCGCTGTTGGGACGCGGTGGCTTCGCGCTCGGTCTACTCTTGACATCGCGTCCGCGCAC 180
 41 GtPProLeuLeuGlySerLylGlyPheGlySerValTySerGlyLLeaRgValSerAap 60
 181 AACTTGGCGGTGGCCATTAAAGCAGTGAAGAAAGACCGGATTTCCGATTGGGGAGAACTG 240
 61 AenLeuProValAlaIleLysHhValGluLysAAspArgLLeSerAapTrpGlyLLeu 80
 241 CCCAATGGACCCCGAGTGGCCCATGGAAAGTGCCTCTTGAAGAAAGGTGAGCTCGGACTTC 300
 81 ProAenGlyThaRgValProMetGluValLLeuLeuLysValSerSerGlyLys 100
 301 TCGGGCGTCATTAAGACTTCTGGACTGTTCCAGAGGCGCGATGATGTTTCGTGATCTCG 360
 101 SerGlyValLLeaRgLeuLeuAapTrpPheGluLysProAAspSerHethValLeuL 120
 361 GAGAGGCGCCGAAACCGGTGCAAGACCTTTGACTTTATGACCGAAGAGAGGCGCTTACAG 420
 121 GluAaRProGluProValGlnAAspLeuPheAAspPheIleThrGluAaRgValaLeuGln 140
 421 GAGGACCTCGGCGCCGAGGATTTCTTCTGGCAGGTGCTTGAGAGCGGTGGCGGCACTTGCCCAAC 480
 141 GtGtLLeuLLeaRgSerPhePheTrpGlnValLLeuGluAlaValaRghIscVhSaen 160
 481 TCGGGGGGTCTCCACCGCGACATCAAGAGACGAGAAATCTTAATCGACCTGAGCGCGCGG 540
 161 CySgLyValLeuHhAaRgAapLLeuLysAAspGluAenLLeuLLeaPheLeuAenAaRgGly 180
 541 GAAATCAACATCATGACTTCGCGGTGGGGCGGTGCTCAAGGACACAGTTACACGCGAC 600
 181 GluLeuLysLeuLLeaPheGlySerGlyAlaLeuLeuLysPheThrValTyThrAap 200
 601 TTTGATGGGACCCGAGTGTACAGTCTCTCCAGAGTGGATTCGCTACATCGCTACCGACGGC 660
 201 PheAapGlyThaRgValTySerProProGluTrpLLeaRgTyHhAaRgTyHhSgLy 220
 661 AGGTGGGACGCTGTGCTGCTCCCTGGGAGTCCGCTCTATAGACATGGTCTGCGGAGATATT 720
 221 AaRgSerAlaAlaValTrpSerLeuGlyLLeuLeuTyHhAAspMetValCySgLyAAspIle 240
 721 CCGTTTGAACACAGTGAAGAGATCATCAAGGCGCAAGTATTTCTTCAAGCAAACTGTCTCT 780
 241 ProPheGluHhAAspGluGluLLeaRgGlyGlnValPheAaRgGlnAaRgValSer 260
 781 TCAGAGTGTACAGACTTTATTAATGTGTGCTGCTCCCTGAACCGTCAAGTGGCGGCTTC 840
 261 SerGtLysCySgLHhAAspLeuLLeaRgTrpCySgLeuAlaLeuAaRgProSerAAspAProth 280
 841 TTTGAAGAAATCGGAGAACATCGGTGAGAGAGCGAGGAGTGCCTCTGGCCCAAGGAGTTCT 900
 281 PheGluGluLLeaGlnHhAAspTrpTrpMetGlnAAspValLeuLeuProGlnLutHhAla 300
 901 GAGATCATCTTGACAGTCTGTCAACCGGAGATCCAGCAAG 939
 301 GluLeHhAAspLeuHhSerLeuSerProGlyProSerLys 313

RESULT 8
 US-08-461-379A-26
 ; Sequence 26, Application US/08461379A
 ; Patent No. 5871961
 ; GENERAL INFORMATION:
 ; APPLICANT: Smith, Kendall A. & Beadling, Carol
 ; TITLE OF INVENTION: Nucleic Acids Encoding CRS Polypeptide,
 ; TITLE OF INVENTION: Vector and Transformed Cell thereof, and
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Ratner & Preecia
 ; ADDRESS: .
 ; (B) STREET: One Westlakes-Berwyn

```

1 CITY: Valley Forge
2 STATE: Pennsylvania
3 COUNTRY: USA
4 ZIP: 19482
5
6 COMPUTER READABLE FORM:
7 MEDIUM TYPE: Floppy disk
8 COMPUTER: IBM PC compatible
9 OPERATING SYSTEM: PC-DOS/MS-DOS
10 SOFTWARE: Patent In Release #1.0,
11 SOFTWARE: Version #1.25
12
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/08/461,379A
15 FILING DATE: 5-JUNE-1995
16
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: US9N 08/330,108; 08/104,736
19 APPLICATION NUMBER: & 07/796,066
20 FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-92
21
22 ATTORNEY/AGENT INFORMATION:
23 NAME: Viviana Amzel, Ph. D.
24 REGISTRATION NUMBER: 30,930
25 REFERENCE/DOCKET NUMBER: DART-070
26
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: (610)470-0700
29 TELEFAX: (610)470-0701
30
31 INFORMATION FOR SEQ ID NO: 26:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 313 amino acids
34 TYPE: peptide
35 STRANDEDNESS: n.a.
36
37 TOPOLOGY: n.a.
38
39 MOLECULE TYPE: peptide
40
41 US-08-461-379A-26

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Alignment Scores:			
Pred. No.:	5.44e-136	Length:	313
Score:	1580.00	Matches:	294
Percent Similarity:	97.12%	Conservative:	10
Best Local Similarity:	93.93%	Mismatches:	9
Query Match:	90.34%	Indels:	0
DB:	2	Gaps:	0
US-10-705-757-5 (1-942) x US-08-461-379A-26 (1-313)			
QY	1	ATGTCCTCCGATCAAGATCAATCCCTGGCGCCACCTGGCGCCCGCCCTTGCAACGACCTG	60
Db	1	MetLeuLeuSerLySLeuAlaPProGlySgLuYsgLuProLeuGluSerGlnTygAlnVal	20
QY	61	CACGCGCAACCAAGCTGGCCGCGCGCAAGAGAAGAGAGCCCTCGAGTCGACGATCACAGTG	120
Db	21	HisAlaThrLySLeuAlaPProGlySgLuYsgLuProLeuGluSerGlnTygAlnVal	40
QY	121	GGCCCGCTGTGTGGGAGCGCGTGCTTGGCTTGGCTTACTGCGATCCGCGTGGCGAC	180
Db	41	GlyProLeuLeuGlySerGlyGlyPheGlySerValTySerGlyLyLeuArgValSerArg	60
QY	181	AACCTTGCCGCTGGCCATTAGCAGCTGTGAAGAGACCGGATTTCCGATTGGGGAGAACTG	240
Db	61	AsnLeuProValAlaIleLySHisValGluYsAspArgIleSerAspTrpGlyGluLeu	80
QY	241	CCCAATGGCACCCGAGTGCCCATGGAAGTGTCCTGTGGAAGAAGGTGAGCTCGACCTTC	300
Db	81	ProAsnGlyThrArgValPProMetGluValValLeuLeuLySValSerSerGlyPhe	100
QY	301	TCGGGCGTCATTAGACTTCTGTGAGCTGTGCGAGAGCGCCGATAGATTCCGTGATCTCG	360
Db	101	SerGlyValIleArgLeuLeuAspTrpPheGluArgPProAspSerPheValLeuIleLeu	120
QY	361	GAGAGGCCCGAACCCGGTGCAGAACCTCTTCGACTTATCACCGAAGAGAGGCCCTACAG	420
Db	121	GluArgPProGluPProValGlnAspPheAspPheIleThrGluArgGlyAlaLeuGln	140
QY	421	GAGGACCTGGCCCGAGATTCTTCTGCGAGGTGCTCGAAGGCCGTGGCGCAATTGCCAAC	480


```

Db      141  GUGUleuAlaArgSerPhePheTrpGlnValIleuGlnAlaValArgHisCysHisAsn 160
Qy      481  TGGGGGGTTTCCACCGGACATCAAGAGAGAACTTTAATCCAGCTGAGCCGGCC 540
Db      161  CysGlyValIleuHisArgSerPheIleuArgGlnAsnIleuIleuAspIleuAsnArgGly 180
Qy      541  GAATCAAACTCATCGACTCGGGGTGGGGGCGGTGCTCAAGGACACAGTCTACAGGAC 600
Db      181  GlnIleuIleuIleuIleuAspPheGlySerGlyAlaIleuIleuIleuAspIleuValIleuAsp 200
Qy      601  TTTGATGGACCCGAGTGTACAGTCTCCAGAGTGTGATTCGATCCATCCGCTACAGG 660
Db      201  PheAspGlyThrArgValIleuSerProGlnIleuTrpIleuArgIleuHisArgGly 220
Qy      661  AGGTGGACGCTGTCTGCTGCTTGGGATCTGCTCTATGACATGGTCTGCGGAGATATT 720
Db      221  ArgSerIleuAlaValIleuTrpSerIleuGlyIleuIleuIleuAspMetValCysGlyAspIle 240
Qy      721  CGGTTGAGACAGATGAAGATCATCAAGGCGCAAGTCTTTCAAGGCAAGCTGTCT 780
Db      241  ProPheGlnHisAspGlnIleuIleuIleuArgGlyGlnAlaPhePheArgGlnArgValSer 260
Qy      781  TCAGAGTGTACGACCTTATTAATGTGTGCTGTCTCCAGACCGTCAAGATCCGCGCTCC 840
Db      261  SerGlnCysGlnHisIleuIleuIleuArgTrpCysIleuAlaIleuArgProSerAspArgProThr 280
Qy      841  TTTGAAGAATCCGGAACCATCCGTGTGATGACAGGAGTACTCTGCCCGGAGGACTTCT 900
Db      281  PheGlnGlnIleuIleuGlnHisAspProTrpMetGlnAspValIleuIleuProGlnIleuTrpAla 300
Qy      901  GAGATCATCTGACAGTGTGTCAACGGGATCCAGGAC 939
Db      301  GlnIleuIleuHisSerIleuSerProGlyProSerIleu 313

RESULT 9
US-08-462-390B-26
Sequence 26, Application US/08462390B
Patent No. 5882894
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding C88 Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Ratner & Prestia
ADDRESS: (B) STREET: One Westlakes-Berwyn
CITY: Valley Forge
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,390B
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)407-0700
TELEFAX: (610)407-0701
INFORMATION FOR SEQ ID NO: 26:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: peptide
; STRANDEDNESS: n.a.
; TOPOLOGY: n.a.
; MOLECULE TYPE: peptide
US-08-462-390B-26

Alignment Scores:
Pred. No.: 5,44e-136
Score: 1580.00
Percent Similarity: 97.12%
Best Local Similarity: 93.93%
Query Match: 90.34%
DB: 2 Gaps: 0

US-10-705-757-5 (1-942) x US-08-462-390B-26 (1-313)

Qy      1  ATGCTCTGTCCAAAGTAACTCCCTGGCCACCTGCGGCGCCGCTGCAAGCACTTG 60
Db      1  MetLeuIleuSerIleuHisSerIleuAlaHisIleuArgAlaArgAlaCysAsnAspLeu 20
Qy      61  CACGCCAACAGCTGGCGCGCGCAAGAGAAAGAACCCCTGAGTCCGAGTACAGATG 120
Db      21  HisAlaThrIleuIleuAlaProGlyIleuGlyIleuGlnIleuGlnIleuSerGlnIleuVal 40
Qy      121  GGGCGGCTGTGGGACAGCGGTGCTTGCGCTGCTTACTCTGACATCCGCTCGCCGAC 180
Db      41  GlyProIleuGlnIleuSerIleuGlyPheGlySerValIleuSerGlyIleuArgValSerAsp 60
Qy      181  AACTTCCGGGTGGCCATTAAAGCACGTGAGAAAGAACCGGATTTCCGATTTGGGGAGAAC 240
Db      61  AsnIleuProValAlaIleuHisValGlnIleuAspArgIleuSerAspTrpGlyIleu 80
Qy      241  CCCAATGCAACCCGAGTGGCCATGGAAGTGTCTCTTGAAGAGAGTGAAGTCCGACTTC 300
Db      81  ProIleuGlyThrArgValProMetGlnValIleuIleuIleuValSerSerGlyPhe 100
Qy      301  TGGGCGCTCATTAAGACTTTGGAATGTGTGAGAGGCGCGATATGTTTCTGTGATCTTG 360
Db      101  SerGlyValIleuArgIleuIleuAspTrpPheGlnArgProAspSerPheValIleuIleu 120
Qy      361  GAGAGCGCGGACCCGTGGAAGACCTTCGACTTATGACGGAAGAGAGCCCTTACAG 420
Db      121  GlnArgProGlnProValGlnAspLeuPheAspPheIleuThrGlnArgGlyAlaGln 140
Qy      421  GAGGACCTGCGCGAGAGATTTCTTGGCAGGTGTGAGAGCGGTGCGGATTCGACAAAC 480
Db      141  GlnGlnIleuAlaArgSerPhePheTrpGlnValIleuGlnAlaValArgHisCysHisAsn 160
Qy      481  TGGGGGGTTTCCACCGGACATCAAGAGAGAACTTTAATCCAGCTGAGCCGGCC 540
Db      161  CysGlyValIleuHisArgSerPheIleuArgGlnAsnIleuIleuAspIleuAsnArgGly 180
Qy      541  GAATCAAACTCATCGACTCGGGGTGGGGGCGGTGCTCAAGGACACAGTCTACAGGAC 600
Db      181  GlnIleuIleuIleuIleuAspPheGlySerGlyAlaIleuIleuIleuAspIleuValIleuAsp 200
Qy      601  TTTGATGGACCCGAGTGTACAGTCTCCAGAGTGTGATTCGATCCATCCGCTACAGG 660
Db      201  PheAspGlyThrArgValIleuSerProGlnIleuTrpIleuArgIleuHisArgGly 220
Qy      661  AGGTGGACGCTGTCTGCTGCTTGGGATCTGCTCTATGACATGGTCTGCGGAGATATT 720
Db      221  ArgSerIleuAlaValIleuTrpSerIleuGlyIleuIleuIleuAspMetValCysGlyAspIle 240
Qy      721  CGGTTGAGACAGATGAAGATCATCAAGGCGCAAGTCTTTCAAGGCAAGCTGTCT 780
Db      241  ProPheGlnHisAspGlnIleuIleuIleuArgGlyGlnAlaPhePheArgGlnArgValSer 260
Qy      781  TCAGAGTGTACGACCTTATTAATGTGTGCTGTCTCCAGACCGTCAAGATCCGCGCTCC 840
Db      261  SerGlnCysGlnHisIleuIleuIleuArgTrpCysIleuAlaIleuArgProSerAspArgProThr 280

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Oy      841  TTGTGAAGAAATCCGGAGAACATCCCTGGATGCAGAGGTGACTCTCTGCTCCCGCCAGGACCTTCT  900
          |||||
Db      281  PhegIugIuIIeGInAmshIaProlTpmetGInsePValIleuLeuProGInguIuThraIa  300
          |||||
Oy      901  GAGATCATCTGCACAGTCTGTGCACCGGAGATCCAGCAAG  939
          |||||
Db      301  GIuIIeHIsIeuhIseSerIeuserProGluYProSerIys  313
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RESULT 10
US-08-463-074B-26
; Sequence 26, Application US/08463074B
; Patent No. 6020155
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CRI Fusion Protein, Vector an
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,074B
; FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/104,736
; FILING DATE: 10-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,066
; FILING DATE: 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: peptide
; STRANDEDNESS: n.a.
; TOPOLOGY: n.a.
; MOLECULE TYPE: peptide
US-08-463-074B-26

Alignment Scores:
Pred. No.: 5.44e-136 Length: 313
Score: 1580.00 Matches: 294
Percent Similarity: 97.12% Conservative: 10
Best Local Similarity: 93.93% Mismatches: 9
Query Match: 90.34% Indels: 0
DB: 3 Gaps: 0

US-10-705-757-5 (1-942) * US-08-463-074B-26 (1-313)
Oy      1  ATGCTCTGTCCAGATCAACTCCCTGCGCCACCTGCGCGCCCGCCCTGCAAGCACTGT  60
          |||||
Db      1  MetIeuIeuSerIysIIeIaMserIeulIaHIsIeulAArgAlaIcYseMshPleu  20
          |||||
Oy      61  CACGCGACCAAGCTGGCGCCGCGGCAAGAGAGAGAGCCCTGTGAGATCCGCAATCCAGGT  120
          |||||
Db      21  HIsAlaIrrIyIseIeulAProGluYsgIuYsgIuProIeuGInseIrlInIuVal  40
          |||||

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1 MEDIUM TYPE: floppy disk
2 COMPUTER: IBM PC compatible
3 OPERATING SYSTEM: PC-DOS/MS-DOS
4 SOFTWARE: Patentin Release #1.0, Version #1.0
5
6 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: US/08/465,585C
8 FILING DATE: 5-JUNE-1995
9
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: USSN 08/330,108
12 FILING DATE: 27-OCT-1994
13 APPLICATION NUMBER: USSN 08/104,736
14 FILING DATE: 10-AUG-1993
15 APPLICATION NUMBER: USSN 07/796,066
16 FILING DATE: 20-NOV-1991
17
18 ATTORNEY/AGENT INFORMATION:
19 NAME: Viatiana Amzel, Ph. D.
20 REGISTRATION NUMBER: 30,930
21 REFERENCE/DOCKET NUMBER: P66 38149 (DART-0500)
22 TELECOMMUNICATION INFORMATION:
23 TELEPHONE: (213) 622-7700
24 TELEFAX: (213) 4894210
25
26 INFORMATION FOR SEQ ID NO: 26:
27
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 313 amino acids
30 TYPE: peptide
31 STRANDEDNESS: n.a.
32 TOPOLOGY: n.a.
33
34 MOLECULE TYPE: peptide
35
36 US-08-465-585C-26

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/ FILING DATE: 5-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/465,585
/ FILING DATE: 5-JUN-1995
/ PRIOR APPLICATION DATA: 08/463,081
/ APPLICATION NUMBER: 08/463,081
/ FILING DATE: 5-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/461,379
/ FILING DATE: 5-JUN-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/739,523
/ FILING DATE: 29-OCT-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Viviana Amzel, Ph. D.
/ REGISTRATION NUMBER: 30,930
/ REFERENCE/DOCKET NUMBER: PP66 40035
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 622-7700
/ TELEFAX: (213) 489-4210
/ INFORMATION FOR SEQ ID NO: 26:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 313 amino acids
/ TYPE: peptide
/ STRANDEDNESS: n.a.
/ TOPOLOGY: n.a.
/ MOLECULE TYPE: peptide
/ US-08-652-446-26

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Alignment Scores:
Pred. No.: 5,44e-136 Length: 313
Score: 1580.00 Matches: 294
Percent Similarity: 97.12% Conservative: 10
Beet Local Similarity: 93.93% Mismatches: 9
Query Match: 90.34% Indels: 0
DB: 3 Gaps: 0
US-10-705-757-5 (1-942) x US-08-652-446-26 (1-313)

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QY 1 ATGCTCTGTCCAAAGTCAACTCCCTGCGCCCGCCCTGCAACGACTTG 60
DB 1 MetLeuLeuSerIysIleAenSerLeuLAlaIleuAlaArgLAcysAenApeLeu 20
QY 61 CAGGCCACCAAGCTGGCGCGCGGCAAGAGAGAGCGCCCTGAGTCCGACTGACGTG 120
DB 21 HAlaIAlaThIryLeuAlaIaProGlyLysGluLysGluProLeuLLeuSerGlnIryLAlaI 40
QY 121 GGCCTCGTGTGGGAGCGGCTTCTGCGCTCGCTCTACTCTGCAATCCGCGTGGCGAG 180
DB 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValSerAap 60
QY 181 AACTTCGCGGTGGCCATTAAAGCAGCTGAGAGAAGACCGGATTTCCGATTTGGGAGAACTG 240
DB 61 AenLeuProValAlaIleLysHAlaGluLysAaAArgIleSerAapTrpGlyGluLeu 80
QY 241 CCAATGGGACCGGAGTGGCCATGAGAGTGTCTGTGTAAGAGGAGCTGAGACTTC 300
DB 81 ProAenGlyThIryArgValProMetGluValValLeuLeuLysValSerSerGlyPhe 100
QY 301 TCGGGCGTCAATTAGACTTCTGACTGCTGTGAGAGGCGCCGATGTTCTGTGATCTTG 360
DB 101 SerGlyValIleArgLeuLeuAaPTripPheGluArgProAaSerPheValIleuIleLeu 120
QY 361 GAGAGGCCGAGACCGGTGCAAGACTTCTGACTTTATCCAGGAGAGAGCCCTACAG 420
DB 121 GluArgProGluProValGlnAaPheLeuPheAaPheIleThIryGluArgGlyAlaLeuGln 140
QY 421 GAGAGCTGGCGCGAGGATCTTCTGCGAGGTGTGAGGCGCGTGGGCAATTGCCCAAC 480
DB 141 GluGluLeuAlaIrySerPhePheTrpGlnValLeuGluValAlaArgHISCySHASen 160
QY 481 TGGGGGTTCTCCAGCCGAGCATCAAGAGAGAGAACTTAATCGACTTGACCGCGAGC 540

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DB 161 CysGlyValLeuHISArgAaPTripLysAaPheGluAenIleLeuLAlaPheLeuAaArgGly 180
QY 541 GAATCAAACTGATGCACTTCGAGGTGCGGCGGCTGCTCAAGAGACAGTCTACAGGAC 600
DB 181 GluLeuLysLeuIleAaPheGlySerGlyAlaLeuLeuLysAaPheThIryThIryAaP 200
QY 601 TTTGATGGACCCGAGTGTACAGTCTTCAGAGTGGATTCGCTACCATGCTTACCAAGCC 660
DB 201 PheAaPheGlyThIryArgValTyrSerProProGluTrpIleArgTyrHISArgTyrHIS 220
QY 661 AGTGGGAGCTGTCTGCTCCCTTGGGATCCCTGCTCTTGAACATGCTGCGGAGATTT 720
DB 221 ArgSerAlaAlaValTrpSerLeuGlyIleLeuLeuTyrAaPheValCysGlyAaPhe 240
QY 721 CCGTTTGGACAGATGAGATCATCAAGAGGCGCAAGTGTCTTCAAGGCAACTGTCTCT 780
DB 241 ProPheGluHISArgGluGluIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
QY 781 TCAGAGTGTACAGACCTTAATGATGCTGTCTGCTGAGACCGTCAAGTGGCGCTTC 840
DB 261 SerGluCysGlnHISLeuIleArgTyrCysLeuAlaLeuArgProSerAaPArgProThr 280
QY 841 TTTGAAGAAATCCGGAACCATCTCGTGAATGACAGGCTGACCTTCCCGCAGGCACTTCT 900
DB 281 PheGluGluIleGlnAaHISProTrpMetGlnAaPheValLeuLeuProGluGlnThIryAla 300
QY 901 GAGATCCATCTGACAGTCTGTACCGGAGTCCAGCAAG 939
DB 301 GluIleHISLeuHISerLeuSerProGlyProSerLys 313

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RESULT 13
US-07-857-224B-41
Sequence 41, Application US/07857224B
Patent No. 5958784
GENERAL INFORMATION:
APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting folded Structures of Proteins
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSER: Steven A. Benner
STREET: Hadlabastrasse 151
CITY: Zurich
STATE: none
COUNTRY: Switzerland
ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1 632 2830
TELEFAX: (International) 41 1 262 2437
TELEX: none
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 257
TYPE: amino acid
MOLECULE TYPE: linear
MOLECULE TYPE: protein
DESCRIPTION:
ORGANISM: rat
FEATURE: Protein kinase; Table 8 Column 46
PUBLICATION INFORMATION:
AUTHORS:
AUTHORS: Hanke, S. K.
AUTHORS: Ouinm, A. M.

```

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;
; AUTHOR8: Hunter, T.
; TITLE: The protein kinase family
; JOURNAL: Science
; VOLUME: 241
; PAGES: 42-52
; DATE: 1988
US-07-857-224B-41

Alignment Scores:
Pred. No.: 1,67e-115 Length: 257
Score: 1355.50 Matches: 256
Percent Similarity: 98.84% Conservative: 0
Beet Local Similarity: 98.84% Mismatches: 0
Query Match: 77.50% Indels: 3
DB: Gaps: 2

US-10-705-757-5 (1-942) x US-07-857-224B-41 (1-257)

QY 106 TCGCAGTACGAGGCGGCGCTGTTGGGAGCGGCTTGGCTCGCTGCTACTGCGC 165
DB 1 SerGlnTrpGlnValGlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGly 20
QY 166 ATCCGCTCCGCGCAACTTGGCGGTGCGCATTAAGACGCGGAGAACCGGATTTCC 225
DB 21 IleArgValAlaIlePheLeuLeuProValAlaIleIleValIleGlyValIleSer 40
QY 226 GATTGGGAGAACTGCCCAATGGCACTCCGAGTCCCATGGAAGTGTCTGTTGAAGAG 285
DB 41 AspTrpGlyGlu-----AenGlyThrArgValProMetGlyValIleLeuLeuValLeu 58
QY 286 GTAGAGCTCGGAGCTTCTGGGCGTGCATTAAGACTTGTGAGCTTGGAGGCGCGATG 345
DB 59 ValSerSerAspPheSerGlyValIleArgLeuLeuAspTrpPheGlyValGlyProAspSer 78
QY 346 TTGCTGCTGATCTCGAGAGGCGCGCAACCGGTGCAAGACTTTCGACTTATCACCGAA 405
DB 79 PheValIleuIleLeuGlnIleuArgProGluProValGlnAspPheAspPheIleMetGlu 98
QY 406 CGAGAGCCCTTACAGAGAACCTTGGCCCGAGAACTTTCGAGAGTGTGAGGCGCGTG 465
DB 99 ArgGlyAlaLeuGlnIleuAspLeuAlaArgGlyPhePheTrpGlnValIleuGlnAlaVal 118
QY 466 CGGATTTGGCAACAATGCGGGGTTCTCCACCGGACATCAAGAGCAAGCAATCTTAATC 525
DB 119 ArgHisGlyHisIleAsnGlyValIleuHisArgAspIleLeuAspGlyIleuIleValIle 138
QY 526 GACCTGAGCGCGCGCAAACTCAATGACTTGGGTGCGGGGCGGTCTCAAGAGC 585
DB 139 AspLeuSerArgGlyIleuIleValLeuIleAspPheGlySerGlyAlaLeuLeuValAsp 158
QY 586 ACAAGTACACGAGCTTGTAGAGAGCCGAGGTACAGTCTTCCAGAGTGAGATTCCGTAC 645
DB 159 ThrValTyrThrAspPheAspGlyThrArgValTyrSerProProGluTrpIleArgTyr 178
QY 646 CATGCTACACGCGCAGAGTGGCAGAGTGTGCTGCTTGGGACTTCTGCTTATGACATG 705
DB 179 HisArgTyrHisGlyArgSerAlaIleValIleTrpSerLeuGlyIleuLeuTyrAspMet 198
QY 706 GTGCGCGAGATATTCGGTTT---GAGCAGAGTAAAGATCATCAAGGCGCAAGTTC 762
DB 199 ValCysGlyAspIleProPheAspGlnHisAspGlnIleIleIleValGlyValIlePhe 218
QY 763 TTCAGGCAACGTGCTTTCAGAGTGCACAGCTTATTAATGAGTCCGTGCTGAGAG 822
DB 219 PheArgGlnThrValIleSerSerGlyCysGlnHisIleuIleIleValTyrCysLeuSerLeuArg 238
QY 823 CCGCAGATGCGCGCTCTTGAAGAAATCCGAAACATCCGTCGAGAGCGAGAGC 879
DB 239 ProSerAspArgProSerPheGlnGluIleArgHisIleProTrpMetGlnGlyAsp 257

RESULT 14
US-09-237-543-5
; Sequence 5, Application US/09237543A

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; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-237-543-5

Alignment Scores:
Pred. No.: 4.3e-94 Length: 455
Score: 1122.50 Matches: 213
Percent Similarity: 81.33% Conservative: 31
Beet Local Similarity: 71.00% Mismatches: 43
Query Match: 64.18% Indels: 13
DB: Gaps: 5

US-10-705-757-5 (1-942) x US-09-237-543-5 (1-455)

QY 1 ATGCTCTGTCCAGATCAATGCTGCGCCACCTGCGCGCCCGCTGC----- 51
DB 130 MetLeuLeuSerGlyPheGlySerLeuAlaHisLeu-----CysGlyProGly 145
QY 52 -----AAGACCTGACCGCCACCAAGCTGGCGCGCGGCAAA---GAGAGGAGCCCGTG 102
DB 146 GlyValAlaHisIleuProValIleValIleGlnProAlaIleValAlaAspIleGlySerPhe 165
QY 103 GAGTCCAGTACCAAGGTGGGCGCGCTGTTGGGAGCGGTGCGTTCGCTCGCTACTGCT 162
DB 166 GlnIleValTyrGlnValGlyAlaValIleuGlySerGlyGlyPheGlyThrValTyrAla 185
QY 163 GGCATCCGCGTGGCGCAACTTGGCGGTGCGCATTAAGACGTCGAGAGACCGGATT 222
DB 186 GlySerArgIleHisAspGlyLeuProValAlaValIleHisIleValIleGlyValIle 205
QY 223 TCGATTTGGGGAAGTGGCCCAATGGCACCGGATGCGCATGAGTGCCTTGAAG 282
DB 206 ThrGlnTrpGlySerIleu---GlyGlyMetAlaValProLeuIleValIleuLeuVal 224
QY 283 AAGGTG-----AGCTCGGACTTCTCGGCGGTGATTAAGACTTTCGACTGTTGAGAGG 336
DB 225 LysValGlyAlaIleGlyAlaArgGlyValIleArgLeuLeuAspTrpPheGlyVal 244
QY 337 CCGGATAGTTTGTGCTGATCTCGAGAGCGCGCAACCGGTGCAAGACTTTCGACTTT 396
DB 245 ProAspGlyPheLeuLeuValIleuGlnIleuArgProGluProAlaGlnAspPheAspPhe 264
QY 397 ATACAGCAACGAGAGACCTTACAGAGACCTTGGCCCGGAGATTTCTTGGCAGGTGCTG 456
DB 265 IleThrGlnArgGlyAlaLeuAspGlnProLeuAlaArgArgPheHisIleGlnValIle 284
QY 457 GAGCGCGTGGGAGTGGCAACAATGCGGGGTTCTCCACCGGCAATCAAGAGCAAGAAC 516
DB 285 AlaIleValArgHisGlyHisIleAsnGlyValIleValHisArgAspIleIleAspGlnIle 304
QY 517 ATCTTAATGACTGAGCGCGCGCAATCAATCATGACTTTCGGGTGCGGGCGCTG 576
DB 305 LeuLeuValAlaAspLeuArgSerGlyIleuLeuValIleAspPheGlySerGlyAlaVal 324
QY 577 CTCAGAGCAACAGTCTACACAGCACTTGTAGGAGCCGAGTGTACAGTCTCCAGAGTGG 636
DB 325 LeuIleAspPheThrValTyrThrAspPheAspGlyThrArgValTyrSerProProGluTrp 344
QY 637 ATTCGCTACATGCTACCAAGCGCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 696
DB 345 IleArgTyrHisArgTyrHisGlyArgSerAlaThrValTrpSerLeuGlyValIleuLeu 364

```

QY 697 TATGACATGCTGCGGAGATATTCGTTGAGACGATGAGATCATCAAGGCGCA 756
DB 365 TyrAspMetValCyseGlyAspIleProPheGlnGlnAspGluIleLeuArgGlyArg 384
QY 757 GTGTTCTTCAGGCAAACTGTCTTCAGAGTGTACAGACCTTAATTAATGTCCTGTCC 816
DB 385 LeuPhePheArgArgValSerProGlnCyseGlnIleLeuIleGlnIleProIlePheLeuSer 404
QY 817 CTGAGACCGTCAGATCGGCGCTCTTTGAAGAAATCCGAAACCATCCGTTGAGATGCAAGGT 876
DB 405 LeuArgProSerGlnArgProSerLeuAspGlnIleAlaIleAspProIlePheLeuGly 424

RESULT 15
US-09-644-450-5
; Sequence 5, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-644-450-5

Alignment Scores:
Pred. No.: 4,3e-94 Length: 455
Score: 1122.50 Matches: 213
Percent Similarity: 81.33% Conservative: 31
Best Local Similarity: 71.00% Mismatches: 43
Query Match: 64.18% Indels: 13
DB: 3 Gaps: 5

US-10-705-757-5 (1-942) x US-09-644-450-5 (1-455)

QY 1 ATGCTCTGTGCAAGATCACTCCCTGGCCACCTGCGCGCCGCGCCCTGC----- 51
DB 130 MetLeuLeuSerIleYsPheGlnSerLeuAlaIleLeu-----CysGlnProGly 145
QY 52 -----AACGACTGCACGCGCACCAACCTGCGCGCGGCAAA--GAGAAAGAGCCCTG 102
DB 146 GlyValAspHisLeuProValIleLeuGlnProAlaLeuAspIleYsGlnSerPhe 165
QY 103 GAGTCGACGTACAGAGTGAGCGCGCTGTGAGGACGCGTTCGCGCTGAGTCTACTCT 162
DB 166 GlnIleValIleTyrGlnValIleGlnAlaValIleGlnIleSerIleGlnIlePheGlnIleTyrAla 185
QY 163 GGCATCCGCGCTGCGCGCAACTTGCCTGCGGCACTTAAGCAGCTGAGAAAGACCGGATT 222
DB 186 GlySerArgIleAlaAspGlnLeuProValAlaValIleHisValIleValIleArgVal 205
QY 223 TCCGATTGGGAGAACTGCCCAATGACCCGAGTGCCTGAGAGTGGTCTGTGTAAG 282
DB 206 ThrGlnIlePheGlnSerLeu--GlnGlyMetAlaValProLeuGlnValIleLeuArg 224
QY 283 AAGGTG-----AGCTCGACCTTCTCGGGCGTCACTTGACTTCGAGCTGTCGAGAG 336
DB 225 LysValGlnAlaIleGlnIleAlaArgGlnValIleArgLeuLeuAspIlePheGlnArg 244
QY 337 CCGGATAGTTTCGTGCTGATCTGAGAGGCGCGAAACGGTGCAGACCTTTCGACTTT 396
DB 245 ProAspGlnPheLeuLeuValIleGlnIleArgProGlnProAlaGlnAspLeuPheAspPhe 264
QY 397 ATGACCGAGACGAGAGCCCTTACAGAGAGACCTGGCCCGAGAGATTCTTCTGCAAGTGTG 456
DB 265 IleThrGlnArgGlnAlaLeuAspGlnProLeuAlaArgArgPhePheAlaGlnValLeu 284

QY 457 GAGCGGTGCGGCAATTGCGCAACTGCGGGGTTTCCACCGGACATCAAGACGAGAAC 516
DB 285 AlaAlaValArgHisCysHisAsnCyseGlyValIleValHisArgAspIleLeuAspGlnAsn 304
QY 517 ATCTTAATGACCTGAGCGCGCGCAAAATCAACTCATGACTTCGGGTGCGGGCGCTG 576
DB 305 LeuLeuValAspLeuArgSerGlnIleLeuIleAspPheGlnIleAspPheGlnIleVal 324
QY 577 CTCAAGACACAGCTTACACGCACTTTGATGGGACCGGAGTGTACAGTCTCCATGAGTGG 636
DB 325 LeuLysAspThrValIleTyrHisPheAspGlnIleArgValIleSerProProGlnIleP 344
QY 637 ATTGCTACATCGCTACACGCGGACAGTGCAGGCTGTCTGCTCCCTTGGAGTCTGTCTC 696
DB 345 IleArgTyrHisArgTyrHisGlnIleArgSerAlaThrValIlePheLeuGlnIleLeuLeu 364
QY 697 TATGACATGCTGCGGAGATATTCGTTGAGACGATGAAAGATCATCAAGGCGCA 756
DB 365 TyrAspMetValCyseGlyAspIleProPheGlnGlnAspGlnIleLeuArgGlyArg 384
QY 757 GTGTTCTTCAGGCAAACTGTCTTCAGAGTGTACAGACCTTAATTAATGTCCTGTCC 816
DB 385 LeuPhePheArgArgValSerProGlnCyseGlnIleLeuIleGlnIleProIlePheLeuSer 404
QY 817 CTGAGACCGTCAGATCGGCGCTCTTTGAAGAAATCCGAAACCATCCGTTGAGATGCAAGGT 876
DB 405 LeuArgProSerGlnArgProSerLeuAspGlnIleAlaIleAspProIlePheLeuGly 424

Search completed: September 22, 2005, 17:24:43
Job time : 32.7742 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 22, 2005, 15:57:45 ; Search time 123 Seconds
(without alignments)
5924.037 Million cell updates/sec

Title: US-10-705-757-5
Perfect score: 1749
Sequence: 1 atgcctcctgcacagatca.....cacccggatcacgacagtag 942

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ n2p.model -DEV=xlp
-Q/cg2.1/USPTO.epool_p/US10705757/runat_22092005_115014_22122/app_query.fasta_1.5333
-DB=A.GeneSeq -QMT=fastcan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPRN=pco -NOR=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10705757_QCGN_1_1_753_@runat_22092005_115014_22122 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: A.GeneSeq_16Dec04:.*
2: geneSeqp19808:.*
3: geneSeqp19808:.*
4: geneSeqp20018:.*
5: geneSeqp20028:.*
6: geneSeqp20038:.*
7: geneSeqp20038:.*
8: geneSeqp20048:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1668	95.4	313	5	ABG33015 Mouse pro
2	1668	95.4	313	6	AAO19790 Murine PI
3	1668	95.4	313	7	ABR62940 Mouse ser
4	1668	95.4	313	8	ADN97347 Murine PI
5	1668	95.4	313	8	ADR88371 Mus muscu
6	1584	90.6	313	5	ABR63016
7	1584	90.6	313	6	AAO19789 Rat PIM1
8	1584	90.6	313	7	ABR62938 Rat serin
9	1582	90.5	313	5	ABP54943 Human PIM
10	1582	90.5	313	5	ABG33017 Human pro

11	1582	90.5	313	6	AAO19788	AAO19788 Human PIM
12	1582	90.5	313	7	ABU61613	ABU61613 Human PIM
13	1582	90.5	313	7	ABR62939	ABR62939 Human ser
14	1582	90.5	313	7	ADBS5368	ADBS5368 Human pro
15	1582	90.5	313	8	ADP45083	ADP45083 Human kin
16	1582	90.5	313	7	ADP45083	ADP45083 Human kin
17	1582	90.5	313	8	ADP45083	ADP45083 Human PRO
18	1582	90.5	313	8	ADP45083	ADP45083 Human PIM
19	1580	90.3	313	2	AAO08139	AAO08139 Human cys
20	1580	90.3	313	3	AAH79959	AAH79959 Human CR7
21	1580	90.3	313	3	AD157202	AD157202 Human PIM
22	1580	90.3	313	8	ADN03170	ADN03170 Human PIM
23	1355.5	75.2	257	8	AAV43942	AAV43942 Rat prote
24	1315	75.2	253	8	AD157241	AD157241 PIM1 dom1
25	1215.5	69.5	254	8	ADR71853	ADR71853 Human kin
26	1131	64.7	323	8	ADR88376	ADR88376 Colutrix
27	1123.5	64.2	326	6	AAO19792	AAO19792 Murine PI
28	1123.5	64.2	326	7	ABR62933	ABR62933 Mouse pro
29	1123.5	64.2	326	8	ADP60032	ADP60032 CRH sigma
30	1123.5	64.2	326	8	ADR88375	ADR88375 Mus muscu
31	1122.5	64.2	326	5	AAO20524	AAO20524 Protein 8
32	1122.5	64.2	326	6	AAO19791	AAO19791 Rat PIM3
33	1122.5	64.2	326	7	ABR62936	ABR62936 Rat prote
34	1122.5	64.2	455	5	AAE23836	AAE23836 Rat KID-1
35	1122.5	64.2	455	5	ABG33013	ABG33013 Rat prote
36	1122.5	64.2	455	7	ADBS5366	ADBS5366 Rat prote
37	1119	64.0	326	2	AAV06886	AAV06886 HWHU20 p
38	1119	64.0	326	4	AAAB29788	AAAB29788 Human ser
39	1119	64.0	326	5	AAE23834	AAE23834 Human HKI
40	1119	64.0	326	5	ABG33011	ABG33011 Human ser
41	1119	64.0	326	7	ABR62932	ABR62932 Human pro
42	1119	64.0	326	8	ADP96625	ADP96625 Human cal
43	1119	64.0	326	8	ADU97960	ADU97960 Human PIM
44	1119	64.0	382	8	ADP20314	ADP20314 Human PRO
45	1119	64.0	382	8	ADP55593	ADP55593 Human PRO

ALIGNMENTS

RESULT 1	ABG33015	standard; protein; 313 AA.
ID	ABG33015	
AC	ABG33015	
DT	20-DEC-2002	(first entry)
XX		
DB	Mouse protein kinase phosphorylation site.	
KW	HKID-1; serine/threonine kinase; cellular proliferative disorder;	
KW	differentiative disorder; cancer; hematopoietic neoplastic disorder;	
KW	acute promyeloid leukaemia; APL; Chronic myelogenous leukaemia; CML;	
KW	Waldenstrom's macroglobulinaemia; WM; mouse.	
XX		
OS	Mus musculus.	
XX		
PN	US2002115120-A1.	
XX		
PD	22-AUG-2002.	
XX		
PF	04-OCT-2001; 2001US-00971791.	
XX		
PR	26-JAN-1999; 99US-00237543.	
XX		
PR	23-AUG-2000; 2000US-00644450.	
XX		
PA	(MILL-) MILLENNIUM PHARM INC.	
XX		
PI	Kapeller-Libermann R, Rudolph-Owen LA, Macbeth K;	
XX		
DR	WPI; 2002-712471/77.	
XX		
PT	Modulating levels or activity of HKID-1 polypeptides, a member of serine/threonine kinase superfamily, for treating cancer, by contacting	

PT cell expressing the polypeptide with a modulator of the polypeptide.

XX Example 3, Page 38-39, 48pp, English.

CC The invention describes a method of modulating the level or activity of
 CC human HKID-1 polypeptide, a member of serine/threonine kinase
 CC superfamily. The method involves contacting a cell expressing the
 CC polypeptide or nucleic acid with an agent to modulate the level or
 CC activity of polypeptide, or level of nucleic acid molecule. The method is
 CC useful for modulating the level or activity of HKID-1 polypeptide or
 CC polynucleotide in a subject having or predisposed to having a disorder
 CC involving cancer. Modulating HKID-1 expression or activity is useful for
 CC therapeutic purposes, for treating cellular proliferative and/or
 CC differentiative disorders including cancer or hematopoietic neoplastic
 CC disorders e.g. Acute promyeloid leukemia (APML), Chronic myelogenous
 CC leukemia (CML) and Waldenstrom's macroglobulinemia (WM). This is the
 CC amino acid sequence of a mouse protein kinase phosphorylation site

XX Sequence 313 AA;

SQ Alignment Scores:

Pred. No.: 5.03e-139 Length: 313
 Score: 1668.00 Matches: 313
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 95.37% Indels: 0
 DB: Gaps: 0

US-10-705-757-5 (1-942) x ABG33015 (1-313)

QY 1 ATGCTCTGTCCAGATCAACTCCCTGGCCCACTGCGCGCCGCTTCAGACGACTG 60
 |||||||
 Db 1 MetleuleuserlylleahsenSerleuAlahleuAlargProCyshamblen 20
 |||||||
 QY 61 CAGCCACCAAGCTGCGCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
 |||||||
 Db 21 HleAlathrllyleuAlargProGlyLysGlyLysGlyLysGlyLysGlyLysGly 40
 |||||||
 QY 121 GGGCGCGCTGTGGGAGCGGCTGCGCTGCGCTGCTACTCTGGCATCCGCGCGCGAG 180
 |||||||
 Db 41 GlyProleuleuendlyserGlyGlyPheGlySerValTyrSerGlylleargValAlaasp 60
 |||||||
 QY 181 AACTGCGCGGTGACCTTAAAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 |||||||
 Db 61 AsnleuProValAlahleuYshleValGlyLysAspArgIleSerAspTrpGlyLys 80
 |||||||
 QY 241 CCCAATGGCACCCGAGTCCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 |||||||
 Db 81 ProAsnGlyThrArgValAlaProMetGlyValAlaValleuleuYshleValSerSerAspPhe 100
 |||||||
 QY 301 TCGGCGGTGACTTGAATCTTGGAGCTGTTGAGAGAGAGAGAGAGAGAGAGAGAG 360
 |||||||
 Db 101 SerGlyValAlahleuArgleuAspTrpPheGlyLysArgProAspSerPheValleuleu 120
 |||||||
 QY 361 GAG 420
 |||||||
 Db 121 GlyArgProGlyLysProValGlnAspLeuPheAspPheIleThrLysArgGlyAlaLeuGln 140
 |||||||
 QY 421 GAG 480
 |||||||
 Db 141 GluAspLeuAlaArgGlyPhePheTrpGlnValleuGlnAlaValAlaArgIshCyshAsn 160
 |||||||
 QY 481 TGGGGGGTCTGACCGCGAGCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 |||||||
 Db 161 CyshGlyValleuAlaArgAspIleLysAspGlyAsnIleleuleuAspLeuSerArgGly 180
 |||||||
 QY 541 GAATCAAACTCATCGACTTCGGGTGCGGCGCGCTGCAAGAGAGAGAGAGAGAGAGAG 600
 |||||||
 Db 181 GluIleleuAspLeuAspPheGlySerGlyAlaLeuLeuYshAspThrValTyrThrAsp 200
 |||||||
 QY 601 TTTGATGGAGACCGAGGTGACAGTCTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
 |||||||
 Db 201 PheAspGlyThrArgValTyrSerProGlyLysTrpIleArgTyrHisArgTyrHisGly 220
 |||||||

QY 661 AGTGGGAGAGTGTCTGAGTCCCTTGGAGTCTGTCTATGACATGATGTCGAGAGATATT 720
 |||||||
 Db 221 ArgSerAlaAlaValAlaTrpSerleuendlylleuleuYshAspMetValCyshLysAspIle 240
 |||||||
 QY 721 CCGTTTGAGCAGATGAGAGAGATCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
 |||||||
 Db 241 PropheGlnAlaAspGlnGlnIlelleYshGlyGlnValPhePheArgGlnThrValSer 260
 |||||||
 QY 781 TGAAGTGTGACGACCTTATTAAATGTGCTGTCTCCGAGACCGTCAATGCGCGCTCC 840
 |||||||
 Db 261 SerGlyLysGlnIleleuIlelleYshTrpCyshLeuSerLeuArgProSerAspArgProSer 280
 |||||||
 QY 841 TTTGAAGAAATCCGAGACCATCCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
 |||||||
 Db 281 PheGlnGlyLysArgAsnIleProTrpMetGlnGlyAspLeuProGlnAlaAsp 300
 |||||||
 QY 901 GAGATCCATCTGACAGTCTGTACCGGAGATCCAGCAAG 939
 |||||||
 Db 301 GluIleleuIleuIleuSerleuSerProGlySerSerLys 313
 |||||||

RESULT 2

AA019790 standard, protein; 313 AA.

AA019790;

11-AUG-2003 (first entry)

Murine PIM1 kinase.

Mouse; PIM1 kinase; PIM3 kinase; pain; analgesic.

Mus sp.

WO200293173-A2.

21-NOV-2002.

13-MAY-2002; 2002MO-EP005234.

11-MAY-2001; 2001DE-01023055.

(CHEF) GRUNENTHAL GMBH.

Weine E, Schaefer MK;

WPI; 2003-120715/11.

N-PSDB; AB269188.

Method for identifying analgesics, useful particularly for treating

chronic pain, by screening compounds for interaction with PIM-1 or -3

kinase, or related compounds.

Claim 11; Fig 1F; 97pp; German.

XX The present invention relates to a method of identifying pain-regulating
 CC compounds, involving screening candidate compounds for interaction with
 CC PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are
 CC useful for treating chronic pain, particularly of neuropathic or
 CC inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or
 CC neurodegenerative diseases). The present sequence is murine PIM1 kinase

XX Sequence 313 AA;

SQ Alignment Scores:

Pred. No.: 5.03e-139 Length: 313
 Score: 1668.00 Matches: 313
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 95.37% Indels: 0
 DB: Gaps: 0

US-10-705-757-5 (1-942) x AAO19790 (1-313)

```

QY 1 ATGCTCTGTCGAAGTCAACTCCCTGGCCCACTGGCGCCGCCCTTGCAACGACTTG 60
DB 1 MetLeuLeuSerLyS11eAenSerLeuAlaH1eLeuArgAlaArgProCyASanAapLeu 20
QY 61 CAGCCCAACGAGTGGCGCGCGGCAAGAGAAGAGAGCCCTGGAGTGCAGTACAGAGTG 120
DB 21 HisAlaThrIySleuAlaProGlyLySgIuLySgIuProLeuGluSerGlnIyrgIuVal 40
QY 121 GGCCTGCTGTGGGACGCGGTGGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValIySerGlyIleArgValAlaAap 60
QY 181 AACTTGCGCGTGGCCATTAAAGCAGTGGAGAAGAGCCGAGATTTCGATTGGGAGAACTG 240
DB 61 AenLeuProValAlaIleLyS11eAenGluLySAspArgIleSerAapTrpGlyGluLeu 80
QY 241 CCCAATGGACCCGAGTGGCCCATGGAAGTGGTCTGCTGTAAGAAGAGTGGAGCTTCG 300
DB 81 ProAenGlyThrArgValIProMetGluValValLeuLeuLyS11eAenSerAapPhe 100
QY 301 TGGCGCGCTATTAGACTTCTGCACTGGTTCGAGAGGCCGATAGTTTCGTGCTGACTTG 360
DB 101 SerGlyValIleArgLeuLeuAapTrpPheGlyIuArgProAapSerPheValIleLeu 120
QY 361 GAAGGCGCCGACCCGCTGCAAGACCTTTGCACTTTATCCGAAAGAGAGCCCTACAG 420
DB 121 GluArgProGluProValGlnAapLeuPheAapPheIleThrGlyIuValAlaLeuGln 140
QY 421 GAGGACCTGGCGCGGAGATTCTTCTGGCAGTGTGAGGCGCGGCGGCGGCGGCGGCGG 480
DB 141 GluAapLeuAlaArgIyPhePheTrpGlnValLeuGlnAlaValAlaGlySCySHAsp 160
QY 481 TGGCGGCTTCTCCACCGCGCATCAAGAGAGAGAACTTTAATCGACTGACCGCGCGC 540
DB 161 CySGIyValIleuH1sArgAapIleLySAspGluAenIleLeuIleAapLeuSerArgGly 180
QY 541 GAAATCAAACTCATCGACTTCGGGTCGGGGCGCTGCTCAAGACACAGTCTACAGGAC 600
DB 181 GluIleLySleuLeuAapPheGlySerGlyAlaLeuLeuLySAspThrValIyTrpAsp 200
QY 601 TTTGATGGGACCCGAGTGTACAGTCCCGAGAGGATTTGGTACCATGGCTCCACGCGC 660
DB 201 PheAapGlyThrArgValIySerProGluTrpIleArgIyH1sArgIyH1sGly 220
QY 661 AGCTCGGACAGTCTGCTGCTCTTGGAGTCTGCTCTATGACATGCTCGGAGATATT 720
DB 221 ArgSerAlaIleValIleTrpSerIleuGlyIleLeuLeuIyTrpAapMetValCySgIyAapIle 240
QY 721 CCGTTTGAGCAGATGAAGATCATCAAGGCGCAAGTGTCTTTCAGGCAACTGTCTCT 780
DB 241 ProPheGluH1sAapGluGluIleIleLySgIuValIlePheAapArgIleThrValIser 260
QY 781 TCAGAGTGTAGAGACCTTATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
DB 261 SerGluCySgIuH1sAenIleLyS11eAenSerLeuArgProSerAapArgProSer 280
QY 841 TTTGAAGAAATCCGGAACCATCGGTGATGACAGGAGTACCTCTGCGCCGAGAGCTTCT 900
DB 281 PheGluGluIleArgAenH1sProTrpMetGlnGlyAapLeuLeuProGlnAlaIleAser 300
QY 901 GAGATCCATGTGCAAGTCTGTCAACCGGAGTCCAGCAAG 939
DB 301 GluIleH1sAenH1sSerLeuSerProGlySerSerLyS 313

```

RESULT 3

ABR62940 standard, protein; 313 AA.

AC ABR62940;
 XX
 DT 04-DEC-2003 (first entry)

```

XX Mouse serine/threonine protein kinase P1M-1.
DE
XX
DE Mouse; P1M-1; protein kinase; enzyme.
KW
XX
XX Mus musculus.
OS
XX
XX W02003060130-A2.
PN
XX
XX 24-JUL-2003.
PD
XX
XX 20-JAN-2003; 2003W0-EP000492.
PF
XX
XX 19-JAN-2002; 2002EP-00001401.
PR
XX
XX (AVET ) AVENTIS PHARMA DEUT GMBH.
PA
XX
XX Korn M, Mueller G, Schneider R, Techank G;
PI
XX
XX WPI; 2003-598536/56.
DR
XX
XX PT New human or murine P1M-3 DNAs or polypeptides, useful for as a screening
PT agent for identifying anti-type 2 diabetes mellitus drugs, or for
PT treating insulin resistance or type 2 diabetes mellitus.
XX
XX
XX Example 2; Page 40; 40pp; English.
PS
XX
XX The present sequence is the protein sequence of the murine
CC serine/threonine protein kinase and proto-oncogene, P1M-1. P1M-1 proteins
CC are the paralogues of novel human and murine P1M-3 proteins (see ABR62932
CC and ABR62933) of the invention, which are therefore expected to be
CC involved in cancer and cell growth regulation. P1M-3 is also involved in
CC the development of insulin resistance and type 2 diabetes mellitus. The
CC invention relates to the use of P1M-3 nucleic acids and proteins in:
CC screening assays for compounds that modulate insulin resistance or type 2
CC diabetes mellitus; detection assays for detecting insulin resistance or
CC type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing,
CC forensic biology); predictive medicine (e.g. diagnostic or prognostic
CC assays, monitoring clinical trials, pharmacogenomics); and for the
CC preparing a medicament for the treatment of insulin resistance or type 2
CC diabetes mellitus
XX
XX
XX SQ Sequence 313 AA;

```

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score: 1668.00	313	313	0	0	0	0
Percent Similarity: 100.00%						
Best Local Similarity: 100.00%						
Query Match: 95.37%						
DB: 7						

US-10-705-757-5 (1-942) x ABR62940 (1-313)

```

QY 1 ATGCTCTGTCGAAGTCAACTCCCTGGCCCACTGGCGCCGCCCTTGCAACGACTTG 60
DB 1 MetLeuLeuSerLyS11eAenSerLeuAlaH1eLeuArgAlaArgProCyASanAapLeu 20
QY 61 CAGCCCAACGAGTGGCGCGCGGCAAGAGAAGAGAGCCCTGGAGTGCAGTACAGAGTG 120
DB 21 HisAlaThrIySleuAlaProGlyLySgIuLySgIuProLeuGluSerGlnIyrgIuVal 40
QY 121 GGCCTGCTGTGGGACGCGGTGGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValIySerGlyIleArgValAlaAap 60
QY 181 AACTTGCGCGTGGCCATTAAAGCAGTGGAGAAGAGCCGAGATTTCGATTGGGAGAACTG 240
DB 61 AenLeuProValAlaIleLyS11eAenGluLySAspArgIleSerAapTrpGlyGluLeu 80
QY 241 CCCAATGGACCCGAGTGGCCCATGGAAGTGGTCTGCTGTAAGAAGAGTGGAGCTTCG 300
DB 81 ProAenGlyThrArgValIProMetGluValValLeuLeuLyS11eAenSerAapPhe 100

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QY 301 TCGGGCGTATTGACTTCTGAGCTGGTTGAGAGGCCCGGATGTTGCTGATCTCTG 360
    |||
DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleLeu 120
QY 361 GAGAGGCCCGAACCAGTGCAGACCTCTTGACTTTATCAACGAGAGAGCCCTACAG 420
    |||
DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
QY 421 GAGGACCTGGCCCGGAGAGATTCTTCTGACAGTCTCTGAGAGCCCTGGGCACTTGCACAC 480
    |||
DB 141 GluAspLeuAlaArgGlyPhePheTrpGlnValLeuGlnAlaValArgHisCysHisAsn 160
QY 481 TGGGGGTTCTCCACCGGACATCAAGAGAGAGAACTTTATCGACCTGAGCCCGGCG 540
    |||
DB 161 CysGlyValLeuHisArgAspIleArgAspGlnAsnIleLeuIleAspLeuSerArgGly 180
QY 541 GAATCAAACTCATCTGACTTCGGGTCGGGGCGCTCTCAAGGACACAGTCTACACGAGAC 600
    |||
DB 181 GluIleIleLeuIleAspPheGlySerGlyAlaIleLeuIleuAspThrValTyrThrAsp 200
QY 601 TTTGATGGGACCCGAGTGTACATCTCTCCAGAGTGGATTGCTACCATGCTACACGGC 660
    |||
DB 201 PheAspGlyThrArgValTyrSerProGluTrpIleArgTyrHisArgTyrHisArgGly 220
QY 661 AGGTCCGACAGCTGTCTGATCTCTGGGATCTCTGCTCATGACATGCTGCGGAGATATT 720
    |||
DB 221 ArgSerHisAlaValIleTrpSerLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
QY 721 CCGTTTGAGACGATGAAGAGATCATCAAGGGCCAAAGTCTTTCAGGCAAACTGTCTCT 780
    |||
DB 241 ProPheGluHisAspGluGluIleIleIleGlyGlnValPhePheArgGlnThrValSer 260
QY 781 TCAGATGTCTCAGACCTTATTAATGTGCTGCTCCCTGAGACGCTGAGATGCGCCCTCC 840
    |||
DB 261 SerGluCysGlnHisIleuIleIleTyrCysLeuSerLeuArgProSerAspArgProSer 280
QY 841 TTTGAAGAATCCGGAACCATCTCGTGAATGACGGTGAATCTCTGCGCCAGCAGCTTCT 900
    |||
DB 281 PheGluGluIleArgHisAspTrpMetGlnGlyAspLeuLeuProGlnAlaAsp 300
QY 901 GAGATCCATCTGCACAGTCTGTCAACCGGAGTCCAGCAAG 939
    |||
DB 301 GluIleHisIleHisSerLeuSerProGlySerSerIle 313

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RESULT 4

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ADN97347
ID ADN97347 standard; protein; 313 AA.
XX
AC ADN97347,
XX
DT 01-JUL-2004 (first entry)
XX
DE Murine p1ml SEQ ID NO:6.
XX
KW mouse; probasin; promoter; transgenic mouse; c-myc; prostate cancer;
    p1ml.
OS Mus musculus.
XX
PN MO2004000010-A2.
XX
PD 31-DEC-2003.
XX
PF 23-JUN-2003; 2003MO-US019818.
XX
PR 21-JUN-2002; 2002US-0390692P.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Sawyers CL, Ellwood-Yen KB,
XX
DR WPI; 2004-099050/10.

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XX
PT New transgenic mouse, useful as model system for the study of prostate
PT cancer and its progression comprising a nucleic acid construct comprising
PT a promoter operably linked to c-myc gene encoded in prostate cells of
PT transgenic mouse.
XX
PS Claim 7, SEQ ID NO 7, 65bp; English.
XX
CC The invention relates to a novel transgenic mouse whose genome comprises
CC a nucleic acid construct comprising a promoter having a fully defined
CC nucleotide sequence comprising 310 bp (ADN97347), where the promoter is
CC operably linked to c-myc having a fully defined nucleotide sequence
CC comprising 1320 bp (ADN97342) where the c-myc protein encoded is
CC expressed in prostate cells of the transgenic mouse at detectable levels.
CC The transgenic mouse can be used as an in vivo model system for the study
CC of prostate cancer and its progression. It can also be used in
CC preclinical and clinical models to test novel diagnostic and therapeutic
CC modalities including drug therapies relevant to prostate cancer
CC prevention and progression. The transgenic animal can also be used to
CC identify molecular markers that can be mediators of progression.
CC Identification of the mediators is useful since they are potential
CC therapeutic targets. The present sequence represents murine p1ml.
XX
SQ Sequence 313 AA;

```

Alignment Scores:	Pred. No.:	Length:	Matches:
Score:	5,03e-139	313	1668,00
Percent Similarity:	100,00%	Conservative:	0
Best Local Similarity:	100,00%	Mismatches:	0
Query Match:	95,37%	Gaps:	0
DB:	8		

```

US-10-705-757-5 (1-942) x ADN97347 (1-313)
QY 1 ATGCTCTGTCCTCAAGATCAATCTCTGCGCCCACTGCGCGCCCTCTGCAACGACTTG 60
    |||
DB 1 MetLeuLeuSerLeuIleAsnSerLeuAlaHisLeuArgAlaArgProCysAsnAspLeu 20
QY 61 CACGCCACCAACCTGCGCGCGCGGCAAGAGAGAGAGCCCTGAGTGGCAGTACCAAGTGG 120
    |||
DB 21 HisAlaThrLysLeuAlaProGlyLysGluLysGluProLeuGlnSerIleTyrGlnVal 40
QY 121 GGCCTGCTGTTGGGAGCGGTGGCTTGGCTGCTACTCTGAGATCCGCTGCGCGAGC 180
    |||
DB 41 GlyProLeuLeuGlySerGlyIlePheGlySerValTyrSerGlyIleArgValAlaAsp 60
QY 181 AACTTGCCTGCGGCAATTAAAGCATGTGAGAGAGACCGGATTTCCGATTGGGAGAACTG 240
    |||
DB 61 AsnLeuProValAlaIleIleHisIleValGluLysAspArgIleSerAspTrpGlyGluLeu 80
QY 241 CCCAATGGACCCCGGAGTGGCCCATGGAAGTGTCTGTTGAAGAAGTGAAGTCCGACTTC 300
    |||
DB 81 ProAsnGlyThrArgValaProMetGluValValIleLeuLysValaSerSerAspPhe 100
QY 301 TCGGGCGTATTGACTTCTGAGCTGGTTGAGAGGCCCGGATGTTGCTGATCTCTG 360
    |||
DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleLeu 120
QY 361 GAGAGGCCCGAACCAGTGCAGACCTCTTGACTTTATCAACGAGAGAGCCCTACAG 420
    |||
DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
QY 421 GAGGACCTGGCCCGGAGAGATTCTTCTGACAGTCTCTGAGAGCCCTGGGCACTTGCACAC 480
    |||
DB 141 GluAspLeuAlaArgGlyPhePheTrpGlnValLeuGlnAlaValArgHisCysHisAsn 160
QY 481 TGGGGGTTCTCCACCGGACATCAAGAGAGAGAACTTTATCGACCTGAGCCCGGCG 540
    |||
DB 161 CysGlyValLeuHisArgAspIleArgAspGlnAsnIleLeuIleAspLeuSerArgGly 180
QY 541 GAATCAAACTCATGACTTCGGGTCGGGGCGCTCTCAAGGACACAGTCTACACGAGAC 600
    |||

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QY 901 GAGATCCATCTGCACAGTCTGTCCACGGGATCCAGAG 939
 |||||
 Db 301 GIUILEHLEUHISSerLeuSerProGlySerSerIys 313

RESULT 6
 ABG33016

ID ABG33016 standard; protein; 313 AA.

XX ABG33016;

DT 20-DEC-2002 (first entry)

DE Rat protein kinase phosphorylation site #2.

KM HKID-1; serine/threonine kinase; cellular proliferative disorder;
 KW differentiative disorder; cancer; haematopoietic neoplastic disorder;
 KM acute promyeloid leukaemia; APLM; Chronic myelogenous leukaemia; CML;
 KM Waldenstrom's macroglobulinaemia; WM; rat.

XX Rattus norvegicus.

PN US2002115120-A1.

PD 22-AUG-2002.

PF 04-OCT-2001; 2001US-00971791.

PR 26-JAN-1999; 99US-00237543.

PR 23-AUG-2000; 2000US-00644450.

PA (MILL-) MILLENNIUM PHARM INC.

PI Kapeller-Libermann R, Rudolph-Owen LA, Machbeth K;

DR WPI; 2002-712471/77.

PT Modulating levels or activity of HKID-1 polypeptides, a member of
 PT serine/threonine kinase superfamily, for treating cancer, by contacting
 PT cell expressing the polypeptide with a modulator of the polypeptide.

PS Example 3; Page 39-40; 48pp; English.

XX The invention describes a method of modulating the level or activity of
 CC human HKID-1 polypeptide, a member of serine/threonine kinase
 CC superfamily. The method involves contacting a cell expressing the
 CC polypeptide or nucleic acid with an agent to modulate the level or
 CC activity of polypeptide, or level of nucleic acid molecule. The method is
 CC useful for modulating the level or activity of HKID-1 polypeptide or
 CC polynucleotide in a subject having or predisposed to having a disorder
 CC involving cancer. Modulating HKID-1 expression or activity is useful for
 CC therapeutic purposes, for treating cellular proliferative and/or
 CC differentiative disorders including cancer or haematopoietic neoplastic
 CC disorders e.g. Acute promyeloid leukaemia (APML), Chronic myelogenous
 CC leukaemia (CML) and Waldenstrom's macroglobulinaemia (WM). This is the
 CC amino acid sequence of a rat protein kinase phosphorylation site

SO Sequence 313 AA;

Alignment Scores:

Pred. No.: 1,45e-131 Length: 313
 Score: 1584.00 Matches: 295
 Percent Similarity: 96.81% Conservative: 8
 Best Local Similarity: 94.25% Mismatches: 10
 Query Match: 90.57% Indels: 0
 DB: 5 Gaps: 0

US-10-705-757-5 (1-942) x ABG33016 (1-313)

QY 1 ATGCTCTGTCCGAAGATCACTCCCTGGCCGACCTGGCCGCTCCGACGACGCTG 60
 |||||
 Db 1 MetLeuSerIysIleAsnSerLeuAlaIleValGAlaIaProCyAsnAspLeu 20

QY 61 CAGGCCACCAAGCTGGCCGCGGCAAGAAAGAGCCCTGGAGTCCGACGATCCAGGCTG 120
 |||||
 Db 21 HIsAlaAnuLySLeuAlaProGlySerGlyProLeuGluSerGlnTyrGlnVal 40
 QY 121 GGGCCGCTGTTGGGACGGGTGGCTTCGGCTCCGCTACTCTGGCATCCGCTCCCGAC 180
 |||||
 Db 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValAlaAsp 60
 QY 181 AACTGGCCGGTGGCCATTAAAGCAGTGGAGAAAGACCGGATTTCCGATTGGGAAACTG 240
 |||||
 Db 61 AsnLeuProValAlaIleIleValIleValGlnValAspArgIleSerAspTyrGlyLeu 80
 QY 241 CCCAATGGACCCCGAGTGGCCCAATGGAGTGGCTCTGTGAAAGAGTGAAGCTTCGACTTC 300
 |||||
 Db 81 ProAsnGlyThrArgValProMetGluValValLeuLeuLySValSerSerGlyPhe 100
 QY 301 TGGGCGCTCATTAAGCTTCTGGACGTGTTCCAGAGAGCCCGAATGTTTGGTGTACTCCG 360
 |||||
 Db 101 SerGlyValIleArgLeuLeuAspTyrPheGluArgProAspSerPheValLeuIleLeu 120
 QY 361 GAGAGCCCGAAGCCGGTGAAGACCTTCGACTTTATCAACGAAAGAGAGCCCTTACG 420
 |||||
 Db 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
 QY 421 GAGGACCTGGCCCGAGATTTCTTGGCAGGTGTGAGAGCCGTGCGGCTATTCGACAAC 480
 |||||
 Db 141 GluGluLeuAlaArgSerPhePheThrGlnValLeuGlnAlaValArgHisCysHisAsn 160
 QY 481 TGGCGGGTCTTCCACCGGACATCAAGAGCAAGCAATCTTAATGACCTGAGCCGCGGC 540
 |||||
 Db 161 CysGlyValLeuHisArgAspIleLyAspArgGluAsnIleLeuIleAspLeuAsnArgGly 180
 QY 541 GAAATCAAACTCATGCACTTCGAGTGGGAGCGCTGCTCAAGAGACAGTCTTACAGGAC 600
 |||||
 Db 181 GluLeuLySLeuIleAspPheGlySerGlyAlaLeuLeuLySAspThrValTyrThrAsp 200
 QY 601 TTTGATGGACCCGAGTGTACAGTCTCCAGAGTGATTTGGTACCATCGCTTACCAAGCC 660
 |||||
 Db 201 PheAspGlyThrArgValTyrSerProProGluTyrIleArgTyrHisArgTyrHisGly 220
 QY 661 AGGTGGGACGCTGTGTGGTCCCTTGGGATCCCTGCTTATGACATGCTCGGCAATATT 720
 |||||
 Db 221 ArgSerAlaAlaValTyrSerLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
 QY 721 CCGTTTGAAGCAGATGAAGATCATCAAGAGGCGCAAGGTTCTTCAAGGCAACTGTCTCT 780
 |||||
 Db 241 ProPheGlnHisAspGluGluIleValLySValGlnValTyrPheArgGlnArgValSer 260
 QY 781 TCAGAGTGTCAAGCACTTATTAATGTGTGCTGTCTCTGAGACCGTCAAGATCGCCCTCC 840
 |||||
 Db 261 SerGluCysGlnHisLeuIleValTyrGlySerLeuValArgProSerAspArgProSer 280
 QY 841 TTTGAAGAAATCCGAAACCATCCGTGATGACAGGAGTGAACCTTCCGCGGACAGTTCT 900
 |||||
 Db 281 PheGluGluIleGlnHisAspTyrProTyrMetGlnAspValLeuLeuProGlnAlaThrAla 300
 QY 901 GAGATCCATCTGCACAGTCTGTCCACGGGATCCAGAG 939
 |||||
 Db 301 GIUILEHLEUHISSerLeuSerProSerProSerIys 313

RESULT 7

AA019789

ID AA019789 standard; protein; 313 AA.

XX AA019789;

DT 11-AUG-2003 (first entry)

DE Rat PIM kinase.

KM Rat; PIM1 kinase; PIM3 kinase; pain; analgesic.

XX Rattus sp.

CC screening assays for compounds that modulate insulin resistance or type 2
 CC diabetes mellitus; detection assays for detecting insulin resistance or
 CC type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing,
 CC forensic biology); predictive medicine (e.g. diagnostic or prognostic
 CC assays, monitoring clinical trials, pharmacogenomics); and for the
 CC preparing a medication for the treatment of insulin resistance or type 2
 CC diabetes mellitus
 XX
 XX

SQ Sequence 313 AA;

Alignment Scores:

Pred. No.:	Length:	313
Score:	1,456-131	295
Percent Similarity:	1584.00	8
Best Local Similarity:	96.81%	Conservative: 10
Query Match:	94.25%	Mismatches: 0
	90.57%	Indels: 0
		Gaps: 0

US-10-705-757-5 (1-942) x ABR62938 (1-313)

QY 1 ATGCTCTGTCCAAAGATCAACTCCCTGGCCACCTTGCGGCGCCGCTGCAACGACTTG 60
 DB 1 MetLeuLeuSerLysIleAsnSerLeuAlaHisLeuArgAlaAlaProCysAsnAspLeu 20
 QY 61 CACGCCACCAAGCTGGCGCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
 DB 21 HisAlaAsnLysLeuAlaProGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGly 40
 QY 121 GGGCCGCTGTGGGCGCGCGCTTGCGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 DB 41 GlyProLeuLeuLysGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
 QY 181 AACTTGGCGGTGGCGCTTAAAGACGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 DB 61 AsnLeuProValAlaIleLysHisValGluLysAspArgLysSerAspTrpGlyGluLeu 80
 QY 241 CCCAATGAGACCCGAGTGGCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 DB 81 ProAsnGlyThrArgValProMetGluValValLeuLeuLysValSerSerGlyPhe 100
 QY 301 TCGGGCGCTGATTGACTTCTGCACTGGTTCAGAGAGCGCGATGCTTCTGCTGCTGCTG 360
 DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleLeu 120
 QY 361 GAGAGGCCGAGACCCGAGTGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
 QY 421 GAGGACCTGGCCGAGAGATTTCTTGGAGGTGCTGAGAGCGCTGGCGGATTTGCCAAG 480
 DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGluAlaValAlaArgHisCysHisAsn 160
 QY 481 TCGGGGGTTCTCCACCGGACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 DB 161 CysGlyValLeuHisArgAspIleLysAspGluAsnIleLeuLeuAspLeuAsnArgGly 180
 QY 541 GAAATCAAACTCATGCACTTGGGCTGGGGGCGCTGCTCAAGAGAGAGAGAGAGAGAGAG 600
 DB 181 GlnLeuLysLeuLysPheGlySerGlyAlaLeuLeuLysAspThrValTyrTrpAsp 200
 QY 601 TTTGATGGGACCCGAGTGTACAGTCTCCAGAGTGTATTCGATACCATCGCTCAACGAG 660
 DB 201 PheAspGlyThrArgValTyrSerProProGluTrpIleArgTyrHisArgTyrHisGly 220
 QY 661 AGGTGGGACGCTGTGGTCCCTTGGAGATCTGCTCTATGACATGGTCTGGCGGAGATATT 720
 DB 221 ArgSerAlaAlaValTyrPheLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
 QY 721 CGGTTGAGACGATGAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
 DB 241 ProPheGlnHisAspGluGluIleValLysGlyGlnValTyrPheArgGlnArgValSer 260
 QY 781 TCAGAGTGTACAGCACTTATTAAATGAGTGCCTGCTCCCTGAGACCGTCAAGATCGCCCTCC 840

DB 261 SerGluCysGlnHisLeuIleArgTyrCysLeuSerLeuArgProSerAspArgProSer 280
 QY 841 TTTGAGAAATCCGGAACATCCGAGATGCAAGGATGCACTTCCGCCAGGACGCTTCT 900
 DB 281 PheGluGluIleGlnAsnHisPheProTrpMetGlnAspValLeuProGlnAlaThrAla 300
 QY 901 GAGATCCATCTGCACAGTCTGTCAACCGGAGATCCAGCAAG 939
 DB 301 GlnIleHisLeuHisSerLeuSerProSerProSerLys 313

RESULT 9

ABP54943
 ID ABP54943 standard; protein; 313 AA.

AC ABP54943;

DT 13-JAN-2003 (first entry)

DE Human Pim1.

KW Pim1; tyrosine threonine kinase; TTK; protein kinase; enzyme;

KW mitotic checkpoint; colon cancer; breast cancer; tumour; cytostatic;

KW human; gene therapy.

OS Homo sapiens.

PN WO200268444-A1.

PD 06-SEP-2002.

PF 21-FEB-2002; 2002WO-US005278.

PR 21-FEB-2001; 2001US-0271254P.

PA (CHIR) CHIRON CORP.

PI Reinhard C, Jefferson AB, Chan VW;

DR MPI: 2002-698650/75.

DR N-PsDB: ABV73989.

PT Reducing growth of cancer cells comprises reducing Tyrosine Threonine

PS disclosure; Page 80-81; 113pp; English.

CC The present sequence is the protein sequence of human Pim1, a protein

CC related to tyrosine threonine kinase (TTK, see ABP54938) . TTK

CC polynucleotides and polypeptides of the invention encompasses

CC polynucleotides and polypeptides having sequence similarity or sequence

CC identity to human TTK and other genes and gene products related to TTK,

CC such as Pim1. The invention is based on the finding that TTK is

CC differentially expressed in various forms of cancer. It provides methods

CC for the identification of cancerous cells, especially breast cancer and

CC colon cancer cells, by detection of expression levels of TTK, as well as

CC diagnostic, prognostic and therapeutic methods. These methods can be used

CC as the basis of rational therapy. Assays for identifying molecules that

CC modulate the activity of these genes in cancers, as well as methods of

CC inhibiting tumour growth by inhibiting the activity of TTK are also

CC provided

SQ Sequence 313 AA;

Alignment Scores:

Pred. No.:	Length:	313
Score:	2,186-131	294
Percent Similarity:	1582.00	Conservative: 10
Best Local Similarity:	97.12%	Mismatches: 9
Query Match:	93.93%	Indels: 0
	90.45%	Gaps: 0

US-10-705-757-5 (1-942) x ABP54943 (1-313)

```

QY 1 ATGCTCTGTTCAGATCAATCCCTGGCCCACTGGCGCCGCCCTGCAAGACTTG 60
DB 1 MetLeuLeuSerIysIleAsnSerLeuAlaHisLeuArgAlaAlaProCysAsnAspLeu 20
QY 61 CAGGCCACCAAGCTGGCGCGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 21 HisAlaThrIleValLeuAlaProGlyLysGlyLysGlyLysGlyLysGlyLysGly 40
QY 121 GGGCCGCTGTGGCAGCGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 180
DB 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValIleArgValSerAsp 60
QY 181 AACTTGCCGGTGGCCATTAAAGCAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 61 AsnLeuProValAlaIleValHisLeuValGlyLysAspArgIleSerAspTrpGlyGlyLeu 80
QY 241 CCCAATGGCAACCGGAGTGGCCATGAAGTGGTCTGTTGAAGAGAGAGAGAGAGAG 300
DB 81 ProAsnGlyThrArgValProMetGlyValValLeuLeuValValSerSerGlyPhe 100
QY 301 TCGGCGCTCATTTAGACTTTCGACTGGTTCGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 101 SerGlyValIleArgLeuLeuAspTrpPheGlyLysArgProAspSerPheValLeuLeu 120
QY 361 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 121 GluArgProGlyLysProValGlnAspLeuPheAspPheIleThrGlyLysGlyAlaLeuGln 140
QY 421 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 141 GlnGlnLeuValAlaAspSerPhePheTrpGlnAlaLeuValAlaValAspHisCysHisAsn 160
QY 481 TGGCGGGTTCCTCCACCGGACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 161 CysGlyValLeuHisAspArgPheIleValAspGlyLysAsnLeuLeuLeuAspLeuAsnArgGly 180
QY 541 GAAATCAAACTCATCGACTTCGGGTCGGGGCGCGCTGCTCAAGAGAGAGAGAGAG 600
DB 181 GluLeuLeuSerLeuIleAspPheGlySerGlyAlaLeuLeuValAspThrValIleThrAsp 200
QY 601 TTTGATGGAGACCGGAGGTACAGTCTCCAGAGTGGATTCGATTCGATTCGATTC 660
DB 201 PheAspGlyThrArgValIleSerProGlyLysArgIleArgIleValAspGlyLysGly 220
QY 661 AGGTCGAGAGTGTCTGGTCCCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 720
DB 221 ArgSerAlaAlaValIlePheSerLeuGlyIleLeuLeuValAspMetValCysGlyAspIle 240
QY 721 CCGTTTGAGAGCAGTGAAGAGATCATCAAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 241 ProPheGlyLysIleAspGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGly 260
QY 781 TCAAGAGTTCAGCACTTATTAAATGGTGGCTGCTCCCTGAGAGAGAGAGAGAG 840
DB 261 SerGlyLysGlnHisLeuIleArgTrpCysLeuAlaLeuArgProSerAspArgProThr 280
QY 841 TTTGAAGAATCCGGAGACATCCGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 281 PheGlnIleValIleGlnAsnHisProTrpMetGlnAspValLeuLeuProGlnIleThrAla 300
QY 901 GAGATCCATCTGCAAGTCTGTCAACCGGAGATCCAGCAAG 939
DB 301 GluIleHisLeuHisSerLeuSerProGlyProSerIleAsp 313

```

DT 20-DEC-2002 (first entry)

DE Human protein kinase phosphorylation site.

KW HKID-1; serine/threonine kinase; cellular proliferative disorder;
 KW differential disorder; cancer; haematopoietic neoplastic disorder;
 KW Acute promyeloid leukaemia; APL; Chronic myelogenous leukaemia; CML;
 KW Waldenstrom's macroglobulinaemia; WM; human.

OS Homo sapiens.

PN US2002115120-A1.

PD 22-AUG-2002.

PP 04-OCT-2001; 2001US-00971791.

PR 26-JAN-1999; 99US-00237543.
 PR 23-AUG-2000; 2000US-00644450.

PA (MILL-) MILLENNIUM PHARM INC.

PI Kapeller-Lidemann R, Rudolph-Owen JA, Macbeth K;
 WPI; 2002-712471/77.

XX Modulating levels or activity of HKID-1 polypeptides, a member of
 PT serine/threonine kinase superfamily, for treating cancer, by contacting
 PT cell expressing the polypeptide with a modulator of the polypeptide.
 XX

PS Example 3; Page 40-41; 48pp; English.

XX The invention describes a method of modulating the level or activity of
 CC human HKID-1 polypeptide, a member of serine/threonine kinase
 CC superfamily. The method involves contacting a cell expressing the
 CC polypeptide or nucleic acid with an agent to modulate the level or
 CC activity of polypeptide, or level of nucleic acid molecule. The method is
 CC useful for modulating the level or activity of HKID-1 polypeptide or
 CC polynucleotide in a subject having or predisposed to having a disorder
 CC involving cancer. Modulating HKID-1 expression or activity is useful for
 CC therapeutic purposes, for treating cellular proliferative and/or
 CC differentiative disorders including cancer or haematopoietic neoplastic
 CC disorders e.g. Acute promyeloid leukaemia (APL), Chronic myelogenous
 CC leukaemia (CML) and Waldenstrom's macroglobulinaemia (WM). This is the
 CC amino acid sequence of a human protein kinase phosphorylation site
 CC

SO Sequence 313 AA:

Alignment Scores:

Pred. No.:	Length:	313
Score:	1582.00	294
Percent Similarity:	97.12%	10
Best Local Similarity:	93.93%	9
Query Match:	90.45%	0
DB:	5	Gaps:

US-10-705-757-5 (1-942) x ABG33017 (1-313)

```

QY 1 ATGCTCTGTTCAGATCAATCCCTGGCCCACTGGCGCCGCCCTGCAAGACTTG 60
DB 1 MetLeuLeuSerIysIleAsnSerLeuAlaHisLeuArgAlaAlaProCysAsnAspLeu 20
QY 61 CAGGCCACCAAGCTGGCGCGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 21 HisAlaThrIleValLeuAlaProGlyLysGlyLysGlyLysGlyLysGlyLysGly 40
QY 121 GGGCCGCTGTGGCAGCGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 180
DB 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValIleArgValSerAsp 60
QY 181 AACTTGCCGGTGGCCATTAAAGCAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 61 AsnLeuProValAlaIleValHisLeuValGlyLysAspArgIleSerAspTrpGlyGlyLeu 80

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QY 241 CCCAATGGACCCGAGTGGCCATGGAAGTGGTCTGTTGAAGAAGGCTGGACTTC 300
DB 81 ProSerGlyThrArgValProMetGluValLeuLeuLysValSerSerGlyPhe 100
QY 301 TCGGGCGTCATTAGACTTCTGAGCTGGTTGAGAGGCCGAGATAGTTTCTGCTGATCTTG 360
DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProSerPheValIleLeu 120
QY 361 GAGAGGCCCGAACCAGTGGCAAGCCTTCTGACTTATCAACCGAAGAGAGCCCTACAG 420
DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
QY 421 GAGACCTGGCCCGAGGATCTTCTGGCAGAGCTCTGAGAGCCGTGGCGCATTCACAAC 480
DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGluAlaValArgHisCysHisAsn 160
QY 481 TGGCGGGTTCTCCACCGCGCATCAAGAGCAGAAACATCTTAATCGACTGAGCCGCGC 540
DB 161 CysGlyValIleuHisArgAspIleLysAspGluAsnIleuIleAspLeuAsnArgGly 180
QY 541 GAATCAAACTCATCGACTTGGGTTGGGGCGCTGTCAGAGCAAGTCTACAGGAC 600
DB 181 GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyrTrpAsp 200
QY 601 TTGATGGGACCCGAGTGTACAGTCTCTCAGAGTGGATTGCTACCATCGCTACACGCGC 660
DB 201 PheAspGlyThrArgValTyrSerProProGluTrpIleArgTyrHisArgTyrHisGly 220
QY 661 AGGTGGGAGCTGTCTGGTCCCTTGGAGTCTGCTCTATGACATGGTCTGGCGAATATT 720
DB 221 ArgSerAlaIaValIleTrpSerLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
QY 721 CCGTTGAGACGATGAAGAGATCATCAAGGCGCAAGTCTTCAAGCGCAACTGTCTCT 780
DB 241 ProPheGluHisAspGluGluIleLeuArgGlyGlnAlaPhePheArgGlnArgValSer 260
QY 781 TCAGAGTGTACAGACCTTATTAATGGTGGCTGCTGCTGAGACCGTCAGATCGGCCCTCC 840
DB 261 SerGluCysGlnHisLeuIleArgTyrCysLeuAlaLeuArgProSerAspArgProThr 280
QY 841 TTGGAAGAAATCCGGAACCATCCGATGAGTACAGAGTGAACCTCTGCCCCAGGCACTTCT 900
DB 281 PheGluGluIleGlnAsnHisProTyrMetGlnAspValLeuLeuProGlnGluTrpAla 300
QY 901 GAGATCCATCGACAGTCTGTCAACCGGAGATCCAGCAG 939
DB 301 GluIleHisLeuHisSerLeuSerProGlyProSerLys 313

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RESULT 11

AAO19788 standard; protein; 313 AA.

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XX AAO19788;
AC AAO19788;
DT 11-AUG-2003 (first entry)
XX Human P1M1 kinase.
XX Human; P1M1 kinase; P1M3 kinase; pain; analgesic.
OS Homo sapiens.
XX
XX W0200293173-A2.
PD 21-NOV-2002.
XX
XX 13-MAY-2002; 2002MO-BP005234.
XX
XX 11-MAY-2001; 2001DE-01023055.
XX
XX (CHEP ) GRUENENTHAL GMBH.
XX

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PI 1 weine B, Schaefer MK;
XX
XX WPI; 2003-120715/11.
DR N-PDB; ABZ69186.
XX
XX Method for identifying analgesics, useful particularly for treating
PT chronic pain, by screening compounds for interaction with P1M-1 or -3
PT kinase, or related compounds.
XX
XX Claim 1; Fig 1B; 97p; German.
XX
XX The present invention relates to a method of identifying pain-regulating
CC compounds, involving screening candidate compounds for interaction with
CC P1M1 or P1M3 kinase. P1M1 and P1M3 proteins and coding sequences are
CC useful for treating chronic pain, particularly of neuropathic or
CC inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or
CC neurodegenerative diseases). The present sequence is human P1M1 kinase
XX
XX Sequence 313 AA;
SQ
Alignment Scores:
Pred. No.: 2,18e-131 Length: 313
Score: 1582.00 Matches: 294
Percent Similarity: 97.12% Conservative: 10
Best Local Similarity: 93.93% Mismatches: 9
Query Match: 90.45% Indels: 0
DB: 6 Gaps: 0
US-10-705-757-5 (1-942) x AAO19788 (1-313)
QY 1 ATGCTCTGTCCAAAGATCAATCCCTGGCCCACTGGCGCGCCGCTTGCACGACTTG 60
DB 1 MetLeuLeuSerLysGlnLeuSerLeuAlaHisLeuArgAlaAlaProCysAsnAspLeu 20
QY 61 CACGCCCAACCACTGGCGCGCGCGGCAAGAGAGAGCCCTGAGTCCAGTACCAAGG 120
DB 21 HisAlaThrLysLeuAlaProGlyLysGlnLysGluProLeuGlnSerGlnTyrGlnVal 40
QY 121 GGCCTGCTTTGGGAGCGGAGGCTTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 41 GlyProLeuLeuGlnLysSerGlyGlyPheGlySerValTyrSerGlyIleArgValSerAsp 60
QY 181 AACTGGCGGTGGGCACTTAAGACGCTGAGAAAGAACCGGATTTCCGATTGGGGAGAACTG 240
DB 61 AsnLeuProValAlaIleLysHisValGluLysAspArgIleSerAspTrpGlyGluLeu 80
QY 241 CCCAATGGACCCGAGTGGCCCATGGAAGTGGTCTGTTGAAGAAGTGAAGTCTCGACTTC 300
DB 81 ProSerGlyThrArgValProMetGluValValLeuLeuLysValSerSerGlyPhe 100
QY 301 TCGGGCGTCATTAGACTTCTGAGCTGGTTGAGAGGCCGAGATAGTTTCTGCTGATCTTG 360
DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProSerPheValIleLeu 120
QY 421 GAGACCTGGCCCGAGGATCTTCTGGCAGAGCTCTGAGAGCCGTGGCGCATTCACAAC 480
DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGluAlaValArgHisCysHisAsn 160
QY 481 TGGCGGGTTCTCCACCGCGCATCAAGAGCAGAAACATCTTAATCGACTGAGCCGCGC 540
DB 161 CysGlyValIleuHisArgAspIleLysAspGluAsnIleuIleAspLeuAsnArgGly 180
QY 541 GAATCAAACTCATCGACTTGGGTTGGGGCGCTGTCAGAGCAAGTCTACAGGAC 600
DB 181 GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyrTrpAsp 200
QY 601 TTGATGGGACCCGAGTGTACAGTCTCTCAGAGTGGATTGCTACCATCGCTACACGCGC 660
DB 201 PheAspGlyThrArgValTyrSerProProGluTrpIleArgTyrHisArgTyrHisGly 220

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QY 661 AGGTCGACAGCTGTCCTGCTGAGATCCTGCTATGACATGAGTCTGCGAGATATT 720
 CC |||||
 Db 221 ArgSerLeuAlaValITPserLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
 CC |||||
 QY 721 CCGTTGAGACGACGATGAAGATCATCAAGCGCCAGAGTCTTTCAGCGCAACTGTCTCT 780
 CC |||||
 Db 241 ProPheGluIleHisAspGluGluIleIleArgGlyGlnValIlePhePheArgGlnArgValSer 260
 CC |||||
 QY 781 TCAGAGTGCAGACCTTATTAAATGCTGCTGCTGCTGAGACCTGACATCGGCTCC 840
 CC |||||
 Db 261 SerGluCysGlnHisLeuIleArgTyrCysLeuAlaLeuArgProSerAspArgProThr 280
 CC |||||
 QY 841 TTGAAGAATCCGGAACCATCCGATGAGAGGATGACCTCTGCCCCAGGAGCTTCT 900
 CC |||||
 Db 281 PheGluGluIleGlnHisAspTyrProTyrMetGlnAspValLeuLeuProGlnIleThrAla 300
 CC |||||
 QY 901 GAGATCCATCTGCACAGCTGTGTCAACCGGATCCAGCAAG 939
 CC |||||
 Db 301 GluIleHisLeuHisSerLeuSerProGlyProSerIys 313
 CC |||||

RESULT 12
 ABU61613
 ID ABU61613 standard; protein; 313 AA.
 XX
 AC ABU61613;
 XX
 DT 11-AUG-2003 (first entry)
 XX
 DE Human PIM1 protein.
 XX
 KM Human; tyrosine threonine kinase; TTK; cancer; cytostatic;
 XX
 KM mitotic checkpoint gene; PIM1.
 XX
 OS Homo sapiens.
 XX
 PN US2003045491-A1.
 XX
 PD 06-MAR-2003.
 XX
 PF 21-FEB-2002; 2002US-00081119.
 XX
 PR 23-FEB-2001; 2001US-0289813P.
 XX
 PA (RETN/) REINHARD C.
 XX
 PA (JEPF/) JEFFERSON A B.
 XX
 PA (CHAN/) CHAN V W.
 XX
 PI Reinhard C, Jefferson AB, Chan VW;
 XX
 DR MPI; 2003-456566/43.
 XX
 DR N-PSDB; ACA62265.
 XX
 PT Detecting cancer in a subject, by comparing expression levels of tyrosine
 PT threonine kinase polypeptide or polynucleotide in a subject cell and a
 PT normal cell, where an increase in the expression level in the test cell
 PT is indicative of cancer.
 XX
 PS Disclosure; Page 34-35; 79pp; English.
 XX
 PS The invention relates to detecting cancer (other than ovarian cancer) in
 CC a subject, comprising comparing the expression levels of tyrosine
 CC threonine kinase (TTK, a mitotic checkpoint gene) polypeptide and
 CC polynucleotide in a test cell obtained from the subject and in a normal
 CC non-cancer cell, where an increase in the expression level of TTK protein
 CC or nucleic acid in the test cell compared to that in the normal cell,
 CC indicates the presence of cancer other than ovarian cancer. Also included
 CC are reducing growth of a cancerous cell (by contacting a cancerous cell
 CC with an amount of an agent effective to reduce TTK polypeptide activity
 CC in the cell), an assay for identifying a candidate agent that reduces
 CC growth of a cancerous cell (comprising: (i) detecting the activity of a
 CC TTK polypeptide in the presence of a candidate agent; and (ii) comparing
 CC the activity of TTK polypeptide in the presence of a candidate agent

CC relative to TTK polypeptide activity in the absence of the candidate
 CC agent), identifying an agent that reduces TTK activity (comprising: (i)
 CC contacting a cancerous cell displaying elevated expression of a TTK-
 CC encoding polynucleotide with a candidate agent; and (ii) determining the
 CC effect of the candidate agent on TTK polypeptide activity) and assessing
 CC the prognosis of a cancerous disease other than ovarian cancer in a
 CC subject (comprising: (i) detecting expression of TTK -encoding
 CC polynucleotide in a test cancer cell of a subject; and (ii) comparing a
 CC level of expression of TTK-encoding polynucleotide in the test cancer
 CC cell with a level of expression of the polynucleotide in a control non-
 CC cancer cell, where the level of expression of TTK in the test cancer cell
 CC is indicative of the prognosis of the cancerous disease). The methods are
 CC useful for detecting cancer (other than ovarian cancer) in a subject;
 CC reducing growth of a cancerous cell; identifying a candidate agent that
 CC reduces growth of a cancerous cell; identifying an agent that reduces TTK
 CC activity and assessing the prognosis of a cancerous disease other than
 CC ovarian cancer. The methods are also useful for determining the ability
 CC of a subject to respond to a particular therapy e.g. as a basis of
 CC rational therapy. The present sequence represents a closely related
 CC protein to human TTK, in this case human PIM1 (not defined)

XX
 SQ Sequence 313 AA;
 XX

Alignment Scores:
 Pred. No.: 2,186-131 Length: 313
 Score: 1582.00 Matches: 294
 Percent Similarity: 97.12% Conservative: 10
 Best Local Similarity: 93.93% Mismatches: 9
 Query Match: 90.45% Indels: 0
 DB: 7 Gaps: 0

US-10-705-757-5 (1-942) x ABU61613 (1-313)

QY 1 ATGCTCTGTCCAAAGATCAACTCCCTGAGCCACTGCGCGCCCTGCAAGCACTG 60
 CC |||||
 Db 1 MetLeuLeuSerIlyeIleAsnSerLeuAlaHisLeuArgAlaAlaProCysAsnAspLeu 20
 CC |||||
 QY 61 CACGCCACCAAGCTGGCGCGCGGCAAGAAAGAGAGCCCTGGAGTGCAGTACCAAGTG 120
 CC |||||
 Db 21 HisAlaThrIleLeuAlaProGlyIleGlyGluProLeuGlnSerGlnIleVal 40
 CC |||||
 QY 121 GGGCGGCTGTGGGCGAGCGGAGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 CC |||||
 Db 41 GlyProLeuLeuGlnSerIlyeIleGlySerValIlyeSerIlyeIleArgValSerAsp 60
 CC |||||
 QY 181 AACTTGCCCGTGGCCATTAAAGCAGTGAAGAGACCGGATTTCCGATTGGGAGAACTG 240
 CC |||||
 Db 61 AsnLeuProValAlaIleIleHisValGlnIlyeAspArgIleSerAspTrpGlyIleLeu 80
 CC |||||
 QY 241 CCGAATGGCAACCGAGTCCCATGGAAGTGTCTGTTGAAGAGTGAAGTCTGCACTTC 300
 CC |||||
 Db 81 ProAsnGlyThrArgValProMetGlnValIleLeuIlyeValSerSerGlyPhe 100
 CC |||||
 QY 301 TGGGGGTCATTAAAGCTTGTGACGTCTGAGAGCCCGGAGATGTTTCGTGTAATCCG 360
 CC |||||
 Db 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleIleLeu 120
 CC |||||
 QY 361 GAGAGGCCGGAACCGGTGCAAGACCTTTCGACTTATGACGGAAGAGAGCCCTTACAG 420
 CC |||||
 Db 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
 CC |||||
 QY 421 GAGAACTGGCCCGAGAGATTTCTTGGCAGGTGCTGAGAGCCGTGCGGATTTCCACAA 480
 CC |||||
 Db 141 GluGluLeuAlaArgSerPhePheTrpGlnValIleGluAlaValArgHisCysHisAsn 160
 CC |||||
 QY 481 TCGGGGGTTTCCACCGGACATCAAGACGGAACATTTAAATGAGTCAAGCCGCGCG 540
 CC |||||
 Db 161 CysGlyValLeuHisIleArgAspIleIlyeAspGlnAsnIleLeuIleAspLeuAsnArgGly 180
 CC |||||
 QY 541 GAATCAAACTCATGCACTTCGGGTGCGGGGCGCTGCTCAAGAGACAGTTCACGAGAC 600
 CC |||||
 Db 181 GluLeuIlyeLeuIleAspPheIlyeSerGlyAlaLeuLeuIlyeAspThrValIlyeThrAsp 200

QY 601 TTGTATGGAGCCGAGTGTACAGTCTCCAGAGTGGATTGCTACCATGCTACAGGCG 660
 |||||
 Db 201 PheAepGlyThrArgValTyrSerProProGluTrpIleArgTyrHisArgTyrHisGly 220
 QY 661 AGGTGGAGAGTGTGTGTGCTGCTTGGAGATCTGCTGTATGACATGGTCTGGAGATATT 720
 |||||
 Db 221 ArgSerAlaIleValTyrPserLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
 QY 721 CGTTTGACACAGATGAAGATCATCAAGGGCAAGTGTCTTCAAGCAACTGCTCT 780
 |||||
 Db 241 ProPheGluHisAspIleGluHisProlTyrMetGlnAspValLeuLeuProGlnGluThrAla 260
 QY 781 TCAGAGTGTACAGACCTTATTAATAGTGTGCTGCTGCTGAGACCTGACAGATCGAGCTCC 840
 |||||
 Db 261 SerGluCysGlnHisLeuIleArgTyrCysLeuAlaLeuArgProSerAspArgProThr 280
 QY 841 TTGTGAAGAAATCCGGAACCATCCGTGATGACAGGGTGAACCTCTGCCCCAGGCACTTCT 900
 |||||
 Db 281 PheGluGluIleGlnHisAspIleArgGlyGlnValPhePheArgGlnArgValSer 300
 QY 901 GAGATCCATCTGCACAGTCTGTACACGGGATCCAGCAG 939
 |||||
 Db 301 GlnIleHisLeuHisSerLeuSerProGlyProSerLys 313
 RESULT 13
 ABR62939
 ID ABR62939 standard, protein; 313 AA.
 AC ABR62939;
 DT 04-DEC-2003 (first entry)
 XX Human serine/threonine protein kinase PIM-1.
 DE Human serine/threonine protein kinase PIM-1.
 KW Human; PIM-1; protein kinase; enzyme.
 OS Homo sapiens.
 PN MO2003060130-AA.
 XX 24-JUL-2003.
 PD 20-JAN-2003; 2003MO-BP000492.
 PF 19-JAN-2002; 2002EP-00001401.
 PR (AVET) AVENTIS PHARMA DEUT GMBH.
 PA Korn M, Mueller G, Schneider R, Techank G;
 PI WPI; 2003-598536/56.
 DR
 XX New human or murine PIM-3 DNAs or polypeptides, useful for as a screening
 PT agent for identifying anti-type 2 diabetes mellitus drugs, or for
 PT treating insulin resistance or type 2 diabetes mellitus.
 XX
 PS Example 2; Page 40; 40pp; English.
 CC The present sequence is the protein sequence of the human
 CC serine/threonine protein kinase and proto-oncogene, PIM-1. PIM-1 proteins
 CC are the paralogues of novel human and murine PIM-3 proteins (see ABR62932
 CC and ABR62933) of the invention, which are therefore expected to be
 CC involved in cancer and cell growth regulation. PIM-3 is also involved in
 CC the development of insulin resistance and type 2 diabetes mellitus. The
 CC invention relates to the use of PIM-3 nucleic acids and proteins in:
 CC screening assays for compounds that modulate insulin resistance or type 2
 CC diabetes mellitus; detection assays for detecting insulin resistance or
 CC type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing,
 CC forensic biology); predictive medicine (e.g. diagnostic or prognostic
 CC assays, monitoring clinical trials, pharmacogenomics); and for the
 CC preparing a medicament for the treatment of insulin resistance or type 2
 CC diabetes mellitus

XX SQ Sequence 313 AA;
 Alignment Scores:
 Pred. No.: 2,186-131
 Score: 1582.00
 Percent Similarity: 97.12%
 Best Local Similarity: 93.93%
 Query Match: 90.45%
 DB: 7 Gaps: 0
 US-10-705-757-5 (1-942) x ABR62939 (1-313)
 QY 1 ATGCTCTGTCCAGATCAACTCCCTGGCCCACTGCGGCCGCCCTGCAACGACTG 60
 |||||
 Db 1 MetLeuLeuSerLysIleIleAsnSerLeuAlaHisLeuArgAlaIleProCysHisAspLeu 20
 QY 61 CACGCCACCAAGCTGAGCGCGCGGCAAGAAAGAGCCCTGGAAGTCCAGTACAGTGG 120
 |||||
 Db 21 HisAlaThrLysLeuAlaProGlyLysGlyLysGluProLeuGluSerGlnTyrGlnVal 40
 QY 121 GGGCCGCTGTGGGAGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 |||||
 Db 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValSerAsp 60
 QY 181 AACTGGCGGTGGCCATTAAAGCAGGTGAGAGAACCGGATTTCCGATTGGGAGAACTG 240
 |||||
 Db 61 AsnLeuProValAlaIleLysHisValGluLysAspArgIleSerAspTrpGlyIleu 80
 QY 241 CCCAATGGCAACCGGAGTCCCATGGAAGTGTCTCTGTGAAGAGAGTGAAGTCCGACTTC 300
 |||||
 Db 81 ProAsnGlyThrArgValProMetGluValIleLeuLysValSerSerGlyPhe 100
 QY 301 TCGGGGCTCATTAAGCTTCTGAGTGTGTGAGAGGCCCGGATGATTTGCTGCTGATCTCG 360
 |||||
 Db 101 SerGlyValIleArgLeuLeuAspTrpPheGluLysProAspSerPheValLeuIleu 120
 QY 361 GAGAGGCCGGAACCGGTGCAAGACTCTTGAATTATCAACGAAAGAGAGCCCTTACAG 420
 |||||
 Db 121 GlnArgProGluProValGlnAspLeuPheAspPheIleThrGlnArgGlyAlaLeuGln 140
 QY 421 GAGAACCTGGCCCGAGAGATTCTTCTGGCAGGTGTCTGAGAGCCGTGGGATTCGCAAC 480
 |||||
 Db 141 GlnGluLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgHisCysHisAsn 160
 QY 481 TCGGGGGTCTCCACCGGCAATCAAGAGCAAGCAATTTATGACCTGAGCCGCGCGC 540
 |||||
 Db 161 CysGlyValLeuHisLeuArgAspIleLysAspGluAsnIleLeuIleAspLeuHisArgGly 180
 QY 541 GAATCAAACTCATGCACTTCCGGTCCGAGGCGCTGCTCAAGAGACACAGTCTTACAGGAC 600
 |||||
 Db 181 GlnLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyrThrAsp 200
 QY 601 TTGTATGGAGCCGAGTGTACAGTCTCCAGAGTGGATTGCTACCATGCTACAGGCG 660
 |||||
 Db 201 PheAepGlyThrArgValTyrSerProProGluTrpIleArgTyrHisArgTyrHisGly 220
 QY 661 AGGTGGAGAGTGTGTGTGCTGCTTGGAGATCTGCTGTATGACATGGTCTGGAGATATT 720
 |||||
 Db 221 ArgSerAlaIleValTyrPserLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
 QY 721 CGTTTGACACAGATGAAGATCATCAAGGGCAAGTGTCTTCAAGCAACTGCTCTCT 780
 |||||
 Db 241 ProPheGluHisAspIleGluHisProlTyrMetGlnAspValLeuLeuProGlnGluThrAla 260
 QY 781 TCAGAGTGTACAGACCTTATTAATAGTGTGCTGCTGCTGAGACCTGACAGATCGAGCTCC 840
 |||||
 Db 261 SerGluCysGlnHisLeuIleArgTyrCysLeuAlaLeuArgProSerAspArgProThr 280
 QY 841 TTGTGAAGAAATCCGGAACCATCCGTGATGACAGGGTGAACCTCTGCCCCAGGCACTTCT 900
 |||||
 Db 281 PheGluGluIleGlnHisAspIleArgGlyGlnValPhePheArgGlnArgValSer 300

QY 901 GAGATCCATCTGCACAGTCTGTCCAGCGGATCCAGCAAG 939
 |||||
 Db 301 GIULIEHISLEUHISSERLEUSERPROGLYPROSERLYS 313

RESULT 14
 ADE55368
 ID ADE55368 standard; protein, 313 AA.

XX ADE55368;

AC ADE55368;

DT 29-JAN-2004 (first entry)

XX Human Protein AAA60089, SEQ ID NO 1183.

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

XX Human pain; neuronal tissue; gene therapy;

Alignment Scores:

Pred. No.: 2,18e-131 Length: 313
 Score: 1582.00 Matches: 294
 Percent Similarity: 97.12% Conservative: 10
 Best Local Similarity: 93.93% Mismatches: 9
 Query Match: 90.45% Indels: 0
 DB: 7 Gaps: 0

US-10-705-757-5 (1-942) x ADE55368 (1-313)

QY 1 ATGCTCCTGTCAAGATCAATCTCCCTGGCCACCTGGCCGCCCTTCGAAGCACTG 60
 |||||
 Db 1 MetleuenuserlysielaenserleualahleuarghlaahlaProCyabnapleu 20
 QY 61 CAGCCCAACAGTGGCGCGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
 |||||
 Db 21 HiealathryleuulapProgllyglulglulProleuglusergintylglnval 40
 QY 121 GGGCCGCTGTGGGCGCGGCTTCCGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTG 180
 |||||
 Db 41 GlyProleuenuiserglyglnyservaltyserglyleargvalserasp 60
 QY 181 AACTGGCGGTGGCCATTAAGACAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 |||||
 Db 61 AsnleuProvalahleuylshlevalglulysabphargliserasptprglgluleu 80
 QY 241 CCCAATGGCAACCGAGTCCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 |||||
 Db 81 ProasnglythryargvalPrometgluvalleuenuysvalserSerglyPhe 100
 QY 301 TCGGCGCTGTAGACTTCTGCACTGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 360
 |||||
 Db 101 Sercllyvalleuargleuenuaprtprpnegluargproasptprpnevalleu 120
 QY 361 GAGAGCGCCGAGACCGGTGCAAGACTCTTGAATTATCAAGAGAGAGAGAGAGAGAG 420
 |||||
 Db 121 GluargProglulProvalGlnaspleuPheaspheliehrclunrgllyaleuGln 140
 QY 421 GAGACCTGGCCCGAGAGATTTCTTGGCAAGTCTGAGAGAGAGAGAGAGAGAGAGAG 480
 |||||
 Db 141 GluGlnleuulargserPhepneptprglnvalleuGlnalvalarghlsCyshleasn 160
 QY 481 TGGGGGTTCTCCACCGCGCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 |||||
 Db 161 CysGlyvalleuulhargasphllyasphglnasnlleuulleasphasnaargly 180
 QY 541 GAATCAAACTCATTCAGCTTGGGTCGGGCGCTCTCAAGAGACAGTCTACAGAGAC 600
 |||||
 Db 181 GluenuyleuuleasphnegllyserglyalaleuenuysasphrthralyrtlnrAsp 200
 QY 601 TTTGATGGAGCCGAGGTGACAGTCTCCAGAGTGAATTGCTTACCATGCTTACAGG 660
 |||||
 Db 201 PheaspglythryargvaltyrserPropoglutprlearglyrharglyrhlsGly 220
 QY 661 AGGTGGCGAGCTGTCTGTCCTTGGAGTCCCTTGAAGTCTTGAAGTCTTGAAGTCT 720
 |||||
 Db 221 ArgseralalalalaltrpserleuglylleuuleuylraspmetvalCysGlyasphle 240
 QY 721 CCGTTGAGCAAGATGAAGATCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
 |||||
 Db 241 ProheglulhlsasphlulglulileleargglylnvalPheheargglnargvalSer 260
 QY 781 TCAAGTGTCAAGCACTTAAATGAGCTGTCTCCCTGAGACCGTCAAGTGGAGCTTCC 840
 |||||
 Db 261 SerGlnCysGlnhlsleuileargtrpCysleuulaleuargproserasptprtr 280
 QY 841 TTTGAAGAATCCGGAACCATCCGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
 |||||
 Db 281 PheglulglulilelnasphllyserProtyrPheGlnasphvalleuenuProglnglnthrAla 300
 QY 901 GAGATCCATCTGCACAGTCTGTCCAGCGGATCCAGCAAG 939
 |||||
 Db 301 GIULIEHISLEUHISSERLEUSERPROGLYPROSERLYS 313

RESULT 15

ADFF45083
ID ADFF45083 standard; protein; 313 AA.

AC ADF45083;

DT 12-FEB-2004 (first entry)

DE Human kinase PIM1.

KW Human; protein kinase; enzyme; inhibitor; PIM1.

OS Homo sapiens.

PN WO2003081210-A2.

PD 02-OCT-2003.

PF 20-MAR-2003; 2003WO-US008725.

PR 21-MAR-2002; 2002US-0366892P.

PA (SUNE-) SUNESIS PHARM INC.

PI Prescott JC, Braisted A;

DR WPI; 2003-865136/80.

PT Identifying ligand binding to inactive conformation of target protein
PT kinase (T) comprises contacting the conformation modified (T) which
PT contains reactive group at binding site, with ligands and detecting
PT kinase-ligand conjugate formation.

PS Disclosure; SEQ ID NO 52; 260pp; English.

CC The present invention relates to a method for identifying a ligand (L),
CC which binds to an inactive conformation of target protein kinase (T). The
CC method involves contacting inactive conformation of (T), which contains
CC or is modified to contain a reactive group at or near a binding site of
CC interest, with one or more ligand candidates capable of covalently
CC bonding to the reactive group thus forming a kinase-(L) conjugate (C).
CC The method is useful for identifying protein kinase inhibitors that
CC preferentially bind to inactive conformation of a target protein kinase.
CC The present sequence is a protein kinase which may be modified via an
CC amino acid substitution, for use in the method of the invention.

SQ Sequence 313 AA;

Alignment Scores:

Pred. No.:	2.18e-131	Length:	313
Score:	1582.00	Matches:	299
Percent Similarity:	97.12%	Conservative:	10
Best Local Similarity:	93.93%	Mismatches:	9
Query Match:	90.45%	Indels:	0
DB:	7	Gaps:	0

US-10-705-757-5 (1-942) X ADF45083 (1-313)

QY 1 AMGCTCTGTCCAAAGTCAACTCCCTCGGCCCACTGGCGCCGCCCTTCGAAAGACTG 60
|||
Db 1 MetLeuLeuSerLy sIleA nSerLeuL hI sLeuA rG lA lA lA ProCy sA nA mP leu 20
|||
QY 61 CACGCCACCAAGTGGGCGCCGGGCAAGAGAGAGAGCCCTCGAGTGGCAGTACCAAGTG 120
|||
Db 21 H sA lA tH rLy sLeuA lA ProG lY lY sG lU lY sG lU ProLeuG lU sSerG l nT yG l nVal 40
|||
QY 121 GGC CGCGCTGTGGGCGACCGGTGGCTTCGCGCTCACTCTGGCATCCGCGTGGCCGAC 180
|||
Db 41 G lY P r o L e u L e u l y s e r G l y G l y P e n e g l y s e r V a l t y s e r G l y l l e a r G v a l s e r A s p 60
|||
QY 181 AACTTCGCGGTGGCCATTAGACATGAGAGAGACCGGATTTCCGATTTGGGAGAACTG 240
|||

[illegible]

Search completed: September 22, 2005, 16:48:01
Job time : 130 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 22, 2005, 16:17:56 ; Search time 30.871 Seconds
(without alignments)
5871.937 Million cell updates/sec

Title: US-10-705-757-5
Perfect score: 1749
Sequence: 1 atgcctcctgcacgaatcaaa.....caccggagcaccgaagtag 942

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Xgapop 10.0, Xgapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame_n2p_model -DEV=xlp
-Q=cg2_1/USPTO_epool_g/US10705757/runat_22092005_115015_22141/app_query.fasta_1.5333
-Db=PIR -Qfmt=faetan -SUFPIX=n2p.rpr -MIMATCH=0.1 -LOOPCT=0 -LOOPEXT=0
-UNTS-bits -START=1 -END=1 -MATRIX=bloum62 -TRANS=human40.cdd -LIST=45
-DOCALLGN=200 -THR SCORE=apct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NORR=ext -HEAPSIZE=550 -MINLEN=0 -MAXLEN=2000000000
-USER=US10705757@cgc 1_1_256 @runat_22092005_115015_22141 -NCP=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1668	95.4	313	1	TVMSPI
2	1584	90.6	313	1	S26298
3	1582	90.5	313	1	TVHUP1
4	861.5	49.3	370	1	S55333
5	628	35.9	363	2	T22255
6	504	28.8	409	2	T15435
7	391.5	22.4	481	2	I49072
8	379	21.7	504	2	T10449
9	379	21.7	504	2	S6730
10	373	21.3	512	1	UC1446
11	373	21.3	1398	2	hypotheical prote
12	372	21.3	1358	2	hypotheical prote
13	370	21.2	511	1	A56009
14	367	21.0	512	2	T52633

15	361	20.6	513	1	S60304	serine/threonine-s
16	360.5	20.6	469	2	B84644	probable protein k
17	358.5	20.5	798	2	UC7500	dik protein - chic
18	357	20.4	512	2	T07788	probable serine/th
19	356	20.4	472	2	B90100	SNF-related kinase
20	355.5	20.3	651	2	S52244	p69Bg3 protein - A
21	353.5	20.2	887	2	T20941	hypotheical prote
22	351.5	20.1	504	2	T07415	probable serine/th
23	344.5	19.7	414	2	UN0323	Ca2/calmodulin-de
24	344	19.7	726	2	T33998	hypotheical prote
25	342.5	19.6	445	2	T50802	serine/threonine p
26	342	19.6	502	2	T02306	probable protein k
27	342	19.6	513	1	S60303	serine/threonine-s
28	338	19.3	1518	2	S37928	probable purine nu
29	334	19.1	746	2	S62365	SNF1-related prote
30	333	19.0	435	2	E84707	probable protein k
31	332.5	19.0	442	2	T48203	hypotheical prote
32	330	18.9	461	2	T14822	probable serine/th
33	330	18.9	520	2	G86414	probable protein k
34	328.5	18.8	1246	2	G89287	protein H3P23.1 l
35	327.5	18.7	745	2	G01025	serine/threonine p
36	327	18.7	774	2	I48609	probable serine/th
37	326.5	18.7	489	2	T04862	probable serine/th
38	326	18.6	473	1	S59941	serine/threonine-s
39	326	18.6	1558	2	T29253	hypotheical prote
40	324	18.5	527	2	A53467	protein kinase SNF
41	323.5	18.5	1152	2	T18611	probable serine/th
42	323	18.5	713	2	S27966	probable serine/th
43	322	18.4	339	2	S56719	serine/threonine-s
44	322	18.4	622	1	S44859	serine/threonine-s
45	321	18.4	423	2	T40224	protein kinase - f

ALIGNMENTS

RESULT 1
TVMSPI
protein kinase (EC 2.7.1.37) pim-1 - mouse
N/Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene prot.
C/Species: Mus musculus (house mouse)
C/Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C/Accession: A24169
R/Selien, G.; Cuypers, H.T.; Boelens, W.; Robanus-Maandag, E.; Verbeek, J.; Domen, J.;
Cell 46, 603-611, 1986
A/Title: The primary structure of the putative oncogene pim-1 shows extensive homology
A/Reference number: A24169; M0ID:86272109; PMID:3015420
A/Accession: A24169
A/Molecule type: DNA
A/Residues: 1-313 <SEL>
A/Cross-references: UNIPROT:P06803; GB:M13945; GB:M13946; NID:G200352; PIDN:AAA39930.1;
C/Comment: Pim-1 autophosphorylates at unknown sites.
C/Genetics:
A/Gene: pim-1
A/Introns: 26/1; 63/3; 80/3; 203/1; 262/1
C/Function:
A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine;
C/Superfamily: kinase-related transforming protein; protein kinase homology
C/Keywords: ATP; autophosphorylation; phosphotransferase; proto-oncogene; serine/threonine
F/36-290/Domain: protein kinase homology <KIN>
F/44-52/Region: protein kinase ATP-binding motif
F/67/Active site: Lys #status predicted

Alignment Scores:

Pred. No.: 4.93e-72 Length: 313
Score: 1668.00 Matches: 313
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.37% Indels: 0
DB: 1 Gaps: 0

US-10-705-757-5 (1-942) x TVMSPI (1-313)

QY 1 ANGCTCTGTCCAAGTCAATCCCTGCGCCACTGCGGCCCGCCCTCGAAGACGCTG 60

Db	1	MetLeuLeuSerLySilleAenSerLeuIahIleuIrrgaIaaGProCyAsnAspLeu	20
QY	61	CACCSCCAACGACTGGCGCCGGGCAAGAGAAGAGCCCTGGAGTGCAGTACAGATG	120
Db	21	HlaBlaThrLySleuAlaIaProGlyLySleGlyIuSgIuProLeuGluSerGlnTyGlnVal	40
QY	121	GGCCCGCGTGTGGGAGCGGCTGGCTTCGAGTCTAATCTGGCATCCCGGCTGCCGAC	180
Db	41	GlyProLeuLeuGlySerGlyGlyPheGlySerValTySerGlyIleArgValAlaAsp	60
QY	181	AACCTGGCCGGTGGCCATTAAACAGTCAGTGAAGAAAGACCGGATTTCCGATGGGGAGA	240
Db	61	AsnLeuProValAlaIleuLySileValGluLyAspArgIleSerAspTrpGlyGluLeu	80
QY	241	CCCAATGGCACCCGAGTGCCCATGAGAACTGGCTGTGAAGAAAGTGAAGCTCGAATTC	300
Db	81	ProAsnGlyThrArgValIProMetGlnValIleuLeuLySlyValSerSerAspPhe	100
QY	301	TCCGGCGCGCATTAACATCTTGGACTGGTTCAGAGAGCCCGCATTAATTCGTGTAATCTG	360
Db	101	SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleLeu	120
QY	361	GAGAGGCCCGAACCAGGTGCAGACCTCTTCACATTTTAACCGGAACAGAGCCCTACAG	420
Db	121	GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln	140
QY	421	GAGACCTGGCCCGGAGATTCTTCTGGCAGGTGTCTGAGGCCGTGGCATTTGCCACAAAC	480
Db	141	GluAspLeuAlaArgGlyPhePheTrpGlnValIleuGlnAlaValAlaGlnIleAsn	160
QY	481	TGGCGGGGTCTCCACCCGACATCAAGAGACGAGAACATTTAACTGACCTGGAGCGGGGC	540
Db	161	CysGlyValLeuAsnIleAspAspIleuLyAspGluAsnIleuIleAspLeuSerArgGly	180
QY	541	GAATCAAACTCATGCACTTCGGGTCCGGGGCGCTGCTCAAGACACAGTCTACAGCAGAC	600
Db	181	GluIleuLyLeuIleAspPheGlySerGlyAlaLeuLeuLyAspThrValTyThrAsp	200
QY	601	TTTGATGGGACCCGAGGTACAGTCTCCAGAGTGGATTCGCTACATCGTACCAAGGC	660
Db	201	PheAspGlyThrArgValTySerTrpProGlnTrpIleArgTyHisArgTyHisGly	220
QY	661	AGGTCCGAGCGTGTGGCTCCCTTGGAGATCTGGCTATGACACAGTCTGGGAGATATT	720
Db	221	ArgSerAlaAlaValTrpSerIleuGlyIleLeuLeuTyArgAspMetValCysGlyAspIle	240
QY	721	CCGTTTGAACAGATGAAGAATCATCAAGGACCAAGTGTCTTCCAGGAAACTGTCTCT	780
Db	241	ProPheGlnIleAspGlnGlnIleIleLySgIuGlnValIlePheAspGlnThrValSer	260
QY	781	TCAGAGTCCAGACCTTATTAATAGTGGCTGGTCCCGTGAACCGTACAGTCCGCGCTCC	840
Db	261	SerGluCysGlnIleLeuIleuLyTrpCysLeuSerIleuArgProSerAspArgProSer	280
QY	841	TTTGAAGAAATCCGGAACCATCCGTGATGACAGGATGACCTCTGCGCCAGAGCTTCT	900
Db	281	PheGlnGlnIleArgAsnHisProTrpMetGlnIleAspLeuLeuProGlnAlaIleSer	300
QY	901	GAGATCCATCTGCACAGTCTGTACACCGGAGATCCAGCAAG	939
Db	301	GluIleHisLeuHisSerLeuSerProGlySerSerTyS	313

RESULT 2
526298
protein kinase (EC 2.7.1.37) p1n-1 - rat
M.ALternate names: kinase-related transforming protein p1n-1; p1n-1 proto-oncogene protein
C.Species: Rattus norvegicus (Norway rat)
C.Date: 25-Feb-1994 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
J.Accession: 526298
R.Wingett, D.; Reeve, R.; Magnusson, N.S.
Nucleic Acids Res. 20, 3183-3189, 1992
A>Title: Characterization of the testes-specific p1n-1 transcript in rat.

A:Reference number: S26298; MUID:92319652; PMID:1620615
A:Accession: S26298
A:Molecule type: mRNA
A:Residues: 1-313 <MIN>
A:Cross-references: UNIPROT:P26794; EMBL:X63675; NID:G56902; PIDN:CAA45214.1; PID:G56903
A:Experimental source: testis
A>Note: testis-specific transcript, is shorter and more stable than the somatic transcript.
C:Comment: Pim-1 autophosphorylates at unknown sites.
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A>Note: in testis may be involved in signal transduction events of normal germ cell matu
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F:36-290/Domain: protein kinase homology <KIN>
F:44-52/Region: protein kinase ATP-binding motif
F:67/Active site: Lys #status predicted

Alignment Scores:			
Pred. No.:	4,58e-68	Length:	313
Score:	1584.00	Matches:	295
Percent Similarity:	96.81%	Conservative:	8
Best Local Similarity:	94.25%	Mismatches:	10
Query Match:	90.57%	Indels:	0
DB:	1	Gaps:	0

US-10-705-757-5 (1-942) x S26298 (1-313)

QY	1	ATGCTCTCTGTCGAATTCACCTCCCTGGCCACCTGGCGCCGCCCTCTGACACGACCTG	60
Db	1	MetLeuLeuSerIysIleAsnSerLeuIahIeLeuArgIaAlaProCysAsnAspLeu	20
QY	61	CACGCCACCAAGCTGGCGCGCCGGCCAAAGAAAGAGAGCCCTCGAGTCGACAGTCCAGGTC	120
Db	21	HisAlaAsnIlyLeuAlaProGlyLysGlyIlySerIlyProLeuGlnSerGlnIlyGlnVal	40
QY	121	GGCGCGCTGTGGGCGAGCGGTGCTTCGCTCGGTCTTACTTGGCATTCGCGCTCGCCGAC	180
Db	41	GlyProLeuLeuIlySerGlyIlyPheGlySerValTyrSerGlyIleArgValAlaAsp	60
QY	181	AACTTGGCCGGTGGCCATTAAAGCAAGTGAAGAAAGACCGGATTTCCGATTGGGAGAACTG	240
Db	61	AsnLeuProValAlaIleIyHisIleValGlnIlyAspArgIleSerAspIleProIlyGlnLeu	80
QY	241	CCCAATGGACCCGAGTCCCATGGAAGTGGTCCGTGTGAAGAAAGTGAAGCTTCGACTTC	300
Db	81	ProAsnGlyThrArgValIleProMetGluValIleLeuLeuIyIyValIleSerSerGlyPhe	100
QY	301	TGGGCGCTATTAGACTTCTTGGACTGGTGTGAGAGGCCCATAGTTTGTTGCTGATCTCG	360
Db	101	SerGlyValIleIleArgLeuLeuAspIleTyrPheGlnArgProAspSerPheValLeuIleLeu	120
QY	361	GAGAGCCCGGACCCGGGCGAAGACCTTGCACCTTTATCAGCGAAGAGAGAGCCCTACAG	420
Db	121	GluArgProGlnProValGlnAspLeuPheAspPheIleTrpGlnArgIyAlaLeuGln	140
QY	421	GAGAACCTGGCCCGAGGATCTTCTGGCAGGTGTGAGGCCGTGCGGCACTTGCACAAC	480
Db	141	GlnGlnLeuAlaArgSerPhePheTrpGlnValIleGlnIlyAlaValArgHisCysHisAsn	160
QY	481	TGGGGGGTCTCCACCGCGCATCAGAGAGAGAAACATCTTAATGAGCTGAGCGCGGC	540
Db	161	CysGlyValLeuHisArgAspIleIyAspGlnAsnIleLeuIleAspLeuAsnArgGly	180
QY	541	GAATCAAACTATCGACTTCGGGTCGGGGCGGTGCTCAAGAACACAGTCTAACCGGAC	600
Db	181	GlnLeuIyAspLeuIleAspPheGlySerGlyAlaLeuLeuIyAspThrValIyThrAsp	200
QY	601	TTTGATGGACCCGAGTGTACAGTCTCCAGAGTGAATTCGCTACCATCGTACCACGGC	660
Db	201	PheAspArgIyThrArgValTyrSerProGlnIlyIleArgIyHisIleArgIyHisGly	220
QY	661	AGGTGGCAGCTGTCTGGTCCCTTGGGATCTGCTCTATGACATGCTCTGCGGACATATT	720

Db 221 argserialaalaValTrpserleuGlyleuleuTrypnaMetValCysGlyAspIle 240

Qy 721 CCGTTTGAAGCAGATGAAGAATCATCAAGGCGCAAGTGTCTTTCAGGCAAACTGTCTT 780

Db 241 ProPheGlnHisMetGlnGluIuileValGysGlnIuValTyrPheArgGlnArgValSer 260

Qy 781 TCAGAGTGCAGCACTTATTAAATGAGCGCTGCGCCGTGAGACCGTCAAGATCGGCGCCGC 840

Db 261 SerGlnCysGlnHisLeuIleArgTrpCysLeuSerLeuAspGlnProSerAspArgProSer 280

Qy 841 TTTGAAGAAATCCGGGAACCATCCGTGATGACAGGATGACCTCTCCGCCCAAGCAAGCTTCT 900

Db 281 PheGlnGluIuileGlnAsnHisProTrpMetGlnAspValleuLeuProGlnIleAspIle 300

Qy 901 GAGATCCATCTGCACACATCTGTCAACCGGGAGATCCAGCAAG 939

Db 301 GluIleHisLeuHisSerLeuSerProSerProSerIlys 313

RESULT 3 TWHUP1

protein kinase (EC 2.7.1.37) p1m-1 - human
N/Alternate names: kinase-related transforming protein p1m-1; p1m-1 proto-oncogene protein
C/Species: Homo sapiens (man)
C/Accession: J1-Mar-1998 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
A/Accession: J00327, A46554; A27476, 158412
R/Reeves, R.; Spies, G.A.; Klefer, M.; Barr, P.J.; Power, M.
Gene 90, 303-307, 1990
A/Title: Primary structure of the putative human oncogene, p1m-1.
A/Accession: J00327, MUID:90382681, PMID:2205533
A/Molecule type: DNA
A/Residues: 1-313 <RER>
A/Cross-references: UNIPROT:P11309; GB:M27903; NID:G189956; PIDN:AAA60090.1; PID:G36702222
R/Meeker, T.C.; Nagarajan, L.; ar-husndi, A.; Croce, C.M.
J. Cell. Biochem. 35, 105-112, 1987
A/Title: Cloning and characterization of the human p1m-1 gene: a putative oncogene related
A/Reference number: A46554; MUID:88115604; PMID:3429489
A/Accession: A46554
A/Molecule type: mRNA
A/Residues: 1-313 <MER>
A/Cross-references: GB:M24779, NID:G1066790, PIDN:AAA81553.1; PID:G1066791
R/Zakut-Houri, R.; Hazum, S.; Givol, D.; Teichman, A.
Gene 54, 105-111, 1987
A/Title: The cDNA sequence and gene analysis of the human p1m oncogene.
A/Reference number: A27476, MUID:87277423, PMID:3475233
A/Accession: A27476
A/Molecule type: mRNA
A/Residues: 1-14, RA, 17-313 <ZAK>
A/Cross-references: GB:M16750; NID:G189956; PIDN:AAA60089.1; PID:G189957
R/Domen, J.; Von Lindern, M.; Hermans, A.; Breuer, M.; Grosveld, G.; Berns, A.A.
Oncogene Res. 1, 103-112, 1987
A/Title: Comparison of the human and mouse p1m-1 cDNAs: Nucleotide sequence and immunoid
A/Reference number: 158412, MUID:88217305, PMID:3328709
A/Accession: 158412
A/Structure: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-313 <DOM>
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C/Comment: p1m-1 autophosphorylates at unknown sites.
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C/Comment: p1m-1 autophosphorylates at unknown sites.
A/Accession: A27476
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A/Accession: A27476
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C/Comment: p1m-1 autophosphorylates at unknown sites.
A/Accession: A27476
A/Structure: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-313 <DOM>
A/Cross-references: GB:M54915; NID:G189961, PIDN:AAA36447.1; PID:G189962
C/Comment: p1m-1 autophosphorylates at unknown sites.
A/Accession: A27476
A/Structure: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-313 <DOM>
A/Cross-references: GB:M54915; NID:G189961, PIDN:AAA36447.1; PID:G189962
C/Comment: p1m-1 autophosphorylates at unknown sites.
A/Accession: A27476
A/Structure: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
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C/Comment: p1m-1 autophosphorylates at unknown sites.
A/Accession: A27476
A/Structure: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-313 <DOM>
A/Cross-references: GB:M54915; NID:G189961, PIDN:AAA36447.1; PID:G189962
C/Comment: p1m-1 autophosphorylates at unknown sites.
A/Accession: A27476
A/Structure: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-313 <DOM>
A/Cross-references: GB:M54915; NID:G189961, PIDN:AAA36447.1; PID:G189962
C/Comment: p1m-1 autophosphorylates at unknown sites.
A/Accession: A27476
A/Structure: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-313 <DOM>
A/Cross-references: GB:M54915; NID:G189961, PIDN:AAA36447.1; PID:G189962
C/Comment: p1m-1 autophosphorylates at unknown sites.
A/Accession: A27476
A/Structure: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-313 <DOM>
A/Cross-references: GB:M54915; NID:G189961, PIDN:AAA36447.1; PID:G189962
C/Comment: p1m-1 autophosphorylates at unknown sites.
A/Accession: A27476
A/Structure: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-313 <DOM>
A/Cross-references: GB:M54915; NID:G189961, PIDN:AAA36447.1; PID:G189962
C/Comment: p1m-1 autophosphorylates at unknown sites.
A/Accession: A27476
A/Structure: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-313 <DOM>
A/Cross-references: GB:M54915; NID:G189961, PIDN:AAA36447.1; PID:G189962
C/Comment: p1m-1 autophosphorylates at unknown sites.
A/Accession: A27476
A/Structure: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-313 <DOM>
A/Cross-references: GB:M54915; NID:G189961, PIDN:AAA36447.1; PID:G189962
C/Comment: p1m-1 autophosphorylates at unknown sites.
A/Accession: A27476
A/Structure: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-313 <DOM>
A/Cross-references: GB:M54915; NID:G189961, PIDN:AAA36447.1; PID:G189962
C/Comment: p1m-1 autophosphorylates at unknown sites.
A/Accession: A27476
A/Structure: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-313 <DOM>
A/Cross-references: GB:M54915; NID:G189961, PIDN:AAA36447.1; PID:G189962
C/Comment: p1m-1 autophosphorylates at unknown sites.
A/Accession: A27476
A/Structure: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-313 <DOM>
A/Cross-references: GB:M54915; NID:G189961, PIDN:AAA36447.1; PID:G189962
C/Comment: p1m-1 autophosphorylates at unknown sites.
A/Accession: A27476
A/Structure: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-313 <DOM>
A/Cross-references: GB:M54915; NID:G189961, PIDN:AAA36447.1; PID:G189962
C/Comment: p1m-1 autophosphorylates at unknown sites.
A/Accession: A27476
A/Structure: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-313 <DOM>
A/Cross-references: GB:M54915; NID:G189961, PIDN:AAA36447.1; PID:G189962
C/Comment: p1m-1 autophosphorylates at unknown sites.
A/Accession: A27476
A/Structure: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-313 <DOM>
A/Cross-references: GB:M54915; NID:G189961, PIDN:AAA36447.1; PID:G189962
C/Comment: p1m-1 autophosphorylates at unknown sites.
A/Accession: A27476
A/Structure: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-313 <DOM>
A/Cross-references: GB:M54915; NID:G189961, PIDN:AAA36447.1; PID:G189962
C/Comment: p1m-1 autophosphorylates at unknown sites.
A/Accession: A27476
A/Structure: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-313 <DOM>
A/Cross-references: GB:M54915; NID:G1

Pred. No.:	5.7e-68	Length:	313
Score:	1582.00	Matches:	294
Percent Similarity:	97.12%	Conservative:	10
Best Local Similarity:	93.93%	Mismatches:	9
Query Match:	90.45%	Indels:	0
DB:	1	Gaps:	0

US-10-705-757-5 (1-942) X TVHUP1 (1-313)

[illegible]

RESULT 4

S55333

protein kinase pim-2 (EC 2.7.1.-) - mouse

C|Species: Mus musculus (house mouse)

C|Date: 10-Oct-1995 #sequence revision 21-Jan-1997 #text_change 09-Jul-2004

C|Accession: S55333; A43093; B43093

R|van der Lugt, N.M.T.; Domen, J.; Verhoeven, E.; Linders, K.; van der Gulden, H.; Allert

EMBO J. 14, 2536-2544, 1995

A|Title: Proviral tagging in E-mu-myc transgenic mice lacking the Pim-1 proto-oncogene 1

A|Reference number: S55333; MUID:95300786; PMID:7781606

A|Accession: S55333

A|Molecule type: mRNA

A|Residues: 1-370 <VAN>

A|Cross-references: UNIPROT:Q62070; GB:I41495; NID:g765065; PIDN:AAA98922.1; PID:g765066

A|Note: 40K form

A|Accession: A43093

A|Molecule type: mRNA

A|Residues: 'M', 27-370 <VA2>

A|Cross-references: GB:I41495; NID:g765065; PIDN:AAA98923.1; PID:g765067

A|Note: 37K form

A|Accession: B43093

A|Molecule type: mRNA

A|Residues: 'M', 61-370 <VA3>

A|Cross-references: GB:I41495; NID:g765065; PIDN:AAA98924.1; PID:g765068

A|Note: 34K form

C|Comment: Pim-2 autophosphorylates at unknown sites.

C|GeneInfo:

A|Gene: Pim-2

A|Map position: X

A|Start codon: CTG

A|Note: locus between A-raf and Act-7, near Kv4.1

C|Function:

A|Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin

C|Superfamily: kinase-related transforming protein; protein kinase homology

C|Keywords: alternative initiators; ATP; autophosphorylation; phosphoprotein; phosphotra

P|89-345/Domain: protein kinase homology <KIN>

P|97-105/Region: protein kinase ATP-binding motif

P|120/Active site: Lys #status predicted

Alignment Scores:

Pred. No.:	5,996-34	Length:	370
Score:	861.50	Matches:	167
Percent Similarity:	69.33%	Conservative:	41
Best Local Similarity:	55.67%	Mismatches:	87
Query Match:	49.26%	Indels:	5
DB:	1	Gaps:	2

US-10-705-757-5 (1-942) x S55333 (1-370)

QY	34	CTGGCGCGCCGCCCTGTGACGACCTGCAGCCGACCAAGCTGGGCGCGGCAAGAG	93
DB	65	LeuGInGlyHisProSerProProValThrProThrGlnProProGlyGlyValAspArg	84
QY	94	GAGCCCTGTGAGTGTGACAGTACAGGTGGGCGCGCTTTGGGCAAGCGGTGGCTGCG	153
DB	85	AlaAlaPheGlnAlaGluTyrArgLeuGlyProLeuLeuGlyValGlyGlyPheGlyThr	104
QY	154	GCTCACTCTGGCATCCGGGTGCGCGACAACTTCCCGGTGGCCATTAAAGCATGGAAG	213
DB	105	ValPheAlaGlyHisArgValThrAspArgArgGlnValAlaIleValIleValIleSerArg	124
QY	214	GACCGGATTTCCGATTGGGAGAACTGCCCAATGGACCCGAGTGGCCCATGGAAGTGTG	273
DB	125	AsnArgValIleLeuGlyTyrPheThrValSerAspSerValThrCysProLeuGlnValAla	144
QY	274	CTGTGGAAGAAAGTG-----AGCTGGACTTCTCGGGCGTCAATTAACTTGGACTGG	327
DB	145	LeuLeuTyrPheValGlyGlyGlyValAsnGlyHisProGlyValIleArgLeuLeuAspTyr	164
QY	328	TTTCGAGAGAGCCCGGATAGTTTGGTGTGATCTCTGAGAGAGCCCGGAACGGGTGCAAGACTC	387
DB	165	PheGlnThrProGlnGlyPheMetLeuValIleuGlnArgProMetProAlaGlnAspLeu	184

QY 388 TTGCACCTTTATACCCGAACAGAGGCCCTTACAGAGAACCTCGGCGCCGAGATTCTTCTGG 447

Db 185 Pheaspryrltlethrglulvvglyproleuylglubsercyserserleasprpethr 204

QY 448 CAGGTGCTGAGGCGCGGCGCATTTGCGACAACTCGCGGGGTTCCTCCACCGCGCATGAG 507

Db 205 Glnlvalvalalaailevalglinhlecyenihlaalargylvalvalhlaargaprllelv 224

QY 508 GACGAGAACATCTTAATCGACCTGACGCCGCGGCGAATCAATCATCTGACTTGGGTCG 567

Db 225 Asprglubsnlleuillleasprleucyaaigdyserlleuylleasprheglyser 244

QY 568 GGGGCGGCTGCTCAAGGACACAGCTACACGGACTTTATGAGGACCCGAGTTACAGTCCT 627

Db 245 Glylaleuueuhlsahargluprotlythrshpheasprglulmargvaltlyserpro 264

QY 628 CCAGAGTGATTCGCTACATCGCTACACCGGACGAGTCGCGAGCTGTCTGGTCCCTTGG 687

Db 265 ProglutprlleserarghlaaglnltyrhlaileuiproalathrValtlrpsertleugly 284

QY 688 ATCTGCTCTTATGACATGCTGTGCGGAGATTTCTCCGTTTGAAGCACATGAAGATCATC 747

Db 285 Valleuleuuryaarmetvalcyeglyasprlleprohegluayagapnglnulleu 304

QY 748 AAGGCGCAAGGTCTTTCAGGCAAACTGTCTCTTCAAGTGTGAGCACTTATTAATGG 807

Db 305 Glulalagluueuhlsahpheproalanhlevalserproahercyscvalaleuulleargarg 324

QY 808 TGCCTGTCCCTGAGACCGCTCAGATCGGCCCTCTCTTGAAGAAATCCGAAACATCGCTGG 867

Db 325 CysleuulapProlysProcysserargProserleuuglnulleuLeuAapProtyr 344

QY 868 ATGCAAGGTGACCTTCCTGCGCCCGGACAGCTTCAAGTCCATCTGCACAGTCGTCCAG 927

Db 345 Metglinsr-----ProalaglnlulapProlleasnserserlyeglyserpro 361

RESULT 5

T22255

hypothetical protein F45H7.4 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T22255

R/Percy, C.

submitted to the EMBL Data Library, June 1994

2/Reference number: Z19538

2/Accession: T22255

1/Status: preliminary; translated from GB/EMBL/DBJ

1/Molecule type: DNA

1/Residues: 1-363 <Wtl>

A/Cross-references: UNIPROT: Q20443; EMBL: Z34800; PIDD: CAA04323.1; GSPDB: GN00021; CESP: F45H7

A/Experimental source: clone F45H7

C/Gene/ID:

A/Gene: CESP:F45H7.4

A/Map position: 3

A/introns: 72/3; 160/3; 310/1

C/Superfamily: kinase-related transforming protein; protein kinase homology

Alignment Scores:

Pred. No.:	6,46e-23	Length:	363
Score:	628.00	Matches:	122
Percent Similarity:	64.15%	Conservative:	48
Best Local Similarity:	46.04%	Mismatches:	89
Query Match:	35.91%	Indels:	6
DB:	2	Gaps:	3

US-10-705-757-5 (1-942) x T22255 (1-363)

QY 103 GAGTCGACGATGAGCGCGCGCTGTGAGGACGAGCTTGCGCTTCGAGCTCGCTACTCT 162

Db 28 Lysllysbahentyrlylsleuylvalgluleucllyargelglyphegilyvalvaltlytharg 47

QY 163 GGCATCGCGCTGCGCGCAACTTGC CGGTGGCATTAAGCACTGTGAGAAAGACCGGATT 222

Db 122 cyenHdargAamMetValhNhdargAapLeuYerProgluamLeuLeuLeuAap--- 140
 QY 532 AGCGCGCGGGAATCAATCATGACTTGGGTGGGGCGCTGCTCAAGACACAGTC 591
 Db 141 SerLySCyavavAllyvAlaerPheGlyLeuSeravnlMetArAargGlyhN 160
 QY 592 TACAGGAGATTGAT---GGGACSSGAGTGTACAGTCTGAGAGGATGAGTGGTACAT 648
 Db 161 PheUlyUthetSerCyvGlySerProventryAlaAlaProgluValIleSerGlyv 180
 QY 649 CGGTACACGAGGAGTGGGAGCTGTGTGCTGCTGGATGCTGTGTATGACATGATC 708
 Db 181 LeuTyAlaGlyProgluValaerValItrPserCyvGlyValIleuTyAlaLeu 200
 QY 709 TGGGAGATATTCGCTTGAAGCAGATGAAGATC-----ATCAAG 750
 Db 201 CyvGlyUthLeuProPheAer---AerGluAvnlIleProavnlPheUlyvIle 219
 QY 751 GGGCAAGTGTTC---TTACAGGCAAGTGTCTTTCAGAGTGTACAGACCTTATTAATG 807
 Db 220 GlyGlyIleTyThLeuProSerhNleuSerSerGlyAlaArgGluLeuIlePro 239
 QY 808 TGGCTGTCTGAGACCGTCAAGTCCGCTCTTGAAGAAATCCGGAACCATCCGATG 867
 Db 240 MetLeuValValaerProMetUlyvArgIleThIleProgluIleArgGlnIlePro 259
 QY 868 ATGCAGGCTGACCTC 882
 Db 260 PheGlnAlaIleU 264

RESULT 9

866730
 hypothetical protein YOL045W - yeast (Saccharomyces cerevisiae)
 N/Alternate names: hypothetical protein O2034
 C/Species: Saccharomyces cerevisiae
 C/Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 16-Aug-2004
 C/Accession: S66730
 R/Annoter: W.; Benes, V.; Rechmann, S.; Schwager, C.; Teodoru, C.; Voss, H.; Wiemann, S.
 submitted to the Protein Sequence Database, July 1996
 A/Reference number: S66723
 A/Accession: S66730
 A/Molecule type: DNA
 A/Residues: 1-1101 <ANS>
 A/Cross-references: UNIPROT:Q08217; EMBL:Z74786; NID:g1419846; PIDN:CAA9051.1; PID:e251
 A/Experimental source: strain S288C
 C/Genetics:
 A/Cross-references: SGD:S0005405
 A/Map position: 15L
 C/Superfamily: protein kinase homology
 C/Keywords: ATP
 F/839-1099/Domain: protein kinase homology <KIN>
 F/847-855/Region: protein kinase ATP-binding motif

Alignment Scores:

Pred. No.: 2 95e-11 Length: 1101
 Score: 379.00 Matches: 91
 Percent Similarity: 55.51% Conservative: 60
 Best Local Similarity: 33.46% Mismatches: 95
 Query Match: 21.67% Indels: 26
 DB: 2 Gaps: 8

US-10-705-757-5 (1-942) x S66730 (1-1101)

QY 106 TCGACATCAAGGTGGCGCGCTGTGTGGCAGCGGTGCTCGCTCGCTACTGTGAC 165
 Db 839 SerAapPheThrlleuGlnValMetGlyGluGlyAlaTyrcIlyvAlaLeuLeuCyv 858
 QY 166 ATCCGCGTGGCGACACTTCCGCGTCCATTAAGCAGTGAAGAAGACCGGATT--- 222
 Db 859 ILeHLaavAargGluHleTyrlleValIleTyMeIlePheUlyvGluTyrlleU 878
 QY 223 ---TCCGATTGG-----GGAGAACTGCGCAATGACACCGAGAGGCC 261

Db 879 ValAerThrlTyValaArgAargUlyvLeuGlyThrlleProSerGluIleGlnIle--- 897
 QY 262 ATGGAATGATCTCTGTTAAAGAGTGAAGTGGACTTTCGGGCGTCAATGAAGTTCG 321
 Db 898 -----MetAlthrlleUavnlAvnSerGlnIlu-----AvnlleUlyvLeuLeu 913
 QY 322 GACTGAGAGAGCGCCGATGATTTCCGTCGATCTGTGAGAGCGCCGAACCGGCGAA 381
 Db 914 AapPhePheGluAapAapAapTyTyTyTle-----GluThrProValhN 929
 QY 382 -----GACCTTTCGACTTATTCACGGAACGAGAGCCCTACAGAG 423
 Db 930 GlyGlyThrcIlySerIleAapPheAerValIleGluPheUlyvAapMetValGlu 949
 QY 424 GACCTGCGCGGAGATTTCTGGCAGGTGCTGAGAGCGCGTGGCATTCGCAATGCG 483
 Db 950 HlsgUalUlyvLeuValaPheUlyvGlnValaIleAserIleUlyvHleUlyvAerGln 969
 QY 484 GGGGTCTCCACCGGACATCAAGACGAGAAATCTTAATGACCTGAGCGCGCGGAA 543
 Db 970 GlyIleValhNhdargAapIleUlyvAerGluAvnlIleValAap---SerhIsgIlyPhe 988
 QY 544 ATCAAACTGATGACTTCGCGGTGCGGGCGCTGCTCAAGACACAGTGTACAGCACTTT 603
 Db 989 ValUlyvLeuIleAapPheUlyvSerAlaAlaTyrlleUlyvSerGlyProPheAerValPhe 1008
 QY 604 GATGGACCCGAGTACAGTCCCTCAAGTGAATTCGTTACATGCTACCAAGGACAG 663
 Db 1009 ValGlyUthMetAapTyrcIlyAlaIleProgluValIleUlyvGlySerSerTyrcIlyv 1028
 QY 664 TCGGACGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 723
 Db 1029 ProGlnAapIleTyrcIlyAlaUlyvLeuGlyValIleUlyvTyrcIlyvGlyvAapPro 1048
 QY 724 TTGACACAGATGAAGATCATCAAGGCGCAAGTCTTCAAGCAACT-----GTC 777
 Db 1049 TyrcIlyvAapIleAapIleUlyvGlnUlyvLeuAargPheAapUlyvSerGlnIleVal 1068
 QY 778 TCTTCAGAGTGTCAAGACCTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 837
 Db 1069 SerGluGlyvGlnIleSerIleUlyvAargIleUthAargGluValaPheUlyvAargPro 1088
 QY 838 TCCTTGAAGAAATCCGGAACCATCCGTGATGACAG 873
 Db 1089 ThrIleAapGluIleTyrcIlyvAapTyrcIlyv 1100

RESULT 10

JCI446
 serine/threonine-specific protein kinase (EC 2.7.1.1-) AK21 - Arabidopsis thaliana
 N/Alternate names: protein kinase SNF1 homolog
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C/Accession: JCI446; S58266; S66334
 R/Lieguen, L.; Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis, M.
 Gene 120, 249-254, 1992
 A/TITLE: Structure and expression of a gene from Arabidopsis thaliana encoding a protein
 A/Reference number: JCI446; MUID:93013041; PMID:3339373
 A/Accession: JCI446
 A/Molecule type: DNA
 A/Residues: 1-512 <LEGS>
 A/Cross-references: UNIPROT:Q08997; GB:M30323; NID:g166599; PIDN:AAA32736.1; PID:g166601
 R/Thummler, F.; Kirchner, M.; Teuber, R.; Dietrich, P.
 submitted to the EMBL Data Library, May 1995
 A/Description: Differential accumulation of the transcripts of 22 novel protein kinase
 A/Reference number: S58266
 A/Accession: S58266
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 144-198 <THU>
 A/Cross-references: EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PID:g928910
 R/Thummler, F.; Kirchner, M.; Teuber, R.; Dietrich, P.
 Plant Mol. Biol. 29, 551-565, 1995
 A/TITLE: Differential accumulation of the transcripts of 22 novel protein kinase genes

A:Reference number: S66314; MUID:96123233; PMID:8534852
A:Accession: S66334
A:Molecule type: DNA
A:Residues: 144-198 <TH2>
A:Cross-references: EMBL:X68666; NID:G928909; PIDD:CA60529.1; NID:G928910
C:Comment: This enzyme plays an important role in a signal transduction cascade regulating
C:Genetics:
A:Gene: AKI10; AK21
A:Introns: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3
C:Function:
A:Description: catalyzes the formation of peptidyl-L-serine-phosphate or peptidyl-L-threonine
C:Superfamily: AMP-activated protein kinase; protein kinase homology
C:Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinases
F:17-27/Domain: protein kinase homology <K1>
F:25-33/Region: protein kinase ATP-binding motif
F:48,67,142,144/Active site: Lys, Glu, Asp, Lys #secret predicted
F:147,151/Binding site: magnesium (Asn, Asp) #secret predicted

Alignment Scores:

Pred. No.:	6,68e-11	Length:	512
Score:	373.00	Matches:	94
Percent Similarity:	52.03%	Conservative:	47
Best Local Similarity:	34.69%	Mismatches:	114
Query Match:	21.33%	Indels:	16
DB:	1	Gaps:	8

US-10-705-757-5 (1-942) x JC1446 (1-512)

OY	94	AAAGCCCTGGAGTGGCAAGTACCAAGTGGAGCCCGCTGTTGGGCAAGCGGTGGCTGGCTGG	153
Db	13	GIuSerIleuProAntyTyluLeuGIygrThyrLeuGIyIleGIySerPheGIyArg	32
OY	154	GTCTACTGTGGCATCCGCGTGGCCGCAACAATGTGCGGTGGCATTAAGACATGGTGAAGAAG	213
Db	33	ValluylIealagIuInIealaleuThrGIyInIyIuValalIaIleIyIleIeuAAsArg	52
OY	214	GACCGGATTTCCGATTTGGGAGAGAACTGCCCAATGGACCCGAGTGGCCATGGAAATGGCTC	273
Db	53	ArgIySIleIyAAsn-----MetGIuMetGIuGIyIuValArgArgGIuIleIyIu	69
OY	274	CTGTGGAGAAAGGTAGTGGCTGGACTTTCGGGCGGTCAATTAAGCTTTGGATGGTGGAG	333
Db	70	IleIeuAAsArgPheMetIleIyProInIu-----IleIleIyArgLeuTyrGIuValIleGIu	87
OY	334	AGGCCCGATGTTTCGTGCTGATCTCTGGAGAGGCCCGCAACCGGTGGCAAGACTTTCGAC	393
Db	88	ThrProThrAerIleTyrLeuValMetGIuTyrValIaAsenr-----GIuIleuPheAer	106
OY	394	TTTATACCCGAACAAGAGAGCCCTACAGAGAGACTCGGCGCGCAAGATTTCTTGGCAAGTG	453
Db	107	TyrIleValIGIuIyIeGIyArgLeuGIInGIuAerGIuValAAsArgAAsPhePheGIInIle	126
OY	454	CTGGAGCGCGGTGGCATTTGCGCACAACTGGCGGGTTCSCACCGCATGCAAGACAGAG	513
Db	127	IleSerGIyValIGIuTyrCueInIeAAsArgAAsMetValIeInIeAAsArgLeuIyProGIu	146
OY	514	AAACATCTTAATCGACCTGAGCGCGCGGCGAATCAAACTCATCGACTTGGGTGGGCGGCG	573
Db	147	AAsnIeuIeuIeuAAsP-----SerIyIeCyuAAsnValIyIealAAsPheGIuIeIySerAAsn	165
OY	574	CTGGCTCAAGAGACACAGTCTACACGGACTTTGAT---GGGACCCGAGTGAAGTCAAGTCTCA	630
Db	166	IleMetAAsArgAerGIuInIePheIeuIyIyThrIeSerCyuGIySerProAntyTylalAAsPro	185
OY	631	GAGTGGATTCGCTACATCGCTTACACGAGCGAGTGGGAGCGAGCTGTGGCTCCCTTGGAGTC	690
Db	186	GIuValIleSerGIyIyIeIyLeuTyrIaGIyProGIuValAAsPheValTyrSerCyuGIyVal	205
OY	691	CTGCTCTTAATGACATGCTGCGGAGATATATTCGTTTGAAGACAGATGAAGAAGATC-----	744
Db	206	IleIeuTyrIaIeIeuIeCyuGIyIyThrIeuProIeAAsP-----AAsGIuAAsnIleProAAsn	224
OY	745	-----ATCAAGGCGCCAAAGTGTTC-----TTCAAGCAAAATGTCTTTCAGAGATGT	789

[illegible]

RESULT 11

hypothetical protein 22E5.8 - fruit fly (*Drosophila melanogaster*)

C;species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence revision 13-Aug-1999 #text change 09-Jul-2004

C/ACCESSION: 113/41
R:Murphy, L.; Harris, D.; Barrell, B.

A:Description: Sequencing the distal X chromosome of *Drosophila melanogaster*.
Submitted to the EMBL Data Library, April 1999

A;Reference number: 217668
A:Accession: T13741

A;Status: preliminary

A;Residues: 1-1398 <MUR>
A;Cross-references: INTIPROT.077268, EMBL.AI.031765.

C;Genetics:
1:Cross-referenced: PjvData.EBcm0000667

A; Introns: 205/3; 227/1;

1

Pred. No.:

Percent Similarity:

Query Match: 21.33%

6
 7
 8
 9
 10
 11
 12

03 1111
QY

```

Db      131  LysLeuLysLeuProIleCArgValGlyPheTyrAspIleGluArgThrIleGlyLysGly  150
QY      142  GGCCTCGGCTCGGTC--TACTCTGGCANCCTGCTCGCCGCAACTTGCGCGTGCACATT  198
        |||  |||  ::  |||  |||  |||  |||  |||  |||  |||  |||
Db      151  AsnPheAlaValAlaLysLeuAlaArgHisArgIleThrLysAsn--GluValAlaIle  165

```

US-10-705-757-5 (1-942) X T13741 (1-1398)

```

QY      85 AAAGAGAAAGAGCCCTGGAG---TCGACATGACAGGTGGGCGCCGCTGTTGGGAGGGGT 141
Db      131 LybLeuulLybLeuulrTomehrarValGlyPhetyrAepilrGluarGthrlleGlyLysG 150
QY      142 GCGCTCGGCGCTGGCTC---TACTCTGGACATCCGCGTGGCGGACAACTTGGCCGTGGCATT 198
Db      151 AsnPhelValValValLybLeuulAarhghrAarGllrEthrlrLysAen---GluValAlaIle 169
QY      199 AAGCAGCTGGAGAAAGAGCCGAGATTCCGATTGGGAGAACTGCCCATGGACCCGAGATG 255
Db      170 LybElleLeuAspLysSerGlnLeu-----AapGlnrThrAsnLeuGlnLysVal 185
QY      259 CCCATGGAGAGTGTCTCGTTGAAGAAAGAGAGCTCGACATTCTGGCGGTCAATAGACTT 318
Db      186 TyrArgGluValAlaGluIleMetLysArgLysGluLysrVhrlsproHs-----IlelleLysLeu 205
QY      319 CTGAGACTGTTCTGAGAGGCGCCGATGATTGCTGATCTTGGAGAGGCCCGAAACCGGTG 376
Db      204 TyrGlnValMetGlnThrLysAsnMetClleryrIleValSerGluTyrAlaSerGln-- 222
QY      379 CAAGACCTCTTGCACCTTTATTCACCGACAGAGAGGCGCTTACAGAGAGACTTGGCCCGAGA 433
Db      223 GlyGluIleLeuAspLysrYrIleAlaLysYrYrGlyArgMetSerGlnSerAlaAlaArgPhe 241
QY      439 TTTCTTGGAGGTGCTGGAGGCGCGTGGCGGACCTTGGCCCAACTGGCGGGATTCTCACCGC 498
Db      243 LysPheThrPrpIlnIleIleSerAlaValAlaGluTyrGlyrVhrlsLysLysGlyIleValHisArg 261
QY      499 GACATCAAGACAGAGAAACATCTTAATCCACTGAGACCGCGCGGAAATCAACTATGAGAC 555
Db      263 AspLeuLysValAlaGluAsnLeuLeuMetSerLeuMet---AsnIleLysIleLysAlaSp 281

```


base of Saccharomyces cerevisiae.

A:Reference number: A56009; MUID:94217693; PMID:8164654

A:Accession: A56009

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-511 <MUR>

A:Cross-references: UNIPROT:Q04544; GB:D26602; NID:g496384; PIDN:BA05649.1; PID:g496385

C:Function:

A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine

C:Superfamily: AMP-activated protein kinase; protein kinase homology

C:Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase

F:17-271/Domain: protein kinase homology <KIN>

F:25-33/Region: protein kinase ATP-binding motif

F:48-67/142,144/Active site: Lys, Glu, Asp, Lys #status predicted

F:147,151/Binding site: magnesium (asn, asp) #status predicted

Alignment Scores:

Pred. No.: 9,266-11 Length: 511

Score: 370.00 Matches: 93

Percent Similarity: 51.64% Conservative: 49

Best Local Similarity: 33.82% Mismatches: 117

Query Match: 21.15% Indels: 16

DB: 1 Gaps: 8

US-10-705-757-5 (1-942) x A56009 (1-511)

QY 82 GCGAAGAGAAAGAGCCCTGAGTGCAGTACAGTGGCGCCGCTGTGGGCAAGCGT 141

DB 9 GlySerSerValGluSerPheLeuArgAsnTyrLysLeuGlyLysThrLeuGlyIleGly 28

QY 142 GCGTTCGCGTGGTCTGCTGTCGATCCGCGTGCAGCAACTGGCCGGCCATTAG 201

DB 29 SerPheGlyLysValLysIleAlaGluHisThrLeuThrGlyHisLysValAlaValLys 48

QY 202 CAGGTGAGAGAGAGCCGAGATTCCGATTGGGAGAACTGCCCAATGGACCCGAGTCCC 261

DB 49 IleLeuAsnArgArgLysIleLysAsn-----MetGluMetGluLysValArg 65

QY 262 ATCGAAGTGGTCTGTGTAAGAGAGAGTGCAGTCTCGGGCCCTTGTAGCTTCG 321

DB 66 ArgGluIleLysIleLeuArgLeuPheMetHisProHis-----IleIleArgLeuTyr 83

QY 322 GACTGTTGAGAGAGCCGAGTATTGCTGATCTGATCTGAGAGAGCCCAACCGGTGCA 381

DB 84 GluValValGluThrProSerArgIleTyrValValMetGluTyrValLysSer---Gly 102

QY 382 GACTCTTGTGACTTTATTCACCGAAGAGAGCCCTTACAGAGAGACTGGCCGAGGATTC 441

DB 103 GluLeuPheAspTyrIleValGluTyrGlyArgLeuGluLysArgLysPhe 122

QY 442 TTCTGACAGGTGCTGAGAGCCGCGGCAATTGCCAACACTGGCGGTTCTCCACCGGAC 501

DB 123 PheGluGluHisIleSerGlyValGluTyrCysHisArgAsnMetValHisIleArgAsp 142

QY 502 ATCGAAGAGAGAGACTTTAATGACCTGAGCCGCGGAGAACTCAACTGCACTTC 561

DB 143 LeuLysProGluAsnLeuLeuLeuAsp---SerLysTyrAsnValLysIleHisIleAspPhe 161

QY 562 GGGTCCGGGGCGCTGCTCAAGACACAGTCTACAGGACTTTGAT---GGAGCCGAGTGC 618

DB 162 GlyLeuSerAsnIleMetArgAspGlyHisPheLeuLysThrSerCysGlySerProAsn 181

QY 619 TACAGCTCCAGAGAGAGATTGGTCACTGATCCGTAACAGGAGCGTCCGAGAGTCTGG 678

DB 182 TyrAlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTyr 201

QY 679 TCCCTTGGAGTCTGCTGTTATGACATGATCTGCGAGATATTCGTTTGACAGATGA 738

DB 202 SerCysGlyValIleLeuTyrAlaLeuLeuLeuCysGlyThrLeuProPheAsp---AspGlu 220

QY 739 GAGATC-----ATCAG--GGCCAGTGTCTTCAAGCAACTGTC 777

DB 221 AsnIleProAsnLeuPheLysIleLysIleGlyGlyMetIleSerLeuProSerHisLeu 240

QY 778 TCTTCAGAGTGCAGACCTTATTAAATGATGCTGCTGCAGACCGTGCAGATCGGCC 837

DB 241 SerAlaGlyAlaArgAspLeuIleProArgMetLysIleValAspProMetLysArgMet 260

QY 838 TCCCTTGAAGAAATCCGAGACCATCGGTGATGACAGGATGACCTC 882

DB 261 ThrIleProGluIleArgMetHisProTyrPheGluHisIleLeu 275

RESULT 14

T52633

serine/threonine-specific protein kinase (EC 2.7.1.-) AKIN1 [validated] - Arabidopsis t

N:Alternate names: SNF1 protein kinase omolog AKIN1

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004

C:Accession: T52633

R:Balazs, R.P.; Salchert, K.; Bako, L.; Okresz, L.; Szabados, L.; Muranaka, T.; Machid

Proc. Natl. Acad. Sci. U.S.A. 96, 5322-7, 1999

A:title: Regulatory interaction of PRL1 WD protein with Arabidopsis SNF1-like protein ki

A:Reference number: 225116; MUID:99238528; PMID:10220464

A:Accession: T52633

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-512 <BHA>

A:Cross-references: UNIPROT:P2958; EMBL:X99279; PIDN:CAA67671.1

A:Experimental source: cultivar Columbia

C:Genetics:

A:Gene: AKIN1

C:Function:

EC 2.7.1.-; serine/threonine-specific protein kinase AKIN1 [validated,]

C:Superfamily: AMP-activated protein kinase; protein kinase homology

C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

Alignment Scores:

Pred. No.: 1,286-10 Length: 512

Score: 367.00 Matches: 95

Percent Similarity: 52.40% Conservative: 47

Best Local Similarity: 35.06% Mismatches: 113

Query Match: 20.98% Indels: 16

DB: 2 Gaps: 8

US-10-705-757-5 (1-942) x T52633 (1-512)

QY 94 GAGCCCTGAGAGTGCAGTACAGAGTGGGCGCGTGTGGGAGCGGTGCTTGCCTGC 153

DB 14 GluSerIleLeuProAsnTyrLysLeuGlyLysThrLeuGlyIleGlySerPheGlyLys 33

QY 154 GTTACTCTGGCATCCGCGTGCAGCAACTTGCCTGGCCATTAAAGCAGTGAAG 213

DB 34 ValLysIleAlaGluHisIleValAlaThrGlyHisLysValAlaIleLysIleLeuAsnArg 53

QY 214 GACCGGATTCGAGATTGGGAGAACTGCCCAATGGACCCGAGTCCCATGAGTGC 273

DB 54 ArgLysIleLysAsn-----MetGluMetGluGlyValArgArgGluLysLys 70

QY 274 CTGTGGAAGAGTGAAGTCTGCGATCTTGCAGCACTTGTGAGCTGCTGAG 333

DB 71 IleLeuArgLeuPheMetHisProHis-----IleIleArgGluTyrGluValIleGlu 88

QY 334 AGCGCCGATGATGCTGATCTGATCTGAGAGAGCCGGAACCGGTGCAAGACTTTGCAC 393

DB 89 ThrThrSerAspIleTyrValValMetGluTyrValLysSer---GlyGluLeuPheAsp 107

QY 394 TTTATTCACGAAACGAGAGACCTTACAGAGAGACTGGCCGAGATTTCTTGGCAGGTG 453

DB 108 TyrIleValGluLysGlyArgLeuGluGluLysArgLysValAspPhePheGluGluIle 127

QY 454 CTGAGAGCGCGTGGCATTGGCCAACTGCGCGGTTCTCACCGGAGATCAAGAGCAG 513

DB 128 IleSerGlyValGluTyrCysHisIleArgAsnMetValHisIleArgAspLeuLysProGlu 147

QY 514 AACATCTTAATGACCTGAGCCGCGGAGAACTCAATCAATGACTTGGGTCGGGGCGG 573

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Db      148 AsnLeuLeuLeuSer---SerArgCyAsnIleIleAlaAspPheGlyLeuSerAsn 166
      574 GTGCTCAAGACACAGCTTACACAGCACTTGAAT---GGACCCGAGTATCACTCTCCA 630
      167 ValMetArgAspGlyHisPheLeuLeuThrSerCysGlySerProAsnTyrAlaAlaPro 186
      631 GAGTGAATTCGCTACCACTCTCCACAGGAGGTGGAGCTGTCTGTCTCTGGATC 650
      187 GluValIleSerGlyLeuLeuTyrAlaGlyProGluValAspValIlePheSerCysGlyVal 206
      691 CTGCTCATGACATGGCTCTGAGGATATATCCGTTTGACAGACAGTGAAGATC----- 744
      207 IleLeuTyrAlaLeuLeuLeuGlyGlyIleTyrThrLeuProSerHisLeuSerGlyAla 225
      745 -----ATCAAGGGCCAGAGTGTTC---TTCAAGCAACTGTCTCTTCAAGTGT 789
      226 LeuPheLeuLeuLeuGlyGlyIleTyrThrLeuProSerHisLeuSerGlyAla 245
      790 CAGCAGCTTATTAATGAGTCCCTGCTCCCTGACAGCCTGACATGGCCCTCTTGAAGA 849
      246 ArgAspLeuLeuProArgMetLeuIleValAspProValIleThrIleProGlu 265
      850 ATCCGAAACCACTCGTGAATGACAGGTC 882
      266 IleArgIleHisArgTyrPheGlnThrHisLeu 276
  
```

RESULT 15

```

S60304
serine/threonine-specific protein kinase (EC 2.7.1.-) BKIN12 (version 2) - barley
C1Date: 19-Mar-1997 #sequence_rev: 15-Aug-1997 #text_change 09-Jul-2004
C1Accession: S60304; S24579
R1Halford, N.G.; Vicente-CarboJose, J.; Sabelli, P.A.; Shewry, P.R.; Hamppel, U.; Kretz
Plant J. 2, 791-797, 1992
A1Title: Molecular analyses of a barley multigene family homologous to the yeast protein
A1Reference number: S60303; PMID:93258420; PMID:1102632
A1Accession: S60304
A1Status: preliminary
A1Molecule type: mRNA
A1Cross-references: UNIPROT:Q40030; EMBL:X65604
R1Halford, N.G.
submitted to the EMBL Data Library, April 1992
A1Reference number: S24578
A1Accession: S24579
A1Status: preliminary
A1Molecule type: mRNA
A1Residues: 1-61, 'A', 63-513 <HA2>
A1Cross-references: EMBL:X65604; NID:gi18933; PDB:CAA46554.1; PID:gi18934
C1Function:
A1Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C1Superfamily: AMP-activated protein kinase; protein kinase homology
C1Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F15-772/Domain: protein kinase homology <KIN>
F123-31/Region: protein kinase ATP-binding motif
F146,65,143,145/Active site: Lys, Glu, Asp, Lys #status predicted
F148,152/Binding site: magnesium (Asn, Asp) #status predicted
  
```

Alignment Scores:

Pred. No.:	2 46e-10	Length:	513
Score:	361.00	Matches:	94
Percent Similarity:	50.72%	Conservative:	46
Best Local Similarity:	34.06%	Mismatches:	120
Query Match:	20.64%	Indels:	16
DB:	1	Gaps:	8

US-10-705-757-5 (1-942) x S60304 (1-513)

```

QY      82 GCGAAGAGAGAGCCCTGAGTCCAGATACAGATGGAGCCGCTGTGGCAGCGGT 141
      8 GlyGlyHisSerGlyValLeuLeuValAsn---TyrAsnLeuGlyLeuThrLeuGlyLeuGly 26
  
```

```

QY      142 GCGTTCGCTCGGTCTACTCTGGACATCCGCGTCCGGAACAATTCGCGGCTTAA 201
      27 ThrPheGlyAspValValAlaGluArgAsnValThrGlyGlnArgValAlaIleLys 46
      202 CAGGTGAAGAAGACCGGATTTCCGATTTGGGAGAACTGCCAATGGACCCGAGTGGCC 261
      47 IleLeuAsnArgArgLysMetGluThrMetGluMetGluGlyLysLysLys----- 64
      262 ATGAAGATGATCTGTGAAGAAGATGATGATGATGATGATGATGATGATGATGATGAT 315
      65 -----GluIleLeuValMetArgLeuPheIleAspPheIleHisProIleIleLeu 82
      316 CTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 375
      83 ValTyrGluValIleGluThrProLysAspIlePheValValMetGluTyrCyAsnAsn 102
      376 GTGCAAGACCTTTCGATTTATACAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 435
      103 ---GlyGluLeuLeuAspTyrIleIleGluAsnGlyArgLeuGlnGluArgAlaArg 121
      436 GGAATCTTTCGAGAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 495
      122 ArgIlePheGlnGlnIleLeuAlaGlyValGluTyrCysHisArgIleMetValHis 141
      496 CCGGACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 555
      142 ArgAspLeuLysProIleAsnLeuLeuAsp---SerArgTyrAsnValLysLeuAla 160
      556 GACTTCGCTCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 612
      161 AspPheGlyLeuSerAsnValMetArgAspGlyHisPheLeuLeuThrSerCysGlySer 180
      613 CAGGTGAAGTCTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 672
      181 LeuAsnTyrAlaAlaProIleIleSerSerLysLeuTyrAlaGlyProGluValAsp 200
      673 GTCTGTCCCTTGGAGATCTCTGATGACAGTCTGCGGAGATATTCCTTTGAGCAC 732
      201 ValTyrSerCysGlyValValLeuTyrAlaLeuLeuCysGlySerValProPheAsp 220
      733 GATGAA-----GAGATCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 774
      221 AspAsnIleProSerLeuPheArgLysIleLysGlyGlyThrTyrIleLeuProSerTyr 240
      775 GTCTTTCAGAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 834
      241 LeuSerAspSerAlaArgAspLeuLeuProLysLeuLeuAsnIleAspProMetLysArg 260
      835 CCTCTCTTGAAGAAGATCCGGAACATCTGTGATGATGATGATGATGATGATGATGAT 882
      261 IleThrPheIleGluIleArgValHisProTyrPheLysValHisLeu 276
  
```

Search completed: September 22, 2005, 17:20:41
 Job time : 40.871 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: September 22, 2005, 15:59:25 ; Search time 155.516 Seconds
(without alignments)
6203.583 Million cell updates/sec

Title: US-10-705-757-5

Perfect score: 1749
Sequence: 1 atgcctctctccacagatcaaa.....caccgggaccagcaagtag 942

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+np.model -DEV=xlp
-Q=cg12.1/USPTO.spool_p/US10705757/runat.22092005.115015.22129/app.query.fasta.1.5333
-DB=uniprot -QFMT=faeatan -SUFPIX=n2p.rup -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdd -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NOR=ext -HEADING=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10705757.QCGN.1.1.980.0runat.22092005.115015.22129 -NCP=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -YGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Uniprot_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1668	95.4	313	1	PIM1_MOUSE
2	1662	95.0	313	1	O8CFN8
3	1584	90.6	313	1	PIM1_FELCA
4	1582	90.6	313	1	PIM1_RAT
5	1582	90.5	313	1	PIM1_HUMAN
6	1574	90.0	313	1	PIM1_BOVIN
7	1131	64.7	326	1	PIM3_MOUSE
8	1123.5	64.2	326	1	PIM3_MOUSE
9	1122.5	64.2	326	1	PIM3_MOUSE
10	1119	64.0	326	1	PIM3_HUMAN
11	1113	63.6	325	1	PIM3_HUMAN
12	1110	63.5	325	2	O811X8
13	1087	49.3	311	2	O8R2P0
14	861.5	49.3	311	2	O8R2P0
15	861.5	49.3	370	1	PIM2_MOUSE
16	856	48.9	311	1	PIM2_HUMAN

17	849	48.5	310	2	Q7ZVU5	Q7ZVU5 brachydanio
18	846	48.4	310	2	O8JFW9	O8JFW9 brachydanio
19	841	48.1	310	1	PIM1_BRARE	O9yfs5 brachydanio
20	839	48.0	310	2	O6DI52	O6DI52 brachydanio
21	697.5	39.9	221	2	O8R1Z0	O8R1Z0 mus musculus
22	628	35.9	441	2	O20443	O20443 caenorhabdit
23	504	28.8	378	2	O8T3F1	O8T3F1 caenorhabdit
24	504	28.8	566	2	O17737	O17737 caenorhabdit
25	415.5	23.8	134	2	O6P2J9	O6P2J9 homo sapien
26	399	22.8	133	1	PASK_MOUSE	O8ce6e mus musculus
27	394	22.5	125	2	O6Q2K5	O6Q2K5 canis famli
28	388	22.2	658	2	O641K5	O641K5 mus musculus
29	385	22.0	1206	2	O6FUT1	O6fui1 candida gla
30	382.5	21.9	432	2	O7OXR8	O7oxr8 giardia lam
31	379	21.7	504	2	P931I3	P931I3 cucumis sat
32	379	21.7	1101	1	KOE5_YEAST	O08217 saccharomyc
33	379	21.7	1336	2	O6FRS7	O6frs7 candida gla
34	378.5	21.6	661	1	ARK5_HUMAN	O60285 homo sapien
35	378.5	21.6	779	1	SNIL_MOUSE	O60670 mus musculus
36	378	21.6	1107	2	O6CJ10	O6c3j0 yarrowia li
37	377.5	21.6	776	1	SNIL_RAT	O9TJUS rattus norv
38	375.5	21.5	643	2	O7R0B9	O7r0b9 giardia lam
39	374.5	21.4	292	2	O7QDP1	O7qdp1 anopheles g
40	374.5	21.4	518	2	O7PR39	O7pr39 anopheles g
41	374.5	21.4	1229	2	O6CKW4	O6ckw4 kluyveromyc
42	373	21.3	535	1	KI10_ARATH	O38997 arabidopsis
43	373	21.3	794	1	KI11_HUMAN	O8cd3c homo sapien
44	373	21.3	1398	2	O77268	O77268 drosophila
45	373	21.3	1398	2	O9W532	O9w532 drosophila

ALIGNMENTS

RESULT 1
ID PIM1_MOUSE STANDARD; PRT; 313 AA.
AC P06803;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Proto-oncogene serine/threonine-protein kinase Pim-1 (BC 2.7.1.37).
GN Name=Pim1; Synonyms=Pim-1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBT:Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86272109; PubMed=3015420; DOI=10.1016/0092-8674(86)90886-X;
RA Sellen G., Cuypers H.T., Boelens W., Robanus-Maandag E., Verbeek J.,
RA Domen J., van Bevern C., Berns A.;
RT "The primary structure of the putative oncogene pim-1 shows extensive
RT homology with protein kinases.";
RL Cell 46:603-611(1986).
RV [2]
RW INTERACTION WITH RP9.
RX MEDLINE=20389540; PubMed=10931201;
RA Maita H., Harada Y., Nagakubo D., Kitaara H., Ikeda M., Tamai K.,
RA Takahashi K., Ariga H., Iguchi-Ariga S.M.M.;
RT "PAP-1, a novel target protein of phosphorylation by Pim-1 kinase.";
RL Eur. J. Biochem. 267:516-5178(2000).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBUNIT: Binds to RP9.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC -1- PTM: Autophosphorylated (By similarity).
CC -1- DISEASE: Frequently activated by provirus insertion in murine
CC leukemia virus-induced T-cell lymphomas.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC subfamily.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strauberg R.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; BC042885; AAH42885.1; -
 DR EMBL; BC053019; AAH53019.1; -
 DR EMBL; BC055316; AAH55316.1; -
 DR MGD; MG1:97584; Pim1.
 DR GO; GO:000524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR007219; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR008271; Ser_thr_pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 313 AA; 35451 MW; 1294P16A03B7CTD7 CRC64;

Alignment Scores:

Pred. No.:	6,066-111	Length:	313
Score:	1662.00	Matches:	312
Percent Similarity:	99.68%	Conservative:	0
Best Local Similarity:	99.68%	Mismatches:	1
Query Match:	95.03%	Indels:	0
DB:	2	Gaps:	0

US-10-705-757-5 (1-942) x Q8CFN8 (1-313)

QY	1	ATGCTCTGTCGAAGTCAACTCCCTGCGCCACCGCCCTGTCACACGACTG	60
DB	1	MetLeuLeuSerIysIleAsnSerLeuAlaHisLeuAlaArgAlaProCysAsnAspLeu	20
QY	61	CACGCCACCAAGCTGGCGCGCGCAAGAGAGAGAGCGCTGGAGTGCAGTACGAGTG	120
DB	21	HisAlaThrIleLeuAlaProGlyIyGluIyGluProLeuIleuSerGlnIyVal	40
QY	121	GCGCCGCTGTTGGGACGCGGCTTCGCTCGCTACTCTGCAATCCGCTGCGGAC	180
DB	41	GlyProLeuLeuIySerGlyIyPheGlyIySerValIySerGlyIleArgValAlaAsp	60
QY	181	AACCTTCGCGTGGCCATTAGACACGTCGAGAGACCGGATTTCCGATTGGGAGAACTG	240
DB	61	AsnLeuProValAlaIleIySerHisValGluIyAspArgIleSerAspTrpGlyGluLeu	80
QY	241	CCCAATGGGACCCGAGTGGCCATGAGAGTGTCTGTGTAAGAGAGGAGCTGCACTTC	300
DB	81	ProAsnGlyThrArgValAlaProMetGluValValLeuLeuIySerValSerSerAspPhe	100
QY	301	TGCGGCGCTATTAGACTTTCGACTGCTGAGAGGCGCGATGTTTCGTGCTGATCTTG	360
DB	101	SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleLeu	120
QY	361	GAGAGGCCCGAACCCTGTCAGACCTCTTGAATTCACCGAAGAGAGCCCTACAG	420
DB	121	GluArgProGluProValAlaGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln	140
QY	421	GAGGACCTGGCGGAGGATCTTCTGGCGAGTCTGGAAGCGCTGGGCGACTGGCAAC	480
DB	141	GluAspLeuAlaArgGlyPhePheTrpGlnValValLeuGluAlaValAlaArgHisCysHisAsn	160
QY	481	TGCGGCGTCTCCACCGCGACATCAAGAGAGAGAAATCTTAAATCGACTGACCGCGCG	540
DB	161	CysGlyValLeuLeuHisArgAspIleIySerAspGluAsnIleLeuIleAspLeuSerArgGly	180

QY	541	GAATCAAACTCATCGACTTCGGGATCGGGGCGCTGCTCAAGAGACAGTCTACACGAC	600
DB	181	GluIleIyLeuLeuIleAspPheGlySerGlyAlaLeuLeuIyAspThrValIyThrAsp	200
QY	601	TTTGATGGAGCCCGAGTGTACAGTCTCCAGAGTGGATTGCTTACATGCTACACGCG	660
DB	201	PheAspGlyThrArgValIySerSerProGluTrpIleArgIyThrAspArgIyHisGly	220
QY	661	AGGTGGGACCTGTCTGTCGTCCTTGGGATCCGCTCTTAAGACATGGCTGGCGAGTATT	720
DB	221	ArgSerAlaIaValIyPheSerLeuGlyIleLeuLeuIyTrpAspValIyGlyAspIle	240
QY	721	CCGTTGACACGATGATGAAGATCATCAAGGCGCAAGTGTCTTTCAGGAACTGTCTC	780
DB	241	ProPheGluHisAspGluGluIleIySerGlyGlnValPhePheArgGlnThrValSer	260
QY	781	TCAGAGTTCAGACCTTAAATGAGCTGTCTCCCTGAGACCGTCAAGTGGCGCTTC	840
DB	261	SerGluCysGlnHisIleLeuIySerIyTrpCysLeuSerLeuArgProSerAspArgProSer	280
QY	841	TTTGAGAAATCCGGAACCATCGTGTGATGACGAGTGAACCTCTCGCCACGAGACTTCT	900
DB	281	PheGluGluIleArgAsnHisProTrpMetGlnGlyAspLeuLeuProGlnAlaIaSer	300
QY	901	GAGATCATCTGCAAGTGTGTACCGGATCCAGCAG	939
DB	301	GluIleHisLeuHisSerLeuSerProGlySerSerIyS	313

RESULT 3

PIM1_FELCA	STANDARD;	PRT;	313 AA.
ID_PIM1_FELCA			

AC	095LTD;
DT	28-FEB-2003 (Rel. 41, Last sequence update)
DT	28-FEB-2003 (Rel. 44, Last annotation update)

05-JUL-2004 (Rel. 44, Last annotation update)

DE Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).

GN Name=PIM1;

OS Felis silvestris catus (cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

OX NCBI_TaxID=9685;

RN [1]

RP SOURCE FROM N.A.

RA Fujino Y., Satoh H., Hiasane M., Masuda K., Ohno K., Tsujimoto H.;

RT "The cDNA sequence of the feline pim-1 oncogene.";

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

CC -1- SUBUNIT: Binds to Rps (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).

CC -1- PTM: Autophosphorylated (By similarity).

CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM subfamily.

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CC EMBL; AB073748; BAB71752.1; -

CC InterPro; IPR011009; Kinase like.

CC InterPro; IPR000719; Prot_kinase.

CC InterPro; IPR008271; Ser_thr_pkin_AS.

CC Pfam; PF00069; Pkinase; 1.

CC ProDom; PD000001; Prot_kinase; 1.

CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

CC PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

CC ATP-binding; Nuclear protein; Phosphorylation; Proto-oncogene;

CC Serine/threonine-protein kinase; Transferase.

KW DOMAIN 38 290 Protein kinase.

FT NP BIND 44 52 ATP (By similarity).
 FT BINDING 67 67 ATP (By similarity).
 FT ACT SITE 167 167 Proton acceptor (By similarity).
 SQ SEQUENCE 313 AA; 35685 MW; C0B8268D638E867 CRC64;

Alignment Scores:

Pred. No.: 2,43e-105 Length: 313
 Score: 1584.00 Matches: 295
 Percent Similarity: 96.81% Conservative: 8
 Best Local Similarity: 94.25% Mismatches: 10
 Query Match: 90.57% Indels: 0
 DB: 1 Gaps: 0

US-10-705-757-5 (1-942) x PIM1_PELCA (1-313)

QY 1 ATGCTCTGTCGAAGTCAACTCCCTGGCCCACTGGCGCCGCCCTTCGAACGACCTG 60
 DB 1 MetLeuLeuSerIyrlleAsnSerLeuAlaH1sLeuAlaGlyThrAlaProCysAsnApeLeu 20
 QY 61 CACGCCACCAAGCTGGCGCGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
 DB 21 HisAlaThrIyrlleuAlaProGlyIyrlleuGlyGlyProLeuGlnSerGlnIyrlleuAla 40
 QY 121 GGGCCGCTGTGGGAGCGGCTTCGCGCTGCTTACTTGGCATCCGCTGCGGAC 180
 DB 41 GlyProLeuGlnIyrlleuGlyIyrlleuGlyIyrlleuGlyIyrlleuGlyIyrlleu 60
 QY 181 AACTTCCCGGCTGGCCATTAAGCAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 DB 61 AsnLeuProValAlaIleuYshIsvaGlnIyAspAArgIleSerApeIyrlleuGlnIyrlleu 80
 QY 241 CCCAATGGACCGGAGTGGCCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 DB 81 ProAsnGlyIyrlleuAlaProMetGlyValIleuLeuIyrlleuYshIsvaIleuSerGlyPhe 100
 QY 301 TCGGGCGCTATTAGACTTCTGAGCTGTGGAGAGCGCCGATAGTTTCTGCTGATCTG 360
 DB 101 SerGlyValIleuAlaIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleu 120
 QY 361 GAGAGCGCCGAGACCGGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 DB 121 GluAlaIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleu 140
 QY 421 GAGAGCGTGGCGGAGAGATCTTCTGGCAGAGCTGTGGAGCGCGGAGCTTSCCAAC 480
 DB 141 GluGlnIleuAlaIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleu 160
 QY 481 TGGGGGTTTCCAGCCGAGCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 DB 161 CysGlyValIleuAlaIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleu 180
 QY 541 GAAATCAAACTCATTCGACTTCGGGGTGGGGGCGCTGCTCAAGAGAGAGAGAGAGAGAG 600
 DB 181 GluLeuIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleu 200
 QY 601 TTTGATGGAGCCGAGGTGACAGTCTCCAGAGTGTGCTGACATCCGCTACCAAGCG 660
 DB 201 PheAspGlyIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleu 220
 QY 661 AGGTGGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 DB 221 ArgSerAlaIaValIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleu 240
 QY 721 CCGTTTGAAGACATGAAGAGATCAAGAGCGCAAGTGTCTTCCAGGCAACGTCTCT 780
 DB 241 ProPheGlnIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleu 260
 QY 781 TCAGAGTGCAGACCTTATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
 DB 261 SerGlnIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleu 280
 QY 841 TTGGAAGAAATCCGGAACATCCGCTGATCCAGGAGTCACTCTGCGCCAGGAGCTTCT 900
 DB 841 TTTGGAAGAAATCCGGAACATCCGCTGATCCAGGAGTCACTCTGCGCCAGGAGCTTCT 900

DB 281 PheGlnIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleu 300
 QY 901 GAGATCCATTCGACAGCTGTGTCACCGGAGATTCAGAGAG 939
 DB 301 GluIleuAlaIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleuAlaIyrlleu 313

RESULT 4

ID PIM1_RAT STANDARD; PRT; 313 AA.
 AC P26754;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Proto-oncogene serine/threonine-protein kinase Pim-1 (EC 2.7.1.37).
 GN Name=Pim1; Synonyms=Pim-1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Testis;
 RX MEDLINE=92319652; PubMed=1620615;
 RA Winget D.; Reeves R.; Magnuson N.S.;
 RT Characterization of the testes-specific pim-1 transcript in rat.
 RL Nucleic Acids Res. 20:3183-3189(1992).
 CC -1-CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1-SUBUNIT: Binds to Rb9 (By similarity).
 CC -1-SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
 CC -1-PTM: Autophosphorylated (By similarity).
 CC -1-SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM subfamily.

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CC EMBL; X63675; CAA45214.1; -.
 DR PIR; S26298; S26298.
 DR RGD; 3330; Pim1.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR008271; Ser_Thr_pkin_AS.
 DR Pfam; PF00069; PKinase; 1.
 DR ProDom; PD000001; Prot Kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Nuclear protein; Phosphorylation; Proto-oncogene; Serine/threonine-protein kinase; Transferase.
 FT DOMAIN 38 52 Protein kinase.
 FT NP BIND 44 52 ATP (By similarity).
 FT BINDING 67 67 ATP (By similarity).
 FT ACT SITE 167 167 Proton acceptor (By similarity).
 SQ SEQUENCE 313 AA; 35630 MW; D5757DA9F1821BF9 CRC64;

Alignment Scores:

Pred. No.: 2,43e-105 Length: 313
 Score: 1584.00 Matches: 295
 Percent Similarity: 96.81% Conservative: 8
 Best Local Similarity: 94.25% Mismatches: 10
 Query Match: 90.57% Indels: 0
 DB: 1 Gaps: 0

US-10-705-757-5 (1-942) x PIM1_RAT (1-313)

QY 1 ATGCTCTGTCGAAGTCAACTCCCTGGCCCACTGGCGCCGCCCTTCGAACGACCTG 60
 DB 1 MetLeuLeuSerIyrlleAsnSerLeuAlaH1sLeuAlaGlyThrAlaProCysAsnApeLeu 20

QY	61	CACGCCACCAAGCTGGCCGCCGGCCAAAGAAAGAGAGCCCTGGAGTGCAGTTC	120
Db	21	HSBALAENLylsLEuNAlProGylYbGluYbGluProLeuGluSerGluNTrYbGlnVal	40
QY	121	GGCCCGCTGTGGGCAAGCGGTGGCTTCGCTCGCTCTACTCTGGCATCCGCTGCCGAC	180
Db	41	GlyProLeuLeuGlySerGlyGlyPheGlySerValTySerGlyIleArgValAlaAsp	60
QY	181	AACCTGGCCGCTGGCCATTAAAGCATGTGGAGAAAGACCCGATTTCCATTGGCGAACTG	240
Db	61	AAuLeuProValAlaIleuYbHbValGluTyAspArgIleSerAspTrpGlyGluLeu	80
QY	241	CCCAATAGCACCAGTCGCCCATGAAGATGGTCTCTGTGAAGAAAGGAGACTGGACTTC	300
Db	81	ProAluNglYThrArgValIProMetGluValIleuLeuYbAluYbValSerSerGlyPhe	100
QY	301	TCGGCGCTGATTAGACTTGTGAGCTGGATTCGAGAGGCCCGATAGTTTCGTGATCTTG	360
Db	101	SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleuIleu	120
QY	361	GAGAGGCCCGGAACCCGCTGCAAGACTCTTCGACTTTATCACCGAAGAGAGCCCTACAG	420
Db	121	GluAArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaGln	140
QY	421	GAGGACCTGGCCCGGAGGATTTCTCTGGCAAGGTCTGTGAGAGCCGTGGCGGCACTG	480
Db	141	GluGluLeuAlaArgSerPhePheTrpGlnValIleuGluAlaValArgHbSCYbHbAsn	160
QY	481	TGCGGAGTCTTCACCCGCAATCAAGAGCAGAACATCTTAAATGCACTGAGCCGCGC	540
Db	161	CysGlyValIleuNhlArgAspIleuYbAspGluAsnIleuNhlLeuNhlAspLeuAsnArgGly	180
QY	541	GAATTCAACTGATGCACTTCGGGTGGGGGCGCTGCTCAAGACACAGTCTACAGGAC	600
Db	181	GluLeuYbLeuNhlLeAspPheGlySerGlyAlaLeuLeuYbAspThrValTyTrnAsp	200
QY	601	TTTGAATGGAGCCGAGTGTACAGTCTCCAGAGTGGATTGCTACCATCGCTCCACAGC	660
Db	201	PheAspGlyThrArgValTySerProProGluTrpIleArgTyHbArgTyTrnArgly	220
QY	661	AGGTGGCAGCTGTCTGGTCCCTTGGGAATCTGCTCTATGACATGGTCTGGGAGATATT	720
Db	221	ArgSerAlaAlaValTrpSerLeuGlyIleLeuLeuTyAspMetValCysGlyAspIle	240
QY	721	CCGTTTGAAGCAGATGAAGATCATCAAGGCGCAAGTGTCTTCAGGCAACTGTCTT	780
Db	241	ProPheGluHbAspGluGluIleValIYbGlyGlnValTyPheArgGlnAspValSer	260
QY	781	TCAGAGTGCAGACCTTATTAATTAATGATGTCCTGCCAGACCGACAGATGGCCCTCC	840
Db	261	SerGluCybGlnHbLeuNhlArgTrpCybLeuSerLeuArgProSerAspArgProSer	280
QY	841	TTTGAAGAAATCCGGAACCATCCGTGGATGACAGAGGTGACTCTCTGCCCAAGCAGCTTCT	900
Db	281	PheGluGluIleGluHbAsnHbIProTrpMetGlnAspValIleuLeuProGlnAlaTrnAla	300
QY	901	GAGATCCATCTGCACAGTCTGTCAACCGGATCCAGCAAG	939
Db	301	GluIleHbLeuHbIleSerLeuSerProSerProSerLys	313

OK NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90382681; PubMed=2205533; DOI=10.1016/0378-1119(90)90195-W;
RA Reeves R., Spies G.A., Klefer M., Barr P.J., Power M.;
RT "Primary structure of the putative human oncogene, p1m-1.";
RL Gene 90:303-307(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87277423; PubMed=3475233; DOI=10.1016/0378-1119(87)90352-0;
RA Zakut-Houri R., Hazum S., Givol D., Telemann A.;
RT "The cDNA sequence and gene analysis of the human p1m oncogene.";
RL Gene 54:105-111(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88217305; PubMed=3329709;
RA Domen J., von Lindern M., Hermans A., Breuer M., Grosveld G.,
BA Bens A.;
RT "Comparison of the human and mouse p1m-1 cDNAs: nucleotide sequence
and immunological identification of the in vitro synthesized p1m-1
protein.";
RL Oncogene Res. 1:103-112(1987).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=88115604; PubMed=3429499;
RA Wecker T.C., Nagarajan L., Ar-Rushdi A., Croce C.M.;
RT "Cloning and characterization of the human p1m-1 gene: a putative
oncogene related to the protein kinases.";
RL J. Cell. Biochem. 35:105-112(1987).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen G.M., Schuler G.D.,
RA Altschul S.F., Collins B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Datcenco L., Marzula B., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueffel T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.E., Lonnellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McEwan K.J., Malek J.A., Gharatne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heltón E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE OF 1-202 FROM N.A.
RX MEDLINE=21354098; PubMed=11460166; DOI=10.1038/35085588;
RA Paquautucci L., Neumeister P., Goossens T., Nanjangud G.,
RA Chaganti R.S.K., Kuppert R., Dalla-Favera R.;
RT "Hypermutation of multiple proto-oncogenes in B-cell diffuse large-
cell lymphomas.";
RL Nature 412:341-346(2001).
RN [7]
RP CHARACTERIZATION.
RX MEDLINE=88246418; PubMed=2837645;
RA Telemann A., Amson R., Zakut-Houri R., Givol D.;
RT "Identification of the human p1m-1 gene product as a 33-kilodalton
cytoplasmic protein with tyrosine kinase activity.";
RL Mol. Cell. Biol. 8:1498-1503(1988).
RN [8]
RP FUNCTION.
RX MEDLINE=20130009; PubMed=10664448; DOI=10.1016/S0014-5793(00)01105-4;
RA Koike N., Maita H., Taira T., Ariga H., Iguchi-Ariga S.M.M.;
RT "Identification of heterotritomatin protein 1 (HP1) as a

RT phosphorylation target by Pim-1 kinase and the effect of
RT phosphorylation on the transcriptional repression function of
RT HPI(1) "":
RL FEBS Lett. 467:17-21(2000).
RN (9)
RP SUBCELLULAR LOCATION.
RX MEDLINE=22567470; PubMed=12680209;
RA Ionov Y., Le X., Tunquist B.J., Sweetenham J., Sachs T., Ryder J.,
RA Johnson T., Lilly M.B., Kraft A.S.:
RT "Pim-1 protein kinase is nuclear in Burkitt's lymphoma: nuclear
RT localization is necessary for its biologic effects.";
RL Cancer Res. 23:167-178(2003).
CC -1- FUNCTION: Thought to play a role in signal transduction in blood
CC cells. May affect the structure or silencing of chromatin by
CC phosphorylating HPI gamma/CBX3.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBUNIT: Binds to R99 (by similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
CC -1- TISSUE SPECIFICITY: Expressed primarily in cells of the
CC hematopoietic and germ line lineages.
CC -1- PTM: Autophosphorylated on tyrosine residues.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC subfamily.
CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/PIM1ID261.html".
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL, M27903; AAA6090.1; -;
CC EMBL, M16750; AAA6089.1; -;
CC EMBL, M54915; AAA6447.1; -;
CC EMBL, M24779; AAA8155.1; -;
CC EMBL, BC020224; AAH20224.1; -;
CC EMBL, AF386792; AAK70871.1; -;
CC FIR, JU0327; TVHUP1.
CC DR GeneW; HGNC:8986; PIM1.
CC DR H-InvDB; HIX005835; -;
CC DR MIM; 164960; -;
CC DR GO; GO:0005737; Cytoplasm; TAS.
CC DR GO; GO:000674; P:protein serine/threonine kinase activity; TAS.
CC DR GO; GO:0007275; P:development; TAS.
CC DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
CC DR InterPro; IPR011009; Kinase, like.
CC DR InterPro; IPR000719; Prot kinase.
CC DR InterPro; IPR008271; Ser_Thr_kin_AS.
CC DR Pfam; PF00069; Pkinase; I.
CC DR ProDom; PD000001; Prot_kinase; 1.
CC DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC DR PROSITE; PS50108; PROTEIN_KINASE_ST; 1.
CC DR ATP-binding; Nuclear protein; Phosphorylation; Proto-oncogene;
CC Serine/threonine-protein kinase; Transferase.
CC FT DOMAIN 38 290 Protein kinase.
CC FT NP_BIND 44 52 ATP (By similarity).
CC FT BINDING 67 67 ATP (By similarity).
CC FT ACT_SITE 167 167 Proton acceptor (By similarity).
CC FT CONFLICT 15 16 AP -> RA (in Ref. 2).
CC SEQUENCE 313 AA; 35685 MW; 35BA76D3668E5A3 CRC64;

Alignment Scores:

Pred. No.: 3,39e-105 Length: 313
Score: 1582,00 Matches: 294
Percent Similarity: 97,12% Conservative: 10
Best Local Similarity: 93,93% Mismatches: 9
Query Match: 90,45% Indels: 0
DB: 1 Gaps: 0

US-10-705-757-5 (1-942) x PIM1_HUMAN (1-313)
QY 1 ATGCTCCGTCCAAATCAATCCCTGGCCCACTGGAGCCGCCCTGCAAGACCTG 60
Db 1 MetLeuLeuSerLySylLeuSerLeuAlaHlSLeuAAlaAlaProCySAmNpLeu 20
QY 61 CACGCCCAACCAAGCTGCGCCCGGCAAGAGAGAGAGCCCTGAGTCCGACAGCTG 120
Db 21 HlSAlaThrLySLeuAlaProGlyLySgluLySgluProLeuGluSerClnTyrglnVal 40
QY 121 GCGCCGCTGTTGGGACGGGTGGCTTGGCTGGCTACTCTGCGATCCGCGTCCGAC 180
Db 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTySerglyLyLeaLyValSerAap 60
QY 181 AACTGCGCGTGGCCATTAGACAGTGGAGAGAGAGCCGATTCGATTGGGAGAGACTG 240
Db 61 AmlLeuProValAlaHlLeuAhlSValGlyLySLeuAAlaAlaSerAapTrpLyGluLeu 80
QY 241 CCCAATGGACCCCGAGTCCCAATGGAGTGTCTGTGAGAGAGTGAAGTCCGACCTTC 300
Db 81 ProAmlGlyThrArgValProMetGlyValValLeuLeuLySValSerGlyPhe 100
QY 301 TCGGCGCTCATTAAGACTTCTGACCTGCTTCCAGAGAGCCCGATGTTTGGCTGATCTCG 360
Db 101 SerGlyValHlLeaLyLeuAapTrpPheGlyAaProAapSerPheValLeuLeu 120
QY 361 GAGAGCCCGAAGCCGATGAGAGACTCTTCACTTATCAACCGAAGAGAGCCCTACAG 420
Db 121 GluAaProGlyProValGlnAapLeuAapPheAapPheHlLeuGlnGlyAlaLeuGln 140
QY 421 GAGACCTGGCCCGAGATTTCTTGGACGCTGAGAGCCGTCGCGATTCGACAAAC 480
Db 141 GluGlyLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgHlCySAlaAen 160
QY 481 TCGCGGCTTCTCCACCGGACATCAAGACAGAGAACTTTAATGACCTGAGCCGCGGC 540
Db 161 CySglYValLeuHlAArgAapHlLeuAapArgGlyAmlHlLeuHlAapLeuAapArgGly 180
QY 541 GAATCAATCATGATGATCGGCTGGGCGGCGCTGCTCAAGACAGATCTACAGGAC 600
Db 181 GluLeuLySLeuHlAapPheHlSerGlyAlaLeuLySLeuAapThrValTyThrAap 200
QY 601 TTTGATGGAGCCCGAGTGAAGTCACTCTCCAGAGTGAATTCGTACATGCTACACAGCG 660
Db 201 PheAapGlyThrArgValTySerProProGlyTrpHlArgTyHlAaGlyHlSgl 220
QY 661 AGTTCGAGAGCTGTCTGCTCTTGGATCTGCTCTATGACATGCTTGGCGAGATATT 720
Db 221 ArgSerAlaAlaValTrpSerLeuGlyLyLeuLeuTyZAspMetValCySglYAspPle 240
QY 721 CGCTTGAAGACAGTGAAGATCATCAAGAGGCGCAAGTGTCTTCAAGGAACTGTCTCT 780
Db 241 ProPheGlyHlAapPheGlyGlnHlLeaGlyGlnValPhePheArgGlnArgValSer 260
QY 781 TCGAGTGTCAAGACCTTATTAATAGTGCCTGTGCTCCCTGAGACCGTCAATGCGCCCTGC 840
Db 261 SerGlyCySglnHlLeuHlLeuGlyTrpCySLeuAlaLeuAaArgProSerAapArgProThr 280
QY 841 TTTGAAGAAATCCGAAACCATCCGTGATGACAGGCTGACCTCTGCGCCAGGACCTTCT 900
Db 281 PheGlyGlyHlLeuGlnAapHlSerProTrpMetGlnAapValLeuLeuProGlnGlnThrAla 300
QY 901 GAGATCCATCTGACAGTCTGTACCGGAGATCCAGCAAG 939
Db 301 GluHlLeuAhlSerLeuSerLeuSerProGlyProSerLyS 313

RESULT 6
PIM1_BOVIN
ID PIM1_BOVIN STANDARD; PRT; 313 AA.
AC GAGNDF;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
 GN Name=PIM1;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 NCBI_TaxID=9913;
 RX MEDLINE=21190909; PubMed=11182156; DOI=10.1016/S0165-2427(00)00259-2;
 RA Wang Z., Petersen K., Weaver M.S., Magnuson N.S.;
 RT "CDNA cloning, sequencing and characterization of bovine pim-1";
 RL Vet. Immunol. Immunopathol. 78:177-195(2001).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SUBUNIT: Binds to Rp9 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
 CC -1- PTM: Autophosphorylated (By similarity).
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM subfamily.
 CC -----
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 CC or send an email to license@isb-eb.ch).
 CC -----
 CC EMBL; AF259078; AAF67200.1; -.
 CC DR HSP; O63450; 1A06.
 CC DR InterPro; IPR011009; Kinase like.
 CC DR InterPro; IPR000719; Prot. kinase.
 CC DR InterPro; IPR008271; Ser_Thr_kin_AS.
 CC DR Pfam; PF00069; Kinase; 1.
 CC DR ProDom; PD000001; Prot. kinase; 1.
 CC DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 CC DR PROSITE; PS0011; PROTEIN KINASE DOM; 1.
 CC DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 CC KM ATP-binding; Nuclear protein; Phosphorylation; Proto-oncogene;
 CC Serine/threonine-protein kinase; Transferase.
 CC FT DOMAIN 38 290
 CC FT NP BIND 44 52
 CC FT BINDING 67 67
 CC FT ACT SITE 167 167
 CC FT ACT SITE 167 167
 CC SQ SEQUENCE 313 AA; 35629 MW; 9EF40229A847AD47 CRC64;
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 CC Alignment Scores:
 CC Pred. No.: 1,27e-104 Length: 313
 CC Score: 1574.00 Matches: 292
 CC Percent Similarity: 97.12% Conservative: 12
 CC Best Local Similarity: 93.29% Mismatches: 9
 CC Query Match: 89.99% Indels: 0
 CC DB: 1 Gaps: 0
 CC -----
 CC US-10-705-757-5 (1-942) x PIM1_BOVIN (1-313)
 CC -----
 CC QY 1 ATGCTCTGTGCAAGATCAATCCCTGCGCCGCGCCGCTTGCAGCACTG 60
 CC DB 1 MetLeuLeuSerIysIleAsnSerLeuAlaHleuAlaIleAlaProCySerAspLeu 20
 CC QY 61 CAGGCCAAGAGTGGCGCGCGCAAGAGAGAGCCCTTGAGTGGCACTGACAGG 120
 CC DB 21 HleAlaThrIleuAlaProGlyIleGlyIleGlyIleProLeuIleuSerGlyIleVal 40
 CC QY 121 GGGCCCTGTGGGAGCGGCTTGGCTCGCTGCTACTCTGAGCATCCGCTGCGGAC 180
 CC DB 41 GlyProLeuLeuIleuSerGlyIleGlyIleSerValIleSerIleAlaGlyAlaAsp 60
 CC QY 181 AACTTGGCGGTGCACATTAAGACGTGAGAGAGAGACCGATTTCCGATTGGGAGAACT 240
 CC DB 61 AsnLeuProValAlaIleIleValIleValIleValAspArgIleSerAspTrpGlyIle 80
 CC QY 241 CCAGATGGACCCGAGTGGCCATGAGAGTGGTCTCTGTGAAGAGGTGAGCTGAGCTTC 300

DB 81 ProAsnGlyThrArgValProMetGluValIleuLeuIleuValSerSerGlyPhe 100
 QY 301 TCGGGGCTCATTTGACTCTTGGACTGTTGAGAGCCGCAATGTTTCGTGCTGCTG 360
 DB 101 SerGlyValIleArgIleuLeuAspTrpPheGluArgProAspSerPheValIleu 120
 QY 361 GAGAGGCCGCAACCGGTGCAAGACCTCTTGCATTTATCAAGAGAGAGCCCTACAG 420
 DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
 QY 421 GAGACCTGCGCCGAGAGATTTCTTCTGCAAGTCTGAGAGCCGCTGCGGCAATTGCCAAC 480
 DB 141 GluIleuAlaIleArgSerPhePheTrpGlnValIleuGlnAlaValArgIleSerVal 160
 QY 481 TCGGGGCTTCCACCGCCGACATCAAGAGAGAGACATTTTCACTGACCTGACCGGCG 540
 DB 161 CyGlyValIleuIleAspArgIleIleValAspGlyIleuIleuIleAspLeuAsnArgGly 180
 QY 541 GAATCAACTCATGACTTTCGGGTGGGGCGCTGCTATGACATGCTTACAGGAC 600
 DB 181 GluLeuIleuLeuIleAspPheGlySerGlyAlaLeuLeuIleuAspThrValIleuAsp 200
 QY 601 TTGATGAGACCCGAGTGTACAGTCTCCAGAGTGGATTGCTACCATCGCTACCAAGC 660
 DB 201 PheAspGlyThrArgValIleSerProProGluTrpIleArgGlyIleValIleu 220
 QY 661 AGGTGGAGAGCTGTGCTGCTTGGATCTGCTATGACATGCTTGGAGATATT 720
 DB 221 ArgSerAlaValAlaValIlePheIleuGlyIleLeuLeuIleuValAspMetValCyGlyAsp 240
 QY 721 CCCTTGGAGACGATGAGAGATCATCAAGGCGCAAGTGTCTTTCAGCAACTGCTCT 780
 DB 241 ProPheGluIleAspGluIleValIleArgGlyIleValIlePheAspArgGlnAspVal 260
 QY 781 TCAGATGTCAAGACCTTATTAATGAGTGCCTGCTGCTGAGAGCCGACATGCGGCTCC 840
 DB 261 SerGluCyGlnIleIleuIleAspTrpCyGlnAlaIleuArgProSerAspArgProThr 280
 QY 841 TTGAGAGAAATCCGAGACCATTCGTGATGACAGTGCAGTCTGCTGCGCCAGGACTTCT 900
 DB 281 PheGluGluIleIleGlnIleuIleAspProTrpMetGlnAspValIleuLeuProGlnIleu 300
 QY 901 GAGATCCATCTGACAGTCTGCTGACCGGATCCAGAG 939
 DB 301 GluIleIleuIleSerLeuSerProGlyProSerIys 313
 CC -----
 CC RESULT 7
 CC PIM3_COTUA
 CC ID PIM3_COTUA STANDARD; PRT; 323 AA.
 CC AC G9P085;
 CC DT 28-FEB-2003 (Rel. 41, Created)
 CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
 CC DT 05-JUL-2004 (Rel. 44, Last annotation update)
 CC DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (pim).
 CC GN Name=PIM3; Synonyms=PIM-3;
 CC OS Coturnix coturnix japonica (Japanese quail).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC OC Coturnix.
 CC NCBI_TaxID=93934;
 CC RN (1)
 CC SEQUENCE FROM N.A.
 CC MEDLINE=20180111; PubMed=10713710; DOI=10.1038/sj.onc.1203355;
 CC RA Eichmann A., Yuan L., Breant C., Allitalo K., Koskinen P.J.;
 CC RT "Developmental expression of Pim kinases suggests functions also
 CC outside of the hematopoietic system";
 CC RL Oncogene 19:1215-1224(2000).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- PTM: Autophosphorylated.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM subfamily.
 CC -----

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CC or send an email to license@sb-sib.ch).

DR EMBL; AJ130845; CAB62386.1; -
DR HSSP; Q63450; 1A06
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR00719; Prot Kinase.
DR InterPro; IPR002290; Ser chr kinase.
DR InterPro; IPR008271; Ser chr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
DR PROSITE; PS00101; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_SF; 1.
KW ATP-binding; Phosphorylation; Serine/threonine-protein kinase;
KW Transferase.
FT DOMAIN 40 291 Protein kinase.
FT NP_BIND 46 54 ATP (By similarity).
FT BINDING 69 69 ATP (By similarity).
FT ACT_SITE 168 168 Proton acceptor (By similarity).
SQ SEQUENCE 323 AA; 36597 MW; E2A4FA20B6F6396C CRC64;

Alignment Scores:
Pred. No.: 8.6e-73 Length: 323
Score: 1131.00 Matches: 208
Percent Similarity: 81.61% Conservative: 45
Best Local Similarity: 67.10% Mismatches: 53
Query Match: 64.67% Indels: 4
DB: 1 Gaps: 3

US-10-705-757-5 (1-942) x PIM3_COTUA (1-323)
QY 1 ATGCTCTGTCGAAAGATCACTCCCTGGCCGACCTGGCCGCGCCGCTTCAGACAGACTG 60
DB 1 MetLeuLeuSerIysPheGlySerLeuAlaHisIleCysSerProAlaSerMetAlaPhe 20
QY 61 CACGCCACCAAGCTGGCGCGG-----GGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 114
DB 21 LeuProValIleSerLeuLeuProValIleValGluValGluLeuProPheAspLysValTyr 40
QY 115 CAGGTGGGCGCGCTGTGGGACAGCGGTGGCTGGCTGGCTGACTGATCCGCGTC 174
DB 41 GlnValGlySerValIleuGlySerGlyGlyPheGlyThrValTyrIleGlySerArgThr 60
QY 175 GCGGCAAACTTGGCGGTGGCCATTAGACAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAG 234
DB 61 AlaAspGlyLeuProValAlaValIleValIleValIleValIleValIleValIleValIle 80
QY 235 GAATGCCCAATGACAGCCGAGTGGCCATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 294
DB 81 ThrIle---GlyGlyAlaMetValProLeuGluIleValLeuLeuLysValGlySer 99
QY 295 GACTTCTCGGCGCTCATTAAGCTTGTGAGCTGTGGAGAGAGAGAGAGAGAGAGAGAGAG 354
DB 100 GlyPheArgGlyValIleValIleValLeuLeuAspTrpTyrGlyLeuArgProAspGlyPheLeuIle 119
QY 355 ATCTGTGAGAGAGCGCGAG 414
DB 120 ValMetGluArgProGluLeuValIleValAspLeuPheAspPheIleThrGluLysGlyAla 139
QY 415 CTACAG 474
DB 140 LeuAspGluAspThrAlaArgGlyPhePheArgGlyValLeuGluAlaValAlaArgHisCys 159
QY 475 CACAACTGCGGGGTCTCCACCGGACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 534
DB 160 TyrGlyCysGlyValValIleHisArgAspIleValAspGluAsnLeuValIleAspLeuArg 179

QY 535 CCGCGCAAAATCAATCATGCTCGGCGCGCGCTGCTCAAGACAGACTGAC 594
DB 180 ThrGlyLeuLeuValLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyr 199
QY 595 ACGAATTTGATGGAGCCCGAGTGAAGTCTCTCAAGAGTGGATTCCTACAGAGCTGAC 654
DB 200 ThrAspPheAspGlyThrArgValTyrSerProGluTrpIleArgTyrHisArgTyr 219
QY 655 CACGCGAGTGGCGAGCTGTGCTGCTGGGATCTGCTATGACATGGTGGCGGA 714
DB 220 HisGlyArgSerAlaThrValTyrSerLeuGlyValLeuLeuTyrAspMetValCysGly 239
QY 715 GATATTCGCTTGAACAGATGACAGATGACATGACAGAGAGAGAGAGAGAGAGAGAG 774
DB 240 AspIleProPheGluGlnAspGluValLeuArgGlyValArgLeuTyrPheArgArgArg 259
QY 775 GTCTCTTCAAGATGTCAGACACTTATTAATGTCGCTGCTCCTGAGACCGTCAGATCGG 834
DB 260 IleSerProGluCysGlnGlnIleuLeuIleuLysTrpCysLeuSerLeuArgProSerAspArg 279
QY 835 CCTCTCTTGAAGAAATCCGAAACATCCGTCGAGT---CAGGAGTACCTCGTGGCCGAG 891
DB 280 ProTrpLeuGluGlnIlePheAspHisGlnTrpMetHisLysSerGluValIleLysSer 299
QY 892 GCAGCTTCAAGATCATCTGACAGACTGTG 921
DB 300 GluAspCysAspIleArgLeuArgThrLeu 309

RESULT 8
PIM3_MOUSE STANDARD, PRT, 326 AA.
ID PIM3_MOUSE
AC P58750;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
GN Name=Pim3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon, and Salivary gland;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant P.L., Scheetz T.E.,
RA Brownstein M.T., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.D., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriques S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC subfamily.

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DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding: Phosphorylation; Serine/threonine-protein kinase;
KW transferase.
FT DOMAIN 40 293 Protein kinase.
FT NP_BIND 46 54 ATP (By similarity).
FT BINDING 69 69 ATP (By similarity).
FT ACT_SITE 170 170 Proton acceptor (By similarity).
SQ SEQUENCE 326 AA; 36002 MW; DD6C9BF4635F851E CRC64;

Alignment Scores:
Pred. No.: 3,52e-72 Length: 326
Score: 1122.50 Matches: 213
Percent Similarity: 81.33% Conservative: 31
Best Local Similarity: 71.00% Mismatches: 43
Query Match: 64.18% Indels: 13
DB: 1 Gaps: 5

US-10-705-757-5 (1-942) x PIM3_RAT (1-326)

QY 1 ATGCTCTGTGCAAGATCACTCCCTGGCCACCTGCGCGCCGCTGC----- 51
DB 1 MetLeuLeuSerYspheglYserLeuAlaHisLeu-----CysglYProglY 16
QY 52 -----AACGACCTGCACCGCCACCAAGCTGGCCCGGCGA--GAGAAGAGCCCTG 102
DB 17 GlyValaHisLeuProValYstleleGlnProAlaHisAlaHisPhe 36
QY 103 GAGTCGACGATCAAGAGTGGCCGCTGTGGGAGCGGCTTGGCTGCTCTCT 162
DB 37 GluValaValYrglValGlyAlaValleuGlySerGlyYpheglYThrValY 56
QY 163 GGCATCCGCGCTCGCCGACCACTGGCGGTGGCAATGAAGAGTGTCTGTGAAG 222
DB 57 GlySerYrglIleAlaHisPheLeuProValAlaValHisValValYValY 76
QY 223 TCGGATGGGAGAACTGCGCAATGAGCCGAGTGGCCATGAAGTGTCTGTGAAG 282
DB 77 ThrGluTrpYserLeu---GlyGlyMetAlaValProleuGluValleuLeu 95
QY 283 AAGGTG-----AGCTCGACTTCTCGGGCTGATTAAGCTTGTGACTGTGAGAG 336
DB 96 LysValGlyAlaHisGlyAlaArgGlyValIleArgLeuLeuSerPheGluArg 115
QY 337 CCGGATAGTTGCGTGGATCTGAGAGGCGGAAACCGGTGAGAGCTTGAAGCTT 396
DB 116 ProHisPheLeuLeuValleuGluArgProGluProAlaGlnHisLeuPhePhe 135
QY 397 ATCAGCAGAGAGAGGCTTACAGAGAGCTGCGCCGAGATTTCTTGGCAGTCTG 456
DB 136 IleThrGluArgGlyAlaLeuHisPheGluProleuAlaArgYrPhePheAlaGlnValleu 155
QY 457 GAGGCGGTGGGCTTCCCACTGCGGGGTCTCCACCGGCATCAAGAGAGAGAAC 516
DB 156 AlaAlaValArgHisCysHisAsnCyGlyValValHisArgHisPheIleHisPheGluAsn 175
QY 517 ATCTATATGACCGAGCGCGGGAATAACTGACTTGGGTGGGGGGGCTG 576
DB 176 LeuLeuValHisPheLeuArgSerGlyGlnLeuYleuLeuHisPheGlySerGlyAlaVal 195
QY 577 CTCAGAGACACAGCTTACACGAGCTTGAAGAGCCGAGTGTACAGTCTCCAGAGTGG 636
DB 196 LeuYleuSerThrValYrThrHisPheHisPheGlyThrArgValYrSerProProGluTrp 215
QY 637 ATTCGATCAAGATGCTTACAGAGAGTGGAGAGCTGTGGTCCCTGGAGATCTGCTC 696
DB 216 IleArgYrHisArgYrHisGlyArgSerAlaThrValTrpSerLeuGlyValleuLeu 235

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QY 697 TATGACATGCTGTGGAGATATTCCTTTGAGCAGATGAAGATCATCAGAGGCCAA 756
DB 236 TyrHisMetValCysGlyAlaHisPheProPheGluGlnHisPheGluIleLeuArgGlyArg 255
QY 757 GTGTTCTTGAGCAAACTGTCTCTTCAAGAGTGCAGACCTTTATTAATGTGCTGTCC 816
DB 256 LeuPhePheArgArgArgValSerProGluCysGlnGlnIleuIleGluTrpCysLeuSer 275
QY 817 CTGAGACCGTCAGATGGCGCCCTTCTTGAAGAAATCCGGAACCATCCGTGATGAGAGT 876
DB 276 LeuArgProSerGluArgProSerLeuHisPheGlnIleAlaHisPheProTrpMetLeuGly 295

RESULT 10
PIM3_HUMAN STANDARD; PRT; 326 AA.
ID PIM3_HUMAN
AC O86V86;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
GN Name=PIM3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heselt F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedyn T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Mera M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RS IDENTIFICATION FROM ESTS.
RX MEDLINE=22682943; PubMed=12798037; DOI=10.1016/S1476-9271(02)00095-6;
RA Chichester C., Nikitin F., Raverint J.-C., Lisacek F.;
RT "Consistency checks for characterizing protein forms."
RL Comput. Biol. Chem. 27:29-35 (2003).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announce/
CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL: BC052239; AAH52239.1; ALT INT.
CC InterPro: IPR011009; Pkinase like.
CC InterPro: IPR000719; Pkinase.
CC InterPro: IPR008271; Ser_thr_kinase.
CC Pfam: PF00069; Pkinase; 1.
CC ProDom: PD000001; Prot_kinase; 1.

```


Score: 1113.00 Matches: 208
 Percent Similarity: 80.38% Conservative: 46
 Best Local Similarity: 65.82% Mismatches: 56
 Query Match: 63.64% Indels: 6
 DB: 1 Gaps: 5

US-10-705-757-5 (1-942) x PIM3_XENIA (1-323)

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QY 1 ATGCTCTCTGCAAGATCAACTCCCTGGCCCACTGGCGCGCCGCTTCAGACGACTG 60
   |||||
DB 1 MetLeuLeuSerLysPheGlySerLeuAlaHisLe---CysAsnProSerAsnMetGlu 19
   |||||
QY 61 CAC-----GCCACCAAGCTGGCGCGCGCAAA---GAGAAAGAGCCCTGAGTGCAG 111
   |||||
DB 20 HisLeuProValLysIleLeuGlnProValLysAspLysGluProPheGluVal 39
   |||||
QY 112 TACCAAGTGGCGCCGCTGTTGGCAGCGGTGGCTTCGGTCTTACTTCGACATCCG 171
   |||||
DB 40 TyrGlnValGlySerValValAlaSerGlyGlyPheGlyThrValTyrSerAspSerArg 59
   |||||
QY 172 GTGCGCGCAACTGGCGGTGGCTTAAAGCACTGAGAGAGAGACCGGATTCGATGG 231
   |||||
DB 60 IleAlaSerGlyGlnProValAlaValAlaValAlaValAlaValGlyValThrGluTyr 79
   |||||
QY 232 GAGAACTGGCCCAATGGCAGCCGAGTGCCTGAGAAAGTGGCTTCGTTGAGAGAGTGCAG 291
   |||||
DB 80 GlyThrLeu---AsnGlyValMetValProLeuGlnIleValLeuLeuLysValPro 98
   |||||
QY 292 TCGGACTTCTCGGCGCTCATTAACCTTTCGACTGTTGAGAGCCGATGTTTCGTG 351
   |||||
DB 99 ThrAlaPheArgIleValIleAsnLeuLeuAspTyrTyrGluArgProAspAlaPheLeu 118
   |||||
QY 352 CTGATCCTGGAGAGCGCCGCAACCGGTGACACTTCGACTTATTCACCGAAGAGGA 411
   |||||
DB 119 IleValMetGlnArgProGlnProValLysAspLeuPheAspTyrIleThrGluLysGly 138
   |||||
QY 412 GCCCTACAGAGGAGCACTGGCGCGAGATTCCTTGGCAGTGTGGAGCGCTGCGGCAAT 471
   |||||
DB 139 ProLeuAspGlnLysArgIleAlaGlyPhePheArgGlnValLeuGlnAlaValArgHis 158
   |||||
QY 472 TGGCAACTGGCGGGGTTCTCCACCGGACATCAAGAGAGAGAACTTATTCGACTG 531
   |||||
DB 159 CysTyrAsnGlySerGlyValIleAspArgIleLysAspIleAsnLeuLeuValAspThr 178
   |||||
QY 532 AGCGCGGCAAGTCAAACTGACATTCGCTGGGTGGCGCGGCGCTGCTCAAGAGCAAGTC 591
   |||||
DB 179 ArgAsnGlyGlnLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrVal 198
   |||||
QY 592 TACAGGACTTGTATGGGAGCCGAGTGTACAGTCTTCAGAGTGTGATTCGACTGCG 651
   |||||
DB 199 TyrThrAspPheAspGlyThrArgValTyrSerProProGlnTyrValArgTyrHisArg 218
   |||||
QY 652 TACCAAGGAGGTGGCGAGCTGTGTGCTCCCTTGGATCTGCTCTATGACATGTCTGC 711
   |||||
DB 219 TyrHisGlyArgSerAlaThrValTyrPheSerLeuGlyValLeuLeuTyrAspMetValTyr 238
   |||||
QY 712 GGAAGATTCCTCGTTGAGCAGATGAGAGATGATCAAGGCGCAAGTGTTCCTCAGGCA 771
   |||||
DB 239 GlyAspIleProPheGlnGlnAspGlnGlnIleValArgValArgValLysCysPheArgArg 258
   |||||
QY 772 ACTGTTCTTCAGAGTGTACGACCTTATTAATGTGTGCTGCTTCGCTGAGACCTGAGAT 831
   |||||
DB 259 ArgIleSerThrIleGlySerGlnGlnIleLeuIleTyrProLysLeuSerLeuAspProSerAsp 278
   |||||
QY 832 CGGCGCTCTTGAAGAAATCCGGAACCATCGGTGATG---CAGGATGACTTCGCGCC 888
   |||||
DB 279 ArgProThrLeuGlnGlnIlePheAspHisProTyrMetCysLysCysAspLeuValLys 298
   |||||
QY 889 CAGGAGGCTTCGATGCATTCGACAGTCTGTCAACCGGAGATCCAGC 936
   |||||
DB 299 SerGlnAspCysAspLeuArgLeuArgTyrIleAspAsnAspSerSer 314
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```

RESULT 12

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Q0811X8
ID 0811X8 PRELIMINARY; PRT; 325 AA.
AC 0811X8;
DT 01-JUN-2003 (TRIMBLrel. 24, Created)
DT 01-JUN-2003 (TRIMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRIMBLrel. 26, Last annotation update)
DE KIDL.
GN Name=Pim3; Synonyms=Kidl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBT:Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Yu L.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AY026239; AKK16606.1; -.
DR HSSP; Q03656; 1099.
DR MGI; MGI:1355297; Pim3.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; I.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 325 AA; 35931 MW; 77DBF8E2041B3F4 CRC64;

Alignment Scores:
Pred. No.: 2,786-71 Length: 325
Score: 1110.00 Matches: 212
Percent Similarity: 81.33% Conservative: 32
Best Local Similarity: 70.67% Mismatches: 42
Query Match: 63.64% Indels: 14
DB: 2 Gaps: 6

US-10-705-757-5 (1-942) x Q0811X8 (1-325)
QY 1 ATGCTCTCTGCAAGATCAACTCCCTGGCCCACTGGCGCGCCGCTTCAGACGACTG 51
   |||||
DB 1 MetLeuLeuSerLysPheGlySerLeuAlaHisLeu-----CysGlyProGly 16
   |||||
QY 52 -----AACGACCTGACAGCCCAACCAAGCTGGCGCGCGCAAA---GAGAAAGAGCCCGTG 102
   |||||
DB 17 GlyValAspHisLeuProValLysIleLeuGlnProAlaLysAlaAspLysGluSerPhe 36
   |||||
QY 103 GAGTGCAGTACACAGTGGCGCGGCTGTGGCAGCGGTGCTTCGCTCGGCTCACTCT 162
   |||||
DB 37 GluLysValTyrGlnValGlyValAlaValLeuGlnSerGlyGlyPheGlyThrValTyrAla 56
   |||||
QY 163 GGCATCCGGGTGGCGGCAACTTGGCGGTCATTAAGACAGTGTGAGAGAGACCGGAT 222
   |||||
DB 57 GlySerArgIleAlaAspGlyLeuProValAlaValLysHisValValLysGluTyrVal 76
   |||||
QY 222 TCCGATTGGGAGAACTGGCCCAATGGCAGCCGAGTCCCATGAGATGGTGTGGAG 282
   |||||
DB 77 ThrGluTrpGlySerLeu---GlyIleValAlaValProLeuGlnValValLeuLeuArg 95
   |||||
QY 283 AAGGTG-----AGCTCGGACTTCTCGGCGCTCATTAACCTTTCGACTGTTCGAGAG 336
   |||||
DB 96 LysValGlyAlaAlaGlyGlyValAlaArgGlyValIleArgLeuLeuAspTyrPheGluArg 115
   |||||
QY 337 CCCGATAGTTTGTGCTGATCTCGAGAGAGCCGCAACCGGTGACAGACCTTTCGACTTT 396
   |||||
DB 116 ProAspGlyPheLeuLeuValLeuGlnTyrProGlnProAlaGlnAspLeuPheAspPhe 135
   |||||

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QY 397 ATCACCGAAGAGAGCCCTACAGAGACCTGGCCCGAGATTCTTCTGCGAGGTCTG 456
    |||||
Db 136 ILeThcIuArGgIyAlaLeuAeBgIuPProLeuAlArGrpHePheAlaGlnValLeu 155
    |||||
QY 457 GAGGCGCGTGGCGCATTTGCCAACAATGCGGGGTTCTCACCGCGACATCAAGAGAGAAC 516
    |||||
Db 156 AlAlaValArGrHsCySHsAeNCGeGIyAlValAlHsArGrApRlIeYsApGrLuAsn 175
    |||||
QY 517 ATCTTAATCGACCTGAGCGCCCGCGGAATCAACTCATCTTCAGTTCGGGTGGGGCGCTG 576
    |||||
Db 176 LeuLeuValAspHeuAspYsGrGIyGlnLeuLysLeuLysLeuLysPheGlySergIyAlaVal 195
    |||||
QY 577 CTCAGAGACACAGCTCTACAGCATTTGATGGAGCCGAGGTACAGTCTCTCCAGATGG 636
    |||||
Db 196 LeuLysAspHrValIyTrHrAspPheAspGIyThrArGrValIySerpProGIuTrP 215
    |||||
QY 637 ATTGCTACCATGCTTACACAGCGAGGTGGCGAGCTGTGCTGCTTGGGATCTGCTC 696
    |||||
Db 216 ILeArGrYrHsArGrYrHsGlyArGrSergAlaThrValTrpSerpLeuGlyValLeuLeu 235
    |||||
QY 697 TATGACATGCTGTGCGGAGATATTCCTTTGAGACACATGAAGATCATCAAGGCGCA 756
    |||||
Db 236 TyAspMetValCyGgIyAspIleProPheGlnGlnAspGIuLysLeuArGrGIyArGr 255
    |||||
QY 757 GTGTTCTTACGAGAACTGTCTTTCAGAGGTGACAGCTTATTAATGTCGCTGTC 816
    |||||
Db 256 LeuPhePheArGrArGrValSerpProGlyGlnGlnLeuLysLeuLysLeuLysLeu 275
    |||||
QY 817 CTGAGACCGTACATGCGCCCTCTTTGAAGAAATCCGGAACCATCGGTGATGACAGGT 876
    |||||
Db 276 LeuArGrProSergIuArGrProSerpLeuAspLysLeu----CySHsPrtPrtMetLeuGly 294
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RESULT 13

Q66111 PRELIMINARY; PRT; 318 AA.

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AC 066111; TISSUE=Embryo;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Amphibia; Batrachia; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Reinhold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pehey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzycki M.I., Skalka U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maier M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;

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RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC081340; AA081340.1; -
DR InterPro: IPR011009; Kinase_like.
DR InterPro: IPR000719; Prot Kinase.
DR InterPro: IPR002290; Ser Thr Kinase.
DR InterPro: IPR008271; Ser Thr Kin AS.
DR InterPro: IPR001245; Tyr Kinase.
DR Pfam: PF00069; Kinase_1.
DR ProDom: PD000001; Prot_Kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TyKc; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein.
SQ
SEQUENCE 318 AA; 36547 MW; 48CCFF12797F01FDC CRR64;

Alignment Scores:
Pred. No.: 1,24e-69 Length: 318
Score: 1087.00 Matches: 198
Percent Similarity: 81.36% Conservative: 42
Best Local Similarity: 67.12% Mismatches: 47
Query Match: 62.15% Indels: 8
DB: 2 Gaps: 3

US-10-705-757-5 (1-942) x Q66111 (1-318)

QY 7 CTGTCCAGATCAACTCTGCGCCACCTGGCGCCCGCCCTTCAGACCATCGACGCC 66
    |||||
Db 1 MetSerSerValGlnValIleTyRHs-----GlnLysIleHsAsnTyRHsLeu 17
    |||||
QY 67 ACCAAGCTGCGCGCGGCAAGAG-----AAGAGCCCTGAGTGGCAGTTC 114
    |||||
Db 18 AsnSerValPheTrpLysAspAspLeuProAlaValLysGlnTrpPheGlnLysCysTyR 37
    |||||
QY 115 CAGGTGCGCGCGCGTGGAGCGGCGTGGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 174
    |||||
Db 38 GlnValGlyProValIleGlyThrGlyGlyPheGlyThrValIleSergIyAlaValGlyIle 57
    |||||
QY 175 GCGCAACATTTGCGGTGCGCATTAAGACGTGGAGAGAGACCGATTTCCGATTGGAGA 234
    |||||
Db 58 SerAspLysLeuProValAlaIleTyRHsSValSerArGrAspArGrIleGlyGlyMetLys 77
    |||||
QY 235 GAACTGCCCAATGGACCGCGAGTGGCGATGAGAGTGTCTGTTGAAGAGTGAAGCTG 294
    |||||
Db 78 HsMet---AsnGlyThrLeuValProLeuGlnIleTyRHsLeuLysLysValSerAsn 96
    |||||
QY 295 GACTTCTGCGGCGTCTTGAAGTCTGAGTGGTGGAGAGCGCGATGTTGCTGCTG 354
    |||||
Db 97 GlyCyArGrGIyValIleArGrLeuLeuAspTrpTyRGIuArProAspPheIleIle 116
    |||||
QY 355 ATCTTGAGAGAGCGCCGAAACCGGTGACAGACTCTTGAATTTATCAACGAGAGAGCC 414
    |||||
Db 117 IleMetGluArGrProLysProLysValGlnAspLeuPheAspPheIleThrGluArGrGIyAla 136
    |||||
QY 415 CTACAGAGAGACTGCGCCGAGAGATTTCTTGGCAGGTCTGAGAGCGCGTGGCGCATTTGC 474
    |||||
Db 137 LeuGlyGlnGlnLeuAlaThrAsnPhePheArGrGlnValGlnAlaValArGrHsCyS 156
    |||||
QY 475 CCAACATGCGGGGTTTCCACCGCGGACATCAAGAGAGAGAAATCTTATTCAGCCGAGAC 534
    |||||
Db 157 HsSerCyAspArValAlaHsArGrAspIleLysAspGluAsnIleLeuValAspLeuArGr 176
    |||||
QY 535 CCGCGGAATATCAACTCATGACTTGGGTGCGGGCGCTGCTCAAGAGACAGTCTAC 594
    |||||
Db 177 ThrAlaGlnLeuLysLeuLysPheGlySergIyAlaLeuLeuArGrAspAlaValTyR 196
    |||||
QY 595 ACGAATTTGATGGAGACCGGAGTGTACAGTCTTCCAGAGTGAATTCCTTACGCTAC 654
    |||||
Db 197 ThrAspPheAspGIyThrArGrValTySerProProGIuTrPILeArGrPheHsLysTyR 216
    |||||
QY 655 CACGAGAGTGGAGAGCTGTGCTGCTGCTGAGATCTGCTTATGACATGATGCTGCGGGA 714
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ID P1M2_MOUSE STANDARD; PRT; 370 AA.
AC 062070; 062071; 062072;
AT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase Pim-2 (EC 2.7.1.37).
GN Name=Pim2; Synonyms=Pim-2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95300786; PubMed=7781606;
RA van der Lugt N.M., Domen J., Verhoeven E., Linders K.,
RA van der Gulden H., Allen J., Berns A.;
RT "Proximal tagging in E-mu-myc transgenic mice lacking the Pim-1 proto-oncogene leads to compensatory activation of Pim-2.";
RL EMBL J. 14:2536-2544(1995).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative Initiation;
CC Comment=3 isoforms, 1 (shown here), 2 and 3, are produced by alternative initiation. Isoform 1 and isoform 2 initiate from CUG codons;
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.ch/announce/ or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L41495; AAA98922.1; -;
CC EMBL; L41495; AAA98923.1; -;
CC EMBL; L41495; AAA98924.1; -;
CC PIR; S55333; S55333.
CC HSP; Q63450; 1A06.
CC MGD; MG1:97587; Pim2.
CC GO; GO:0005515; P:protein binding; IPI.
CC GO; GO:0004674; P:protein serine/threonine kinase activity; IDA.
CC GO; GO:0006376; P:apoptotic mitochondrial changes; IDA.
CC GO; GO:0008637; P:apoptotic mitochondrial changes; IDA.
CC InterPro; IPR011009; Kinase like.
CC InterPro; IPR000719; Prot Kinase.
CC InterPro; IPR008271; Ser_Thr_kinase.
CC InterPro; IPR002290; Ser_Thr_kinase.
CC Pfam; PF00069; Kinase; 1.
CC ProDom; PD000001; Prot Kinase; 1.
CC SMART; SM00220; S_TKc; 1.
CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
CC PROSITE; PSS0011; PROTEIN KINASE-DM; 1.
CC PROSITE; PSS00108; PROTEIN KINASE-ST; 1.
CC Alternative initiation; ATP-binding; Phosphorylation;
CC Serine/threonine-protein kinase; Transferase.
CC CHAIN 1 370
CC Serine/threonine-protein kinase Pim-2,
CC isoform 1.
CC FT CHAIN 26 370
CC Serine/threonine-protein kinase Pim-2,
CC isoform 2.
CC FT CHAIN 60 370
CC Serine/threonine-protein kinase Pim-2,
CC isoform 3.
CC FT INIT MET 26 26
CC For isoform 2.
CC FT INIT MET 60 60
CC For isoform 3.
CC FT DOMAIN 91 345
CC Protein kinase.
CC FT NP BIND 97 105
CC ATP (By similarity).
CC FT BINDING 120 120
CC ATP (By similarity).
CC FT ACT_SITE 222 222
CC Proton acceptor (By similarity).
CC SQ SEQUENCE 370 AA; 40059 MW; 12BB70BFD04DBE8A CRC64;

Alignment Scores:

Pred. No.:	2,04e-53	Length:	370
Score:	861.50	Matches:	167
Percent Similarity:	69.33%	Conservative:	41
Beet Local Similarity:	55.67%	Mismatches:	87
Query Match:	49.26%	Indels:	5
DB:	1	Gaps:	2

US-10-705-757-5 (1-942) x P1M2_MOUSE (1-370)

QY	34	CTGCGCGCCGCCCTGCAACGACTGCACGCCAAGCTGGCGCGCAAGAG	93
DB	65	LeuGlnGlyHisIleProSerProProValThrProThrGlnProProGlyGlyAspArg	84
QY	94	GAGCCCTGAGTCGAGCAAGTACAGAGTGGCGCCGCTTTGGGACGCGTGGCTCG	153
DB	85	AlaAlaPheGlnValIleValThrValArgValGlyProLeuLeuGlyValGlyPheGlyThr	104
QY	154	GTTCTACTGTCGATCGCGCTGCGCGCAACTGGCGGCTTAAAGACGTCGAGAAG	213
DB	105	ValPheAlaGlyHisIleArgValThrAspArgValGlnValAlaIleValIleSerArg	124
QY	214	GACCGGATTTCCGATTGGGGAAGTCCCAATGGACCCGAGTCCCATGGAAGTGTG	273
DB	125	AsnArgValLeuGlyTrpSerThrValSerAspSerValThrCysProLeuGlnValAla	144
QY	274	CTGTGAAGAAGT-----AGCTCGACTTCTCGGCGTCACTTGAAGTCTG	327
DB	145	LeuLeuTrpIleValGlyGlnGlyValIleValIleValIleValIleValIleValIle	164
QY	328	TTGAGAGGCGCGCATGTTGTCGTCGATCTGTCGAGAGGCGCGCAAGTGGCAAGCTC	387
DB	165	PheGlnThrProGlnGlyPheMetLeuValIleGlnGlyPheMetProAlaGlnAspLeu	184
QY	388	TTGCAATTTATCAACGAGGAGGCTTACAGAGAACCTGGCGCGGAGATTTCTTGG	447
DB	185	PheAspTyrIleThrGlnIleValGlyProLeuGlyGlnSerCysSerArgSerPhePheThr	204
QY	448	CAGTCTGAGAGGCGCGTGGCGGCTTGGCCCACTGGCGGCTTCCACCGGCAATCAAG	507
DB	205	GlnValValAlaAlaValAlaGlnHisCysHisAlaArgValValAlaIleArgAspIleLeu	224
QY	508	GACGAGATCTTAATGCACTGACGCGCGGGAATCAACTGACACTTGGGCTG	567
DB	225	AspGlnAsnIleLeuIleAspLeuCysArgGlySerIleValLeuIleAspPheGlySer	244
QY	568	GCGGCGCTCTCAAGGACAGTACACGAGCTTGTGAGGACCGGAGTGAAGTCACTCT	627
DB	245	GlyAlaLeuLeuHisAspGlnProTyrThrAspPheAspGlyThrArgValTyrSerPro	264
QY	628	CCAGATGATTCGCTACATCGCTACACGAGAGTCCGAGCTGTCTGCTCTGCTGGG	687
DB	265	ProGlnTrpIleSerArgHisGlnTyrHisAlaLeuProAlaThrValIleTrpSerLeuGly	284
QY	688	ATCGTCTGATGACATGCTGCGGAGATTCGTTGAGACGATGAGGATGATC	747
DB	285	ValLeuLeuTyrAspMetValCysGlyAspIleIleProPheGlnArgAspGlnIleLeu	304
QY	748	AAGGCGCAAGTCTTCAAGGCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTAAATG	807
DB	305	GlnAlaGlnLeuHisAspProAlaHisValSerProAspCysGlyAlaLeuIleArgArg	324
QY	808	TGCTCTCTGCTGAGACGCTGAGATCGGCGCTCTTGAAGAAATCGCAACATCCGTGG	867
DB	325	CysLeuAlaProIleProCysSerArgProSerLeuGlnGlnIleLeuLeuAspProTyr	344
QY	868	ATGCAAGAGGATCTGCTGCGGAGGCTTGCAGATCATCTGACAGTGTGTCGACCG	927
DB	345	MetGlnSer-----ProAlaGlnGlnIleProIleAsnSerSerIleGlySerPro	361

Search completed: September 22, 2005, 17:14:55
Job time : 162.516 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: September 22, 2005, 16:26:26 / Search time 127.935 Seconds
(without alignments)
5993.731 Million cell updates/sec

Title: US-10-705-757-5

Perfect score: 1749
Sequence: 1 agctctctgtccagatca.....caccggatccagcaagtag 942

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1826521 seqs, 407012169 residues

Total number of hits satisfying chosen parameters: 3653042

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPT=0 -LOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62
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Database: Published.Applications_AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1668	95.4	313	9 US-09-971-791-7	Sequence 7, Appl
2	1668	95.4	313	15 US-10-348-081-14	Sequence 14, Appl
3	1668	95.4	313	16 US-10-664-421-2	Sequence 2, Appl
4	1668	95.4	313	16 US-10-377-266-10	Sequence 10, Appl
5	1668	95.4	313	18 US-10-705-757-6	Sequence 6, Appl
6	1668	95.4	313	18 US-10-941-635-2	Sequence 2, Appl
7	1584	90.6	313	9 US-09-971-791-8	Sequence 8, Appl
8	1584	90.6	313	15 US-10-348-081-12	Sequence 12, Appl
9	1584	90.6	313	18 US-10-705-757-4	Sequence 4, Appl
10	1582	90.5	313	9 US-09-971-791-9	Sequence 9, Appl
11	1582	90.5	313	14 US-10-081-119-18	Sequence 18, Appl
12	1582	90.5	313	15 US-10-394-322A-52	Sequence 52, Appl
13	1582	90.5	313	15 US-10-348-081-13	Sequence 13, Appl
14	1582	90.5	313	16 US-10-664-421-1	Sequence 1, Appl
15	1582	90.5	313	16 US-10-664-421-150	Sequence 150, App
16	1582	90.5	313	16 US-10-377-266-9	Sequence 9, Appl
17	1582	90.5	313	17 US-10-951-388-18	Sequence 18, Appl
18	1582	90.5	313	17 US-10-951-406-18	Sequence 18, Appl
19	1582	90.5	313	17 US-10-951-477-18	Sequence 18, Appl
20	1582	90.5	313	18 US-10-977-087-18	Sequence 18, Appl
21	1582	90.5	313	18 US-10-705-757-2	Sequence 2, Appl
22	1582	90.5	313	18 US-10-941-635-1	Sequence 1, Appl
23	1582	90.5	313	18 US-10-941-635-152	Sequence 152, App
24	1580	90.3	313	16 US-10-620-052A-22	Sequence 22, Appl
25	1315	75.2	253	16 US-10-620-052A-71	Sequence 71, Appl
26	1131	64.7	323	16 US-10-664-421-7	Sequence 7, Appl
27	1131	64.7	323	16 US-10-377-266-15	Sequence 15, Appl
28	1131	64.7	323	18 US-10-941-635-7	Sequence 7, Appl
29	1123.5	64.2	326	15 US-10-348-081-6	Sequence 6, Appl
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33	1122.5	64.2	326	18 US-10-348-081-10	Sequence 10, Appl
34	1122.5	64.2	326	18 US-10-705-757-9	Sequence 9, Appl
35	1122.5	64.2	455	9 US-09-971-791-5	Sequence 5, Appl
36	1119	64.0	326	9 US-09-971-791-2	Sequence 2, Appl
37	1119	64.0	326	15 US-10-348-081-2	Sequence 2, Appl
38	1119	64.0	326	16 US-10-664-421-166	Sequence 166, App
39	1119	64.0	326	16 US-10-618-941-82	Sequence 82, App
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42	1113	63.6	323	9 US-09-971-791-6	Sequence 6, Appl
43	1113	63.6	323	15 US-10-348-081-11	Sequence 11, Appl
44	1113	63.6	323	16 US-10-664-421-8	Sequence 8, Appl
45	1113	63.6	323	16 US-10-377-266-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-971-791-7
; Sequence 7, Application US/09971791
; Patent No. US20020115120A1
; GENERAL INFORMATION:
; APPLICANT: Rosanna Kapeller-Libermann
; APPLICANT: Laura A. Rudolph-Owen
; APPLICANT: Kyle Macbeth
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 35800/238856
; CURRENT APPLICATION NUMBER: US/09/971, 791
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/644, 450
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/237, 543
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 313


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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-971-791-7

Alignment Scores:
Pred. No.:      2,676-117      Length:      313
Score:          1668.00        Matches:      313
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    95.37%         Indels:      0
DB:             9              Gaps:         0

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QY      61 CAGCCCAACCAAGCTGGCGCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
      |||
DB      21 Hsialthrileuamlaarproglyyrglulysglulproleuclusergintyrglnval 40

QY      121 GGCCTCGTGTGGGAGCGGCTTGGCTCGCTGCTACTCTGGCATTCGCGTCCGAC 180
      |||
DB      41 Glyproleuenucluserglyyphneglyyphneglyyphneglyyphneglyyphneg 60

QY      181 AACTGGCGGTGGCCATTAGACAGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
      |||
DB      61 Aamleuprovalaiallelyahlsvalglulysaaparglleseraptrpglylnleu 80

QY      241 CCCAATGGCAACCGAGTGCATGAAAGTGTCTGTGAGAGAGAGAGAGAGAGAGAGAG 300
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DB      81 Proaenglytharvalprometglulvalleuenucluserleu 100

QY      301 TCGGGGCTATTAGACTTCTGAGCTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
      |||
DB      101 Serglyvalleargleuenuaprtprphgluargproaerphnevalleuileu 120

QY      361 GAGAGCGCGAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
      |||
DB      121 Gluargproglulprovalgluabreleuaphepneillethrgluarglylnleu 140

QY      421 GAGAGCTGGCCGAGAGATCTTCTGGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAG 480
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DB      141 Gluabreleuamlaarglyrphetrpgrlnvalleuglnvalaarghlsywhsaen 160

QY      481 TCGGGGCTTCCACCGCGCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
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DB      161 Cyeglyvalleuamlaargaprllelysaapgluabreleuileuileuileu 180

QY      541 GAATCAAACTCATGCACTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
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DB      181 Gluileuyleuileuaphepneglyserglyaleuenucluseraptrvallytrnaar 200

QY      601 TTGATGGGAGCCGAGTGTACAGTCTCCAGAGTGTATTCGATCACTGCTACAGAG 660
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QY      721 CCGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
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QY      781 TCAGAGTGCAGCACTTATTAATGAGTGTCTGCTGAGAGAGAGAGAGAGAGAGAG 840
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DB      261 Serglyyeglylnhlsleuileuileuileuileuileuileuileuileuileu 280

QY      841 TTGGAAGAAATCCGGAACCATCGGTGATGAGAGAGAGAGAGAGAGAGAGAGAG 900
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QY      901 GAGATCCATCTGCACAGTCTGTGCACCGGAGATCCAGAGAG 939
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RESULT 2
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; Sequence 14, Application US/10348081
; Publication No. US20040038246A1
; GENERAL INFORMATION:
; APPLICANT: KORN, Marcus
; APPLICANT: MUELLER, Guenter
; APPLICANT: SCHNEIDER, Rudolf
; APPLICANT: TSCHAN, Georg
; TITLE OF INVENTION: P1M-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
; FILE REFERENCE: DE4V2002/0004 US NP
; CURRENT APPLICATION NUMBER: US/10/348,081
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-348-081-14

Alignment Scores:
Pred. No.:      2,676-117      Length:      313
Score:          1668.00        Matches:      313
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    95.37%         Indels:      0
DB:             15              Gaps:         0

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QY      61 CAGCCCAACCAAGCTGGCGCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
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DB      21 Hsialthrileuamlaarproglyyrglulysglulproleuclusergintyrglnval 40

QY      121 GGCCTCGTGTGGGAGCGGCTTGGCTCGCTGCTACTCTGGCATTCGCGTCCGAC 180
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DB      41 Glyproleuenucluserglyyphneglyyphneglyyphneglyyphneglyyphneg 60

QY      181 AACTGGCGGTGGCCATTAGACAGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
      |||
DB      61 Aamleuprovalaiallelyahlsvalglulysaaparglleseraptrpglylnleu 80

QY      241 CCCAATGGCAACCGAGTGCATGAAAGTGTCTGTGAGAGAGAGAGAGAGAGAGAGAG 300
      |||
DB      81 Proaenglytharvalprometglulvalleuenucluserleu 100

QY      301 TCGGGGCTATTAGACTTCTGAGCTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
      |||
DB      101 Serglyvalleargleuenuaprtprphgluargproaerphnevalleuileu 120

QY      361 GAGAGCGCGAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
      |||
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QY      421 GAGAGCTGGCCGAGAGATCTTCTGGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAG 480
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DB      141 Gluabreleuamlaarglyrphetrpgrlnvalleuglnvalaarghlsywhsaen 160

QY      481 TCGGGGCTTCCACCGCGCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
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Db      201  |||||PheAspGlyThrArgValIyrtserProGluIrtPrlleArgTyrtHrAsgTyrtHrAsgIy 220
Qy      661  |||||AGGCGGACGCTGTGGTCCCTTGAGATCGTCTCATATGATGATGCTGCGGAGATATT 720
Db      221  |||||ArgSerAlaAlaValIrtPserLeuGlyIleuLeuLeuYrtAspMetValCySgIYAspIle 240
Qy      721  |||||CCGTTGAGCAGCATGAAGAATCATCAAGGCGCAAGTGTCTTCCAGGCAAGCTGTCT 780
Db      241  |||||ProPheGluIrtHrAspGluIrtleuIleuGlyGlnValPhePheArgGlnIrtHrValser 260
Qy      781  |||||TCGAGGTGACGACCTTATTAAATGCTGCTCTGCTGAGACCGTGACATCGGCGCTCC 840
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RESULT 3

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US-10-664-421-2
/ Sequence 2, Application US/10664421
/ Publication No. US20040142864A1
/ GENERAL INFORMATION:
/ APPLICANT: BREMER, RYAN
/ APPLICANT: KUMAR, ABHINAV
/ APPLICANT: KUMAR, ABHINAV
/ APPLICANT: MANDIYAN, VALISAN
/ APPLICANT: MILBURN, MICHAEL V.
/ TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
/ FILE REFERENCE: 039363/0703
/ CURRENT APPLICATION NUMBER: US/10/664,421
/ CURRENT FILING DATE: 2003-09-16
/ PRIOR APPLICATION NUMBER: 60/412,341
/ PRIOR FILING DATE: 2002-09-20
/ PRIOR APPLICATION NUMBER: 60/411,398
/ PRIOR FILING DATE: 2002-09-16
/ NUMBER OF SEQ ID NOS: 169
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 2
/ LENGTH: 313
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-10-664-421-2

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Alignment Scores:

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Pred. No.: 2,67e-117 Length: 313
Score: 1668.00 Matches: 313
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.37% Indels: 0
DB: 16 Gaps: 0

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US-10-705-757-5 (1-942) x US-10-664-421-2 (1-313)

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Db      1  |||||MetLeuLeuSerIyrtleuAspSerLeuAlaHrIleuAlaGlnAlaArgProCyAspAspLeu 20
Qy      61  |||||CAGGCGACCAAGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 120
Db      21  |||||HisAlaThrIyrtleuLeuAlaArgProGlyIyrtGlnIyrtGlnIyrtGlnIyrtGlnIyrtGlnIyrt 40
Qy      121 |||||GGCGCGCTGTGGGACGCGGCTGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCGAC 180

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Db      41  |||||GlyProLeuLeuGlySerGlyIyrtPheGlySerValIyrtserGlyIrtleuArgValAlaAsp 60
Qy      181  |||||AACTTCCCGGTGGCCATTAAAGCACGTGGAGAGAGACCGGATTTCCGATTGGGGAGAACTG 240
Db      61  |||||AsnLeuProValAlaIleuYsnIleValGlnIyrtAspArgIleIserAspIrtPrgIyrtGluLeu 80
Qy      241  |||||CCCAATGGCAGCCCGAGTGGCCATGAGAGGTGCTCTTTGAGAAAGGTGAGCTGCGACTTC 300
Db      81  |||||ProAsnGlyThrArgValIrtPmetGluValIleuLeuLeuYrtValIserSerAspPhe 100
Qy      301  |||||TCGGGCGTCATTAGACTTGTGAATGTTTGAAGAGCCCGATAGTTGTGCTGATCTG 360
Db      101  |||||SerGlyValIrtleuArgLeuLeuAspIrtPheGluArgProAspSerPheValIleuLeu 120
Qy      361  |||||GAGAGCGCGGACCCGCTGCAAGACCTTCTGCACTTTATACCGCAAGAGAGAGCCCTTACAG 420
Db      121  |||||GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
Qy      421  |||||GAGGACCTGGAGCGGAGATTTCTTCTGCGAGGTGCTGAGAGCGCGTGGCGCATTCGCAAC 480
Db      141  |||||GluAspLeuAlaArgGlyPhePheIrtPrgIrtValIleuGlnAlaValArgHrAsyHrAsn 160
Qy      481  |||||TCGGGCGGTCTCCACCGGACATCAAGACGAGACATCTTAAATGCACTGTAACCGCGCGC 540
Db      161  |||||CySgIYValIleuHrAspIrtleuYsaPrgIrtValIleuIleuIleuIleuIleuIleuIleu 180
Qy      541  |||||GAAATCAACTCATGCACTTCGCGGTGGGCGCGCTCTCAAGACACAGTCTTACAGGAC 600
Db      181  |||||GluileuLeuileuLeuPheglservGlyAlaLeuLeuYsaPthrValIyrtHrAsp 200
Qy      601  |||||TTTGATGGGACCCGAGTGTCACAGTCTCTCCAGAGTGATTCGTAACCATCGGTACCAAGGC 660
Db      201  |||||PheAspGlyThrArgValIyrtserProGluIrtPrlleArgTyrtHrAsgTyrtHrAsgIy 220
Qy      661  |||||AGGCGGACGCTGTGGTCCCTTGAGATCGTCTCATATGATGATGCTGCGGAGATATT 720
Db      221  |||||ArgSerAlaAlaValIrtPserLeuGlyIleuLeuLeuYrtAspMetValCySgIYAspIle 240
Qy      721  |||||CCGTTGAGCAGCATGAAGAATCATCAAGGCGCAAGTGTCTTCCAGGCAAGCTGTCT 780
Db      241  |||||ProPheGluIrtHrAspGluIrtleuIleuGlyGlnValPhePheArgGlnIrtHrValser 260
Qy      781  |||||TCGAGGTGACGACCTTATTAAATGCTGCTCTGCTGAGACCGTGACATCGGCGCTCC 840
Db      261  |||||SerGluCySgIrtHrAspIleuIleuIyrtPcyLeuSerLeuArgProSerAspArgProSer 280
Qy      841  |||||TTTGAAGAATCCGGAACCATCCGTGATGACGAGGTGACTCTCGCCCGGAGGAGCTTCT 900
Db      281  |||||PheGluGluIrtleuArgAspHrAspIrtProIrtPmetGlnGlyAspLeuLeuProGlnAlaIAser 300
Qy      901  |||||GAGATCCATCTGACAGTGTGTCAACCGGATCCAGCAAG 939
Db      301  |||||GluileuIleuHrAspSerLeuSerProGlySerSerIys 313

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RESULT 4

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US-10-377-268-10
/ Sequence 10, Application US/10377268
/ Publication No. US20040171062A1
/ GENERAL INFORMATION:
/ APPLICANT: HIRTH, KLAUS-PETER
/ APPLICANT: MILBURN, MICHAEL VANCE
/ TITLE OF INVENTION: METHOD FOR THE DESIGN OF MOLECULAR SCARFOLDS AND LIGANDS
/ FILE REFERENCE: 039363/0303
/ CURRENT APPLICATION NUMBER: US/10/377,268
/ CURRENT FILING DATE: 2003-02-28
/ PRIOR APPLICATION NUMBER: 60/437,929
/ PRIOR FILING DATE: 2003-01-02
/ PRIOR APPLICATION NUMBER: 60/360,651
/ PRIOR FILING DATE: 2002-02-28
/ PRIOR APPLICATION NUMBER: 60/411,398
/ PRIOR FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: 60/412,341
/ PRIOR FILING DATE: 2002-09-20

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; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 10
 ; LENGTH: 313
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-377-268-10

Alignment Scores:

Pred. No.:	2,67e-117	Length:	313
Score:	1668.00	Matches:	313
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	95.37%	Indels:	0
DB:	16	Gaps:	0

US-10-705-757-5 (1-942) x US-10-377-268-10 (1-313)

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QY 1 ATGCTCTGTCAGATCAATCTCCCTGCGCCACCTGCGCGCCGCCCTTGCAACGACTTG 60
DB 1 MetLeuLeuSerlyslleahnsersleuAlahlsleuAlargProcySabaAbpLeu 20
QY 61 CAGCCCAACCAAGCTGCGCGCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 21 HlsAlathrlYsleuAlaProglYlYsGlnLyluproLeuGlnSerGlnYrGlnVal 40
QY 121 GGGCGCGTGTGGAGCGGCGGCTTCCGCTCGCTACTGCTGCAATCCGCTGCGCGAG 180
DB 41 GlyProLeuLeuGlnSerGlnYlYsGlnLyluproLeuGlnSerGlnYrGlnVal 60
QY 181 AACTGCGCGTGGCCATTAAGACAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 61 AsnLeuProValAlaIleYshlsValGlnLyluproLeuGlnSerGlnYrGlnVal 80
QY 241 CCCAATGGACCCGAGTGGCCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 81 ProAsnGlnYrTharYValProMetGlnValValLeuLeuYlYsValSerSerAapPhe 100
QY 301 TCGGCGCTGATTAGACTTCTGAGCTGGTTCGAGAGCGCGAGTATTCGATGCGTGC 360
DB 101 SerGlnYValIleargleuLeuAapTrpPheGlnLyluproLeuGlnSerGlnYrGlnVal 120
QY 361 GAGAGGCGCGAGCCGAGTGGACAGACTTCTGAGCTTATCAACGAGAGAGAGAGAGAGAG 420
DB 121 GlnArgProGlnLyluproValGlnAapLeuPheAapPheIleThrGlnLyluproVal 140
QY 421 GAGGAGCTGCGCGAGAGATTCCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 141 GlnAapLeuAlaArgGlnPhePheTrpGlnValLeuGlnValAlaArgHlsCyshlsAap 160
QY 481 TGGGCGGCTTCCAGCGCGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 161 CyshGlnYValIleuHlsAapArgIleYshlsAapGlnAapIleuHlsAapLeuSerAapGln 180
QY 541 GAAATCAAACTCATCGACTTCGAGTGGCGCGCGCTGCAAGAGACAGTCTACAGAGAG 600
DB 181 GlnIleYsleuLeuIleAapPheGlnSerGlnLyluproLeuGlnSerGlnYrGlnVal 200
QY 601 TTTGATGGAGCCGAGTGTACAGTCTCCAGAGTGGATTCGCTACCATCGCTACAGAGAG 660
DB 201 PheAapGlnYrTharYValYrSerProGlnLyluproLeuGlnSerGlnYrGlnVal 220
QY 661 AGGTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 221 ArgSerAlaAlaValIlePheSerLeuGlnYlYsleuLeuYrAapPheValCyshGlnAap 240
QY 721 CCGTTTGGAGCAGATGAAGAGATCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 241 ProPheGlnLyluproValGlnAapLeuPheAapPheIleThrGlnLyluproVal 260
QY 781 TCGAGAGTGTCAAGACCTTATTAATGAGTGGCTGCTGCTGAGAGAGAGAGAGAGAGAG 840
DB 261 SerGlnLyluproValIleuHlsAapArgIleYshlsAapGlnAapIleuHlsAapLeu 280
  
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QY 841 TTTGAAGAAATCCGGAACCATCGGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 281 PheGlnLyluproValIleuHlsAapArgIleYshlsAapGlnAapIleuHlsAapLeu 300
QY 901 GAGATTCATCTGCACAGTGTGTACCGGAGATTCACGAG 939
DB 301 GlnIleHlsleuHlsSerleuSerProGlnYrSerSerLys 313
  
```

RESULT 5

US-10-705-757-6

; Sequence 6, Application US/10705757
 ; Publication No. US20040146942A1
 ; GENERAL INFORMATION:

; APPLICANT: GRUBENTHAL, GMBH
 ; TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE OR PIM3-KINASE

; FILE REFERENCE: 029310,5281805
 ; CURRENT APPLICATION NUMBER: US/10/705,757

; CURRENT FILING DATE: 2003-11-12
 ; PRIOR APPLICATION NUMBER: PCT/EP02/05234

; PRIOR FILING DATE: 2002-05-13
 ; PRIOR APPLICATION NUMBER: DE 101 23 055.9

; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Patentin Ver. 2.1

US-10-705-757-6

; LENGTH: 313
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-705-757-6

Alignment Scores:

Pred. No.:	2,67e-117	Length:	313
Score:	1668.00	Matches:	313
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	95.37%	Indels:	0
DB:	18	Gaps:	0

US-10-705-757-5 (1-942) x US-10-705-757-6 (1-313)

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QY 1 ATGCTCTGTCAGATCAATCTCCCTGCGCCACCTGCGCGCCGCCCTTGCAACGACTTG 60
DB 1 MetLeuLeuSerlyslleahnsersleuAlahlsleuAlargProcySabaAbpLeu 20
QY 61 CAGCCCAACCAAGCTGCGCGCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 21 HlsAlathrlYsleuAlaProglYlYsGlnLyluproLeuGlnSerGlnYrGlnVal 40
QY 121 GGGCGCGTGTGGAGCGGCGGCTTCCGCTCGCTACTGCTGCAATCCGCTGCGCGAG 180
DB 41 GlyProLeuLeuGlnSerGlnYlYsGlnLyluproLeuGlnSerGlnYrGlnVal 60
QY 181 AACTGCGCGTGGCCATTAAGACAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 61 AsnLeuProValAlaIleYshlsValGlnLyluproLeuGlnSerGlnYrGlnVal 80
QY 241 CCCAATGGACCCGAGTGGCCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 81 ProAsnGlnYrTharYValProMetGlnValValLeuLeuYlYsValSerSerAapPhe 100
QY 301 TCGGCGCTGATTAGACTTCTGAGCTGGTTCGAGAGCGCGAGTATTCGATGCGTGC 360
DB 101 SerGlnYValIleargleuLeuAapTrpPheGlnLyluproLeuGlnSerGlnYrGlnVal 120
QY 361 GAGAGGCGCGAAGCGGTGCAAGACTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 121 GlnArgProGlnLyluproValGlnAapLeuPheAapPheIleThrGlnLyluproVal 140
QY 421 GAGGAGCTGCGCGAGAGATTCCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 141 GlnAapLeuAlaArgGlnPhePheTrpGlnValLeuGlnValAlaArgHlsCyshlsAap 160
  
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; PRIOR FILING DATE: 1999-01-26
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: FaastSeq for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 313
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-09-971-791-8

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
5,86e-111	313	295	8	10	0	
Score:	1584.00					
Percent Similarity:	96.81%					
Best Local Similarity:	94.25%					
Query Match:	90.57%					

US-10-705-757-5 (1-942) x US-09-971-791-8 (1-313)

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QY 1 ATGCTCTGTCGAAGATCAACTCCCTGGCCACCTGCGGCGCCGCCCTGCAACGACTG 60
   |||||
Db 1 MetleuLeuSerIylleahnsrleuAlahlsleuArgAlahlaProCyshansrleu 20
   |||||
QY 61 CAGGCCAACAGCTGGCGCGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
   |||||
Db 21 HlsAlaahsleuLeuAlaProGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 40
   |||||
QY 121 GGGCCGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
   |||||
Db 41 GlyProleuLeuIylserGlyGlyPheGlySerValIylserGlyIleArgValAlaAsp 60
   |||||
QY 181 AACTGCGCGGTGGCCATTAAAGCAGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
   |||||
Db 61 AenleuProValAlahlsleuValGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 80
   |||||
QY 241 CCCAATGGCAACCGGAGTCCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
   |||||
Db 81 ProahnglyThzArgValProMetGlyValIleuLeuIylserValSerSerGlyPhe 100
   |||||
QY 301 TGGGGGCTGATTGACTTCTGCACTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
   |||||
Db 101 SerGlyValIleArgleuLeuAspTrpPheGlyArgProAspSerPheValIleuLeu 120
   |||||
QY 361 GAGAGCGCCGAGACCGGTGCAAGACTCTTCACTTATATCAACGAGAGAGAGAGAGAGAG 420
   |||||
Db 121 GluArgProGlyProValGlnAspLeuPheAspPheIleThrGlyArgGlyAlaLeuGln 140
   |||||
QY 421 GAGAGCTGGCGCGGAGAGATTCTTCTGCACTGCTGAGAGAGAGAGAGAGAGAGAGAGAG 480
   |||||
Db 141 GluGlnLeuAlaArgSerPhePheTrpGlnValIleuGlnAlaValArgHisCyshAsn 160
   |||||
QY 481 TGGGGGCTTCTGCAACCGGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
   |||||
Db 161 CyseGlyValleuHisArgAspIleIylAspGlyAsnIleuLeuIleAspLeuAsnArgGly 180
   |||||
QY 541 GAATCAAACTCATGCACTTGGGTCGGGCGCGCTGCTCAAGAGAGAGAGAGAGAGAGAGAG 600
   |||||
Db 181 GluLeuIylleuLeuIleAspPheGlySerGlyAlaLeuLeuIylAspThrValIylTrpAsp 200
   |||||
QY 601 TTTGATGGAGACCGGAGGTGACAGTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
   |||||
Db 201 PheAspGlyThzArgValIylSerProProGlyIylleArgTrpHisArgTrpHisGly 220
   |||||
QY 661 AGGTGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
   |||||
Db 221 ArgSerAlaAlaValIylTrpSerleuGlyIleLeuLeuIylAspPheValCyseGlyAspIle 240
   |||||
QY 721 CCGTTGAGACGATGAAGAGATCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
   |||||
Db 241 ProPheGlnHisAspGlyGlnIylleValGlyGlnValIylTrpPheArgGlnAspValSer 260
   |||||
QY 781 TCAAGGTGTGAGACCTTATTAATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
   |||||

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Db 261 SerGlyCyseGlnHisleuIleArgTrpCyseuSerleuArgProSerAspArgProSer 280
   |||||
QY 841 TTTGAAGAAATCCGGAACCATCCGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
   |||||
Db 281 PheGlnGlyIleGlnAspHisProTrpPheGlnAspValleuProGlnAlaThrAla 300
   |||||
QY 901 GAGATCATCTGCAACAGTCTGTCAACGGGAGATCCAGCAAG 939
   |||||
Db 301 GluIleHisleuHisSerleuSerProSerProSerIyls 313
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```

RESULT 8

US-10-348-081-12
 ; Sequence 12, Application US/10348081
 ; Publication No. US20040038246A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KORN, Marcus
 ; APPLICANT: MUELLER, Guenter
 ; APPLICANT: SCHNEIDER, Rudolf
 ; APPLICANT: TSCHANX, Georg
 ; TITLE OF INVENTION: P1W-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
 ; FILE REFERENCE: DE4V2002/0004 US NP
 ; CURRENT APPLICATION NUMBER: US/10/348,081
 ; CURRENT FILING DATE: 2003-01-21
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 12
 ; LENGTH: 313
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-10-348-081-12

Alignment Scores:
 Pred. No.: 5,86e-111
 Score: 1584.00
 Percent Similarity: 96.81%
 Best Local Similarity: 94.25%
 Query Match: 90.57%
 DB: 15
 Gaps: 0

US-10-705-757-5 (1-942) x US-10-348-081-12 (1-313)
 QY 1 ATGCTCTGTCGAAGATCAACTCCCTGGCCACCTGCGGCGCCGCCCTGCAACGACTG 60
 Db 1 MetleuLeuSerIylleahnsrleuAlahlsleuArgAlahlaProCyshansrleu 20
 QY 61 CAGGCCAACAGCTGGCGCGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
 Db 21 HlsAlaahsleuLeuAlaProGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 40
 QY 121 GGGCCGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
 Db 41 GlyProleuLeuIylserGlyGlyPheGlySerValIylserGlyIleArgValAlaAsp 60
 QY 181 AACTGCGCGGTGGCCATTAAAGCAGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 Db 61 AenleuProValAlahlsleuValGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 80
 QY 241 CCCAATGGCAACCGGAGTCCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 Db 81 ProahnglyThzArgValProMetGlyValIleuLeuIylserValSerSerGlyPhe 100
 QY 301 TGGGGGCTGATTGACTTCTGCACTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
 Db 101 SerGlyValIleArgleuLeuAspTrpPheGlyArgProAspSerPheValIleuLeu 120
 QY 361 GAGAGCGCCGAGACCGGTGCAAGACTCTTCACTTATATCAACGAGAGAGAGAGAGAGAGAGAG 420
 Db 121 GluArgProGlyProValGlnAspLeuPheAspPheIleThrGlyArgGlyAlaLeuGln 140
 QY 421 GAGAGCTGGCGCGGAGAGATTCTTCTGCACTGCTGAGAGAGAGAGAGAGAGAGAGAGAG 480
 Db 141 GluGlnLeuAlaArgSerPhePheTrpGlnValIleuGlnAlaValArgHisCyshAsn 160

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QY 181 AACTGCGCGGTGGCCATTAAAGCAGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
   |||||
Db 61 AenleuProValAlahlsleuValGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 80
   |||||
QY 241 CCCAATGGCAACCGGAGTCCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
   |||||
Db 81 ProahnglyThzArgValProMetGlyValIleuLeuIylserValSerSerGlyPhe 100
   |||||
QY 301 TGGGGGCTGATTGACTTCTGCACTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
   |||||
Db 101 SerGlyValIleArgleuLeuAspTrpPheGlyArgProAspSerPheValIleuLeu 120
   |||||
QY 361 GAGAGCGCCGAGACCGGTGCAAGACTCTTCACTTATATCAACGAGAGAGAGAGAGAGAGAGAG 420
   |||||
Db 121 GluArgProGlyProValGlnAspLeuPheAspPheIleThrGlyArgGlyAlaLeuGln 140
   |||||
QY 421 GAGAGCTGGCGCGGAGAGATTCTTCTGCACTGCTGAGAGAGAGAGAGAGAGAGAGAGAG 480
   |||||
Db 141 GluGlnLeuAlaArgSerPhePheTrpGlnValIleuGlnAlaValArgHisCyshAsn 160
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[illegible]

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RESULT 9
US-10-705-757-4
; Sequence 4, Application US/10705757
; Publication No. US20040146942A1
; GENERAL INFORMATION:
; APPLICANT: GRUENTHAL GMBH
; TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE OR PIM3-KINASE
; FILE REFERENCE: 029310.52818US
; CURRENT APPLICATION NUMBER: US/10/705,757
; PRIOR FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/EP02/05234
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: DE 101 23 055.9
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 313
/ TYPE: prt
/ ORGANISM: Rattus norvegicus
US-10-705-757-4

Alignment Scores:
Pred. No.:          5,86e-111      Length:           313
Score:              1584.00         Matches:          295
Percent Similarity: 96.81%         Conservative:     8
Best Local Similarity: 94.25%       Mismatches:       10
Query Match:        90.57%         Indels:            0
DB:                  18             Gaps:              0

US-10-705-757-5 (1-942) x US-10-705-757-4 (1-313)

QY      1 ATGTCCTGTCCAAAGTCAACTGCCCTGGCCACCTGCGGCCGCCCTTGACAAGACTTG 60
        |||||
Db       1 MettleLeuSerIylleAenSeRicuAlAhSlenuATgAlaIaProCyaaenApLeu 20

QY      61 CAGCGCACCAACTGTCGCGCGGGCAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
        |||||
Db       21 HtSAlaenHyLeuAlarProGlyrByGLuLySGluProlendunserGintyrGlnVal 40

QY      121 GGCCCCGCTATTGGAGCGAGCGATGCCTTAGCTCGGTCTACTTGACATCCGCGTCCGAC 180

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Db	41	GIYRPLEULENGLYSERCIYGLPHEGLYSERVALTYSERCIYLLIETRGVALIADAP	60
QY	181	AACTGGCCGGTGGCCATTAAAGCAGCTGGAGAAGAACCCGATTTCCGATTTGGGAGAACTG	240
Db	61	AAenLEuproVALAIaileLYvhiSVaLGIuLYvAPARGIIeSERAPRTGIGIuLEu	80
QY	241	CCCAATGGCAGCCCGAGTGGCCCATGGAAAGTGGCTCTTTAAAGAAAGGTAGCTCGCACTTC	300
Db	81	ProAenGIYThIRaXVALPROMeGIuVALIleuLEuLYvVALISerSergIYpHe	100
QY	301	TCCGGCGCATTAAGACTTCTTGACCTGGTTCGAGAGGCCGATAGTTTCGTGCGTATCTCTG	360
Db	101	SergIYvAlIleuLYuLEuAPRTpRheGIIuYGRProAPserpHeVALIleuIleu	120
QY	361	GAGAGGCCGAAACCCGGTGGAGACACTTTTGAATTATACCGAAGCAGAGAGCCCTACAG	420
Db	121	GIuATGRProGIuProVALGIuAPRLeuPheAPRheIleThGIuYGRGIuAlaLeuGln	140
QY	421	GAGCACTGGCCCGGAGATTTCTTGGCAGGTGCTGGAGAGCCGTGGCGCATTCGCACAC	480
Db	141	GIuGIuLEuAlaARGserPhepHeTRpGInVALIeGInALaVALaRGHISCyvhiVAPh	160
QY	481	TGCGGGGTCTCCAGCCGAGACTCAAGGACCGAGACATTTATATGACCTCGACCCGGCGC	540
Db	161	CySGIuVALIeuhIaARGAPRIleLYvAPRGInuAenIIleuPIleAPRLeuAPhARGIY	180
QY	541	GAATCAAACTCAGACTTCGGGTGCGGGGCGCTGCTCAAGAGCAGACTGTACACGAG	600
Db	181	GIuLEuLYvLEuIIleAPRheIYserGIuAlaLeuLYvAPRphIRhIYALTYRTPIhAPR	200
QY	601	TTTGAATGGACCCGAGGTATACAGCTCTCCAGAGTGATTCGTTACCATCGGTACACAGGC	660
Db	201	PheAPRGIYThIRaXVALTYserProProGIuTRPIleARGTYkhiSARGTYkhiVGLY	220
QY	661	AGGTGGGAGAGCTGTGGTCTCTTGGGATCTTCGCTTAAGACATGGTCTTGGCAAGATATT	720
Db	221	ARGserIaIaIaVALTPserIeudIYIleuLEuTYAPRMeVALCYvGIuAPRIle	240
QY	721	CCGTTTGAAGCAGATGAAGAGATCAATCAAGGGCCAAAGTGTCTTCAAGGCCAAATGTCTCT	780
Db	241	ProPheGIuuhIvAPRGIGIuIleVALIYvGIuGInVALTYvPheARGInAPRGVALISer	260
QY	781	TCAAGAGTCAAGCACTTATTAATAGTGGCTGTGCTCGTGAAGACCGTCAAGTCGGCCCTCC	840
Db	261	SergIuCYvGIuhiSLeuIIleARGTRPYvLeuSERLeuARGProSERAPARGProser	280
QY	841	TTTTGAAGAAATCCGGAACCATCTCGTGGATGACAGGGGTGACCTCTGCCCCAGGAGCTTCT	900
Db	281	PheGIuGIuIleGInAPhIAPROCTpRMeGIuAPRVALIleuLEuProGIuIaThIRaIa	300
QY	901	GAGATCACTTGGACAGTCTGCACCGGGGATCCAGCAAG	939
Db	301	GIuIlehiSLeuhiSLeuSERProserProserLYvS	313

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RESULT 10
US-09-971-791-9
; Sequence 9, Application US/09971791
; Patent No. US20020115120A1
; GENERAL INFORMATION:
; APPLICANT: Rosanna Kapeller-Libermann
; APPLICANT: Laura A. Rudolph-Owen
; APPLICANT: Kyle Macbeth
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HK1D-1-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 35800/238856
; CURRENT APPLICATION NUMBER: US/09/971,791
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/644,450
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/237,543
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 9
; LENGTH: 313
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-971-791-9

Alignment Scores:
Pred. No.:      8.3e-111      Length:      313
Score:          1582.00      Matches:      294
Percent Similarity: 97.12%      Conservative: 10
Best Local Similarity: 93.93%      Mismatches:   9
Query Match:    90.45%      Indels:      0
DB:              9          Gaps:      0

US-10-705-757-5 (1-942) x US-09-971-791-9 (1-313)

QY      1 ATGCTCTGTTCGAAGTCAACTCCCTGGCCCACTGGCGCCGCCGCCCTGCAAGCACTG 60
DB      1 MetleuenseuylsleasenseleuAlahleuAlahlabrocyasanaapleu 20
QY      61 CACGCCAACCAAGCTGGCGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB      21 HleAlathlyleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleu 40
QY      121 GGCCTGCTGTGGCAGCGGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB      41 GlyProleuendlyserglyserglyserglyserglyserglyserglyserglyserglyser 60
QY      181 AACCTGCGGCTGGCCATTAGCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB      61 AahleuProvalAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleu 80
QY      241 CCCAATGGCAACCGGAGTGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB      81 ProhensglytharAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleu 100
QY      301 TCGGCGCTGATTAGACTTCTGCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB      101 SerGlyValIleargleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleu 120
QY      361 GAGAGCGCCGAACCGGAGTGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB      121 GluArgProgluProvalAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleu 140
QY      421 GAGAGCGCCGAACCGGAGTGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB      141 GluGluAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleu 160
QY      481 TCGGCGGCTTCTCAACCGGAGTGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB      161 CyseGlyValIleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleu 180
QY      541 GAATCAAAATCTCACTTCGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
DB      181 GluIleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleu 200
QY      601 TTGATGGGAGCCGAGTGGCAAGTGGCAAGTGGCAAGTGGCAAGTGGCAAGTGGCAAGTGGCAAG 660
DB      201 PhasapGlytharAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleu 220
QY      661 AGGTGGAGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB      221 ArgSerAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleu 240
QY      721 CCGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB      241 ProPhenGlytharAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleu 260
QY      781 TCAGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB      261 SerGlyCysGlnAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleu 280
QY      841 TTGGAAGAAATCCGGAACATCCGTGGATGAGGAGTGAAGTGGAGGAGGAGGAGGAGGAGGAGGAG 900
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DB      281 PheGluGluIleGlnAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleu 300
QY      901 GAGATCCATCTGCACAGTGTGCACCGGAGATCCAGAG 939
DB      301 GluIleAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleu 313

RESULT 11
US-10-081-119-18
; Sequence 18, Application US/10081119
; Publication No. US20030045491A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-081-119-18

Alignment Scores:
Pred. No.:      8.3e-111      Length:      313
Score:          1582.00      Matches:      294
Percent Similarity: 97.12%      Conservative: 10
Best Local Similarity: 93.93%      Mismatches:   9
Query Match:    90.45%      Indels:      0
DB:              14          Gaps:      0

US-10-705-757-5 (1-942) x US-10-081-119-18 (1-313)

QY      1 ATGCTCTGTTCGAAGTCAACTCCCTGGCCCACTGGCGCCGCCGCCCTGCAAGCACTG 60
DB      1 MetleuenseuylsleasenseleuAlahleuAlahleuAlahlabrocyasanaapleu 20
QY      61 CACGCCAACCAAGCTGGCGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB      21 HleAlathlyleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleu 40
QY      121 GGCCTGCTGTGGCAGCGGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB      41 GlyProleuendlyserglyserglyserglyserglyserglyserglyserglyserglyserglyser 60
QY      181 AACCTGCGGCTGGCCATTAGCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB      61 AahleuProvalAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleu 80
QY      241 CCCAATGGCAACCGGAGTGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB      81 ProhensglytharAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleu 100
QY      301 TCGGCGCTGATTAGACTTCTGCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB      101 SerGlyValIleargleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleu 120
QY      361 GAGAGCGCCGAACCGGAGTGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB      121 GluArgProgluProvalAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleu 140
QY      421 GAGAGCGCCGAACCGGAGTGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB      141 GluGluAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleuAlahleu 160
QY      481 TCGGCGGCTTCTCAACCGGAGTGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
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Db      161  Cys61YvalLeuH1sArGApR11eLy6ArG1u6u6n11eLeuH1eArPLeu6Ar6nArG1y 180
Qy      541  GAATCAAACTCATGCACTTCGGGTCGGGGCGCTGCTCAAGACACAGTCTACACGAGC 600
Db      181  GluLeuYserLeuH1eArPheG1ySerG1yAlaLeuLeuYsArPThrValTyThrAsp 200
Qy      601  TTGATGGGACCGGAGGTACAGTCTCCAGAGTGGATTGGCTACCTACCTCCAGAGGC 660
Db      201  PheAr61YThrArGValTyTrSerPro61uTrp11eArG1yGlnValPhePheArG1nArGValSer 220
Qy      661  AGGTGGCACTGTCTGTGCTCCCTTGGATCCGTGCTATGACATGCTGTGCGAGATATT 720
Db      221  ArgSer1Ala1AlaValTrpSerLeuG1y1LeuLeuYrHArPMeValCy61yAr61le 240
Qy      721  CCGTTGAGACACGATGAAGATCATCAAGGCGCAAGTGTCTTCAAGCAAACTGTCTT 780
Db      241  ProPheG1uH1sArG1uG1u11e1eArG1yGlnValPhePheArG1nArGValSer 260
Qy      781  TCAGAGTGCAGACCTTATTAATGGTGCCTGTCCCTGAGACCGTCAAGATCCGGCTCC 840
Db      261  SerG1uYserGlnH1sLeuH1eArG1yTrpCy61u6AlaLeuArGProSerAr6ArGProThr 280
Qy      841  TTGAAGAATCCGGAACCATCCGTGATGCAAGGATGACCTCTGCCCCAGGACGTTCT 900
Db      281  PheG1uG1u11eGlnAr6nH1sProTrpMetG1nAr6ValLeuLeuProG1nG1uThrAla 300
Qy      901  GAGATCCATCTGCACAGTCTGTCAACGGGATCCAGCAAG 939
Db      301  Glu11eH1sLeuH1sSerLeuSerProG1yProSer1y6 313

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RESULT 12

```

US-10-394-322A-52
/ Sequence 52, Application US/10394322A
/ Publication No. US20030232391A1
/ GENERAL INFORMATION:
/ APPLICANT: SUNESIS PHARMACEUTICALS, INC.
/ APPLICANT: Prescott, John C.
/ TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
/ FILE REFERENCE: 39750-0006 US
/ CURRENT APPLICATION NUMBER: US/10/394,322A
/ PRIOR FILING DATE: 2003-03-20
/ PRIOR APPLICATION NUMBER: US 60/366,892
/ NUMBER OF SEQ ID NOS: 70
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 52
/ LENGTH: 313
/ TYPE: PR
/ ORGANISM: Homo sapiens
US-10-394-322A-52

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Alignment Scores:

```

Pred. No.:      8,3e-111      Length:      313
Score:          1582.00      Matches:      294
Percent Simlarity: 97.12%      Conservative: 10
Best Local Simlarity: 93.93%      Mismatches: 9
Query Match:     90.45%      Indels:      0
DB:              15          Gaps:          0

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US-10-705-757-5 (1-942) x US-10-394-322A-52 (1-313)

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Qy      1  ATGCTCTGTTCGAAGATCACTCCCTGGCCCACTGGCGCCGCCCTTGCAGACCTG 60
Db      1  MetLeuLeuSer1y61eAr6nSerLeuH1eLeuArG1Ala1ArProCy6Ar6nAr6Leu 20
Qy      61  CAGCCCAACCAAGCTGGCGCGCGGCAAAAGAGAAGAGCCCTTGAGTGCAGTCCAGGTG 120
Db      21  H1sAla1ThrYsLeuH1sAr6ArProG1y6G1u6YsG1uProLeuG1uSerG1nG1uVal 40
Qy      121  GGGCCGCTGTGGCAGACGGGTGGCTTCGAGTCCGATCTACTTGGACATCCGCTCGCCAG 180
Db      41  G1yProLeuLeuG1ySerG1yG1yPheG1ySerValTySerG1y1eArGValSerAr6 60

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Qy      181  AACTTGGCGGTGGCCATTAAAGCATGTGAGAAAGACCCGATTTCCGATTGGGGAAGACTG 240
Db      61  AsnLeuProValAla11eYsH1sValG1u6YsAr6ArG11eSerAr6TrpG1yG1uLeu 80
Qy      241  CCCAATGGCAACCGGAGTCCCATGAGAGTGGTCCCTGTGAAAGAGAGTGAAGCTGCACTTC 300
Db      81  ProAr6nG1yThrArGValArProMetG1uValValLeuLeuYsValSerSerG1yPhe 100
Qy      301  TCGGGCGCTATTAGACTTTCGACTGTGACTGTTGAGAGGCGCGATAGTTTGGTGTGATCTTG 360
Db      101  SerG1yVal11eArGLeuLeuAr6TrpPheG1uArGProAr6SerPheValLeuH1eLeu 120
Qy      361  GAGAGGCGCCGACACCGGTGCAAGACCTTCTGACTTTATATCAACGAAAGAGAGCCCTTACAG 420
Db      121  GluArGProG1uProValGlnAr6LeuPheAr6Phe11eThrG1uArG1yAlaLeuGln 140
Qy      421  GAGACCTGGCCCGGAGATTTCTTGTGAGAGTGTCTGAGAGCGGTGCGGCAATGCGCAAC 480
Db      141  GluG1uLeuH1sArGSerPhePheTrpG1nValLeuG1uH1sValArG1sCy6H1sAr6n 160
Qy      481  TCGGGGTTCTCCACCGCGACATCAAGACGAGAAACATTTAATGCACTGAGCCGGCGC 540
Db      161  Cy61YvalLeuH1sArGAr611eYsAr6G1u6n11eLeuH1eArPLeu6Ar6nArG1y 180
Qy      541  GAATCAAACTCATGCACTTCGGGTCGGGGCGCTGCTCAAGACACAGTCTACACGAGC 600
Db      181  GluLeuYsLeuH1eArPheG1ySerG1yAlaLeuLeuYsArPThrValTyThrAsp 200
Qy      601  TTGATGGGACCGGAGGTACAGTCTCCAGAGTGGATTGGCTACCTACCTCCAGAGGC 660
Db      201  PheAr61YThrArGValTyTrSerPro61uTrp11eArG1yGlnValPhePheArG1nArGValSer 220
Qy      661  AGGTGGCACTGTCTGTGCTCCCTTGGATCCGTGCTATGACATGCTGTGCGAGATATT 720
Db      221  ArgSer1Ala1AlaValTrpSerLeuG1y1LeuLeuYrHArPMeValCy61yAr61le 240
Qy      721  CCGTTGAGACACGATGAAGATCATCAAGGCGCAAGTGTCTTCAAGCAAACTGTCTT 780
Db      241  ProPheG1uH1sAr61uG1u11e1eArG1yGlnValPhePheArG1nArGValSer 260
Qy      781  TCAGAGTGCAGACCTTATTAATGGTGCCTGTCCCTGAGACCGTCAAGATCCGGCTCC 840
Db      261  SerG1uYserGlnH1sLeuH1eArG1yTrpCy61u6AlaLeuArGProSerAr6ArGProThr 280
Qy      841  TTGAAGAATCCGGAACCATCCGTGATGCAAGGATGACCTCTGCCCCAGGACGTTCT 900
Db      281  PheG1uG1u11eGlnAr6nH1sProTrpMetG1nAr6ValLeuLeuProG1nG1uThrAla 300
Qy      901  GAGATCCATCTGCACAGTCTGTCAACGGGATCCAGCAAG 939
Db      301  Glu11eH1sLeuH1sSerLeuSerProG1yProSer1y6 313

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RESULT 13

```

US-10-348-081-13
/ Sequence 13, Application US/10348081
/ Publication No. US20040038246A1
/ GENERAL INFORMATION:
/ APPLICANT: KORN, Marcue
/ APPLICANT: MUELLER, Guenter
/ APPLICANT: SCHNEIDER, Rudolf
/ TITLE OF INVENTION: P1M-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
/ FILE REFERENCE: DE4V2002/0004 US NP
/ CURRENT APPLICATION NUMBER: US/10/348,081
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 13
/ LENGTH: 313
/ TYPE: PR
/ ORGANISM: Homo sapiens
US-10-348-081-13

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Alignment Scores:

Prod. No.:	8.3e-111	Length:	313
Score:	1582.00	Matches:	294
Percent Similarity:	97.12%	Conservative:	10
Best Local Similarity:	93.93%	Mismatches:	9
Query Match:	90.45%	Indels:	0
DB:	15	Gaps:	0

US-10-705-757-5 (1-942) x US-10-348-081-13 (1-313)

```

QY 1 ATGCTCTGTCCAGATCAATCCCTGGCCACCTGGCCGCCGCCCTTGCAACGACTG 60
Db 1 MetLeuLeuSerLyrlaenSerLeuAlaHleuHrgAlaAlaProCybanaAerLeu 20
QY 61 CAGGCCCAAGCTGGGGCCGGGCAAGAGAGAGCCCTGGAGTGGCAAGTACAGGTG 120
Db 21 HleAlaThrLyseuAlaProGlyLybGluLybGluProLeuGluSerGlnYrGlnVal 40
QY 121 GGCCTGCTTTGGGAGCGGTGGCTTGGCTCGGTACTCTGGCATCCGCTGGCCAG 180
Db 41 G1yProLeuLeuGlySerGlybGlybPheGlySerValYrSerGlylLeaGValSerb 60
QY 181 AACTTGGCGGTGGCCATTAAGACGTGAGAGAGACCGGATTTCCGATTGGGAGAACTG 240
Db 61 AenLeuProValAlaIleYbHleValGluLybAerPrglLeSerAerPrglYgluLeu 80
QY 241 CCCAATGGGACCCGAGTGGCCATTAAGAGTGTCTTGAAGAGGTGAGTCCGACTTC 300
Db 81 ProAenGlyThrArgValProMetGluValValLeuLeuLybValSerSerGlyPhe 100
QY 301 TCGGGCGTCAATAGACTTCTGAGCTGGTTCGAGAGCCGAGTATGTTTGGTGTGATCTG 360
Db 101 SerGlyValIleHrgLeuLeuAerPrglYbGluPrglYbAerPrglYbAerPrglYbAer 120
QY 361 GAGAGGCCGAGACCGGTGCAAGACTTCTGACTTTATCAACGAGAGGCTTACAG 420
Db 121 GluArgProGluProValGlnAerLeuPheAerPheIleHrgGluArgGlyAlaLeuGln 140
QY 421 GAGAGCTGGCCCGGAGATTTCTTGGCAGTGTCTGAGAGCCGCTGGGCTTCCCAAC 480
Db 141 GluGluLeuAlaArgSerPhePhePrglValValLeuAlaValAlaArgHleCybHleAen 160
QY 481 TGGGGGTTCTCCACCGCAGATCAAGAGAGAGAACTTTAATCGACTGACCGGCG 540
Db 161 CybGlyValLeuHleHrgAerPrglYbGlybAerPrglYbAerPrglYbAerPrglYbAer 180
QY 541 GAAATCAACTCATCGACTTCGAGTCCGAGGCGCTGCTCAAGAGACAGTCTACAGGAC 600
Db 181 GluLeuLybLeuIleAerPheGlySerGlyAlaLeuLeuLybAerPrglYrHleAer 200
QY 601 TTTGATGGGACCCGAGTGTACAGCTTCGAGAGTGTGATTCCTGCTCCGCTCAACGCG 660
Db 201 PheAerPrglYrHleArgValYrSerProGluPrglYrHleArgYrHleArgYrHleArgYr 220
QY 661 AGGTGGCAGCTGTGCTGCTTGGAGTCTGCTGATGACATGCTGCTGAGAGATAT 720
Db 221 ArgSerHleAlaValIlePrglYbGlylLeuLeuLybAerPrglYbAerPrglYbAerPrglYb 240
QY 721 CCGTTGAGACAGATGAAGATCATCAAGGCGCAAGTGTCTTCAAGCAACTGTCTCT 780
Db 241 ProPheGluHleAerPrglYrHleArgGlylLeuValPhePheAerGlnArgValSer 260
QY 781 TCAAGATGAGACCTTAATTAATGGCTGCTGCTGCTGAGACCGTCAAGTCCGCTCC 840
Db 261 SerGluLybGlnHleAerPrglYrHleArgYrHleArgYrHleArgYrHleArgYrHleArgYr 280
QY 841 TTTGAAGAAATCCGGAACATCCGCTGATGACAGGAGTCACTCTGCTCCGAGGAGCTTCT 900
Db 281 PheGluGluIleGlnAenHleProTrrMetGlnAerValLeuLeuProGlnGluIleHleAla 300
QY 901 GAGATCCATGTGACAGTGTGTCAACCGGAGTCCAGCAAG 939

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Db 301 GluIleHleuHleSerLeuSerProGlyProSerLyse 313

RESULT 14

US-10-664-421-1

Sequence 1, Application US/10664421

Publication No. US20040142864A1

GENERAL INFORMATION:

APPLICANT: BREMER, RYAN

APPLICANT: IBRAHIM, PRABHA

APPLICANT: KUMAR, ABHINAV

APPLICANT: MANDIRAN, VALSAN

APPLICANT: MILBURN, MICHAEL V.

TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE

FILE REFERENCE: 039363/0703

CURRENT APPLICATION NUMBER: US/10/664,421

CURRENT FILING DATE: 2003-09-16

PRIOR APPLICATION NUMBER: 60/412,341

PRIOR FILING DATE: 2002-09-20

PRIOR APPLICATION NUMBER: 60/411,398

PRIOR FILING DATE: 2002-09-16

NUMBER OF SEQ ID NOS: 169

SOFTWARE: PatentIn Ver. 3.2

SEQ ID NO 1

LENGTH: 313

TYPE: PRT

ORGANISM: Homo sapiens

US-10-664-421-1

Alignment Scores:

Prod. No.:	8.3e-111	Length:	313
Score:	1582.00	Matches:	294
Percent Similarity:	97.12%	Conservative:	10
Best Local Similarity:	93.93%	Mismatches:	9
Query Match:	90.45%	Indels:	0
DB:	16	Gaps:	0

US-10-705-757-5 (1-942) x US-10-664-421-1 (1-313)

```

QY 1 ATGCTCTGTCCAGATCAATCCCTGGCCACCTGGCCGCCGCCCTTGCAACGACTG 60
Db 1 MetLeuLeuSerLyrlaenSerLeuAlaHleuHrgAlaAlaProCybanaAerLeu 20
QY 61 CAGGCCCAAGCTGGGGCCGGGCAAGAGAGAGCCCTGGAGTGGCAAGTACAGGTG 120
Db 21 HleAlaThrLyseuAlaProGlyLybGluLybGluProLeuGluSerGlnYrGlnVal 40
QY 121 GGCCTGCTTTGGGAGCGGTGGCTTGGCTCGGTACTCTGGCATCCGCTGGCCAG 180
Db 41 G1yProLeuLeuGlySerGlybGlybPheGlySerValYrSerGlylLeaGValSerb 60
QY 181 AACTTGGCGGTGGCCATTAAGACGTGAGAGACCGGATTTCCGATTGGGAGAACTG 240
Db 61 AenLeuProValAlaIleYbHleValGluLybAerPrglLeSerAerPrglYgluLeu 80
QY 241 CCCAATGGGACCCGAGTGGCCATTAAGAGTGTCTTGAAGAGGTGAGTCCGACTTC 300
Db 81 ProAenGlyThrArgValProMetGluValValLeuLeuLybValSerSerGlyPhe 100
QY 301 TCGGGCGTCAATAGACTTCTGAGCTGGTTCGAGAGCCGAGTATGTTTGGTGTGATCTG 360
Db 101 SerGlyValIleHrgLeuLeuAerPrglYbGluPrglYbAerPrglYbAerPrglYbAer 120
QY 361 GAGAGGCCGAGACCGGTGCAAGACTTCTGACTTTATCAACGAGAGGCTTACAG 420
Db 121 GluArgProGluProValGlnAerLeuPheAerPheIleHrgGluArgGlyAlaLeuGln 140
QY 421 GAGAGCTGGCCCGGAGATTTCTTGGCAGTGTCTGAGAGCCGCTGGGCTTCCCAAC 480
Db 141 GluGluLeuAlaArgSerPhePrglYbGlylLeuValPhePheAerGlnArgValSer 160
QY 481 TGGGGGTTCTCCACCGCAGATCAAGAGAGAGAACTTTAATCGACTGACCGGCG 540
Db 161 CybGlyValLeuHleHrgAerPrglYbGlybAerPrglYbAerPrglYbAerPrglYbAer 180

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